

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 11, 2005, 21:05:14 ; Search time 117.489 Seconds
(without alignments)
72.421 Million cell updates/sec

Title: US-10-712-812-5

Perfect score: 112
Sequence: 1 MADNGTIVEELKQLLEQWNLV 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database : A_Geneseq_16Dec04:*
1: geneeqp19808:*
2: geneeqp19908:*
3: geneeqp20005:*
4: geneeqp20018:*
5: geneeqp20028:*
6: geneeqp20038:*
7: geneeqp20038:*
8: geneeqp20048:*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 112 | 100.0 | 221 | 8 | AD195325 OSPF-rela |
| 2 | 52 | 46.4 | 16368 | 6 | Abm67171 Phototrab |
| 3 | 51 | 45.5 | 54 | 4 | AAm19303 Peptide # |
| 4 | 51 | 45.5 | 54 | 4 | ABM38595 Peptide # |
| 5 | 51 | 45.5 | 54 | 4 | AAm32049 Peptide # |
| 6 | 51 | 45.5 | 54 | 4 | ABM33710 Peptide # |
| 7 | 51 | 45.5 | 54 | 4 | AAm1757 Protein # |
| 8 | 51 | 45.5 | 54 | 4 | AAm59222 Human bra |
| 9 | 51 | 45.5 | 54 | 4 | ABM33442 Human liv |
| 10 | 51 | 45.5 | 54 | 4 | ABM41571 Human pep |
| 11 | 51 | 45.5 | 206 | 6 | ABU03494 Angiogene |
| 12 | 51 | 45.5 | 206 | 6 | ABU62881 Ras-Fam11 |
| 13 | 51 | 45.5 | 206 | 6 | ADG10624 Human STR |
| 14 | 51 | 45.5 | 206 | 7 | ADJ70216 Human hea |
| 15 | 51 | 45.5 | 206 | 8 | ADQ20631 Human sof |
| 16 | 51 | 45.5 | 206 | 8 | ADQ34469 FOSH prot |
| 17 | 51 | 45.5 | 209 | 7 | ADP14139 Human srt |
| 18 | 51 | 45.5 | 209 | 8 | ADP24705 PRO polyP |
| 19 | 51 | 45.5 | 209 | 8 | ADG34490 FOSH prot |
| 20 | 51 | 45.5 | 246 | 4 | AAU31548 Novel hum |
| 21 | 51 | 45.5 | 351 | 6 | ABU23569 Protein e |
| 22 | 51 | 45.5 | 572 | 2 | AAW68488 Mouse Utl |
| 23 | 50 | 44.6 | 469 | 7 | ABU48797 Actinomye |
| 24 | 50 | 44.6 | 673 | 6 | ABU48797 Protein e |
| 25 | 49 | 43.8 | 123 | 3 | AAW32530 S. lavend |

| | | | | | | |
|----|------|------|------|---|----------|---------------------|
| 26 | 49 | 43.8 | 123 | 7 | ADL10302 | Adel10302 S. lavend |
| 27 | 48.5 | 42.3 | 842 | 3 | AAW69350 | AAW69350 HIV-1 non |
| 28 | 48 | 42.9 | 300 | 7 | ADP07641 | ADP07641 Bacterial |
| 29 | 48 | 42.9 | 401 | 8 | ADG21407 | ADG21407 Bacterial |
| 30 | 48 | 42.9 | 4437 | 6 | ABU11384 | ABU11384 Protein e |
| 31 | 47 | 42.0 | 159 | 8 | ADJ18885 | ADJ18885 Glucoseam |
| 32 | 47 | 42.0 | 508 | 8 | ADJ64176 | ADJ64176 S. cerevi |
| 33 | 47 | 42.0 | 158 | 8 | ADN10681 | ADN10681 Nicotiana |
| 34 | 47 | 42.0 | 508 | 8 | ADN10653 | ADN10653 Nicotiana |
| 35 | 47 | 42.0 | 509 | 8 | ADN10655 | ADN10655 Nicotiana |
| 36 | 47 | 42.0 | 659 | 8 | ADN19947 | ADN19947 Bacterial |
| 37 | 46.5 | 41.5 | 428 | 6 | ABU49306 | ABU49306 Protein e |
| 38 | 46.5 | 41.5 | 849 | 3 | AAW69645 | AAW69645 HIV synth |
| 39 | 46 | 41.1 | 100 | 3 | AAW02044 | AAW02044 Human sec |
| 40 | 46 | 41.1 | 114 | 4 | ABW70970 | ABW70970 Drosophi |
| 41 | 46 | 41.1 | 189 | 5 | ABG59978 | ABG59978 Human DIT |
| 42 | 46 | 41.1 | 216 | 4 | AAW82765 | AAW82765 S. epider |
| 43 | 46 | 41.1 | 216 | 6 | ABU19037 | ABU19037 Pathogen |
| 44 | 46 | 41.1 | 253 | 8 | ADQ37007 | ADQ37007 Rice pro |
| 45 | 46 | 41.1 | 253 | 8 | ADQ15677 | ADQ15677 Rice stre |
| 46 | 46 | 41.1 | 274 | 5 | ABP40434 | ABP40434 Staphyloc |
| 47 | 46 | 41.1 | 274 | 8 | ADG05966 | ADG05966 Staphyloc |
| 48 | 46 | 41.1 | 300 | 6 | ADN12194 | ADN12194 Actinoba |
| 49 | 46 | 41.1 | 300 | 7 | AAW39415 | AAW39415 Actinoba |
| 50 | 46 | 41.1 | 385 | 3 | AAW34981 | AAW34981 Arabidops |
| 51 | 46 | 41.1 | 398 | 3 | AAW23096 | AAW23096 Arabidops |
| 52 | 46 | 41.1 | 420 | 3 | AAW34980 | AAW34980 Arabidops |
| 53 | 46 | 41.1 | 433 | 3 | AAW23095 | AAW23095 Arabidops |
| 54 | 46 | 41.1 | 469 | 4 | ABG09202 | ABG09202 Novel hum |
| 55 | 46 | 41.1 | 469 | 4 | ABG21331 | ABG21331 Novel hum |
| 56 | 46 | 41.1 | 512 | 6 | AAW38226 | AAW38226 Human enz |
| 57 | 46 | 41.1 | 516 | 4 | AAW35470 | AAW35470 Human cyc |
| 58 | 46 | 41.1 | 532 | 7 | ABO63494 | ABO63494 Klebsiell |
| 59 | 46 | 41.1 | 534 | 8 | ABW83406 | ABW83406 Human dia |
| 60 | 46 | 41.1 | 536 | 2 | AAW95110 | AAW95110 Human RPM |
| 61 | 46 | 41.1 | 536 | 7 | ADG58253 | ADG58253 Human pro |
| 62 | 46 | 41.1 | 536 | 8 | ADG40394 | ADG40394 Human pho |
| 63 | 46 | 41.1 | 536 | 8 | ADG75985 | ADG75985 Human pho |
| 64 | 46 | 41.1 | 537 | 7 | ADP04444 | ADP04444 Bacterial |
| 65 | 46 | 41.1 | 545 | 6 | ABU26622 | ABU26622 Protein e |
| 66 | 46 | 41.1 | 553 | 2 | AAW68489 | AAW68489 Human par |
| 67 | 46 | 41.1 | 554 | 8 | ABW83407 | ABW83407 Human dia |
| 68 | 46 | 41.1 | 572 | 5 | ABW32231 | ABW32231 Human Utl |
| 69 | 46 | 41.1 | 572 | 6 | ABP97910 | ABP97910 Amino aci |
| 70 | 46 | 41.1 | 572 | 7 | ADP65307 | ADP65307 Human dth |
| 71 | 46 | 41.1 | 572 | 8 | ADQ18668 | ADQ18668 Human sof |
| 72 | 46 | 41.1 | 792 | 6 | ABW55389 | ABW55389 Human col |
| 73 | 46 | 41.1 | 1052 | 3 | AAW06335 | AAW06335 Rat sublt |
| 74 | 46 | 41.1 | 422 | 6 | ABU50276 | ABU50276 Protein e |
| 75 | 45.5 | 40.2 | 119 | 8 | ADU04570 | ADU04570 M. catarr |
| 76 | 45 | 40.2 | 329 | 8 | ABO58567 | ABO58567 Human gen |
| 77 | 45 | 40.2 | 377 | 3 | AAW20649 | AAW20649 Arabidops |
| 78 | 45 | 40.2 | 377 | 3 | AAW45918 | AAW45918 Arabidops |
| 79 | 45 | 40.2 | 399 | 3 | AAW20648 | AAW20648 Arabidops |
| 80 | 45 | 40.2 | 399 | 3 | AAW45917 | AAW45917 Arabidops |
| 81 | 45 | 40.2 | 404 | 3 | AAW20647 | AAW20647 Arabidops |
| 82 | 45 | 40.2 | 404 | 3 | AAW45916 | AAW45916 Arabidops |
| 83 | 45 | 40.2 | 462 | 3 | ABU25173 | ABU25173 Protein e |
| 84 | 45 | 40.2 | 497 | 7 | ADG64193 | ADG64193 Human pro |
| 85 | 45 | 40.2 | 508 | 8 | ADN10589 | ADN10589 Nicotiana |
| 86 | 45 | 40.2 | 534 | 2 | AAW28404 | AAW28404 63 kd Cam |
| 87 | 45 | 40.2 | 534 | 2 | AAW69720 | AAW69720 Cyclic-GM |
| 88 | 45 | 40.2 | 534 | 2 | AAW11251 | AAW11251 63 kd cal |
| 89 | 45 | 40.2 | 534 | 2 | AAW18038 | AAW18038 Bovine br |
| 90 | 45 | 40.2 | 534 | 2 | AAW71223 | AAW71223 63 kDa Ca |
| 91 | 45 | 40.2 | 534 | 2 | AAW77039 | AAW77039 Bovine br |
| 92 | 45 | 40.2 | 534 | 2 | AAW60751 | AAW60751 63 kDa bo |
| 93 | 45 | 40.2 | 534 | 3 | AAW80977 | AAW80977 Bovine br |
| 94 | 45 | 40.2 | 534 | 8 | ABU58716 | ABU58716 Bovine br |
| 95 | 45 | 40.2 | 534 | 8 | ADG94947 | ADG94947 Rat Prote |
| 96 | 45 | 40.2 | 535 | 7 | ADG58251 | ADG58251 Rat Prote |
| 97 | 45 | 40.2 | 548 | 4 | ABW62383 | ABW62383 Drosophi |
| 98 | 45 | 40.2 | 626 | 5 | ABW49107 | ABW49107 Listeria |

| | | | | | | | | | | | | | |
|-----|------|------|------|---|-----------|---------------------|-----|------|------|------|---|-----------|---------------------|
| 99 | 45 | 40.2 | 626 | 6 | ABU32651 | Abu32651 Protein e | 172 | 44 | 39.3 | 952 | 7 | ABO68769 | AbO68769 Pseudomon |
| 100 | 45 | 40.2 | 643 | 4 | AAU35641 | AAU35641 Haemophil | 173 | 44 | 39.3 | 1577 | 2 | AAAR91047 | AAAR91047 Alpha-D-g |
| 101 | 45 | 40.2 | 633 | 6 | ABU30579 | Abu30579 Protein e | 174 | 43.5 | 38.8 | 189 | 8 | ADG45845 | ADG45845 Staphyloc |
| 102 | 45 | 40.2 | 666 | 5 | ABB90255 | Abb90255 Human pol | 175 | 43.5 | 38.8 | 384 | 3 | AAAG10103 | AAAG10103 Arabidops |
| 103 | 45 | 40.2 | 808 | 7 | ADBE4170 | Adbe4170 Human pro | 176 | 43.5 | 38.8 | 426 | 3 | AAAG10102 | AAAG10102 Arabidops |
| 104 | 45 | 40.2 | 867 | 7 | ADER1288 | Der1288 Novel hum | 177 | 43.5 | 38.8 | 429 | 6 | ABU47911 | Abu47911 Protein e |
| 105 | 45 | 40.2 | 1052 | 3 | AAAB06336 | Abab06336 Mouse sub | 178 | 43.5 | 38.8 | 434 | 7 | ADG94448 | AdG94448 E. faeciu |
| 106 | 45 | 40.2 | 1052 | 3 | AAAB06334 | Abab06334 Human sub | 179 | 43.5 | 38.8 | 477 | 4 | AAU38398 | AAU38398 Salmonell |
| 107 | 45 | 40.2 | 1052 | 3 | AAAY54619 | AAy54619 Human sub | 180 | 43.5 | 38.8 | 523 | 3 | AAAG10101 | AAAG10101 Arabidops |
| 108 | 45 | 40.2 | 1052 | 3 | AAAY69892 | AAy69892 Human sub | 181 | 43.5 | 38.8 | 523 | 8 | ADN73153 | Adn73153 Thale cre |
| 109 | 45 | 40.2 | 1052 | 3 | AAAY84227 | AAy84227 Amino aci | 182 | 43.5 | 38.8 | 540 | 7 | ADFO5702 | Adfo5702 Bacterial |
| 110 | 45 | 40.2 | 1052 | 3 | AAAY84228 | AAy84228 Amino aci | 183 | 43.5 | 38.8 | 619 | 8 | ADSO30170 | Adso30170 Bacterial |
| 111 | 45 | 40.2 | 1052 | 3 | AAU38520 | AAu38520 Human sub | 184 | 43 | 38.4 | 42 | 8 | ABO58010 | ABO58010 Human gen |
| 112 | 45 | 40.2 | 1052 | 5 | AAAE14527 | AAe14527 Human slt | 185 | 43 | 38.4 | 126 | 4 | ABBE62908 | ABBE62908 Drosophil |
| 113 | 45 | 40.2 | 1052 | 5 | AAAE14528 | AAe14528 Hamster s | 186 | 43 | 38.4 | 162 | 7 | ADFO6342 | Adfo6342 Bacterial |
| 114 | 45 | 40.2 | 1052 | 5 | ABG91096 | Abg91096 Human sub | 187 | 43 | 38.4 | 172 | 6 | ABU40649 | Abu40649 Protein e |
| 115 | 45 | 40.2 | 1537 | 4 | AAAB83971 | Abab83971 Amino aci | 188 | 43 | 38.4 | 172 | 8 | ADSA4275 | Adsa4275 Bacterial |
| 116 | 45 | 40.2 | 1677 | 4 | ABG10016 | Abg10016 Novel hum | 189 | 43 | 38.4 | 196 | 4 | ABBO3863 | ABBO3863 Human mus |
| 117 | 45 | 40.2 | 1696 | 7 | ADU69016 | Adj69016 Human hea | 190 | 43 | 38.4 | 196 | 6 | ABU13177 | Abu13177 Novel hum |
| 118 | 45 | 40.2 | 1720 | 4 | AAAM78886 | AAm78886 Human pro | 191 | 43 | 38.4 | 196 | 6 | ADJ29203 | Adj29203 Human mus |
| 119 | 45 | 40.2 | 1720 | 4 | ABO07115 | AbO07115 Novel hum | 192 | 43 | 38.4 | 256 | 3 | AAAY82452 | AAy82452 Spinnach c |
| 120 | 45 | 40.2 | 1721 | 4 | AAAM79870 | AAm79870 Human pro | 193 | 43 | 38.4 | 311 | 6 | ABP96401 | ABp96401 Prochloro |
| 121 | 44.5 | 39.7 | 403 | 4 | AAUS4649 | AAus4649 Propionib | 194 | 43 | 38.4 | 394 | 5 | ABG93276 | ABg93276 C. albica |
| 122 | 44.5 | 39.7 | 403 | 6 | ABMS1168 | Abms1168 Propionib | 195 | 43 | 38.4 | 407 | 7 | ADMO5407 | Admo5407 Human pro |
| 123 | 44.5 | 39.7 | 417 | 8 | ADSA42706 | Adsa42706 Bacterial | 196 | 43 | 38.4 | 429 | 6 | ABM15850 | ABm15850 Mycobacte |
| 124 | 44.5 | 39.7 | 429 | 6 | ABM67843 | Abm67843 Phototrab | 197 | 43 | 38.4 | 467 | 7 | ADG33780 | Adg33780 Actinomyc |
| 125 | 44.5 | 39.7 | 494 | 8 | ADOC26143 | ADoc26143 HIV gp120 | 198 | 43 | 38.4 | 469 | 8 | ADN20290 | Adn20290 Bacterial |
| 126 | 44.5 | 39.7 | 549 | 5 | AAAM52842 | AAms2842 Physcomit | 199 | 43 | 38.4 | 481 | 8 | ADNO1952 | Adno1952 Staphyloc |
| 127 | 44.5 | 39.7 | 619 | 5 | AAU75156 | AAu75156 N-termina | 200 | 43 | 38.4 | 481 | 8 | ADNO1939 | Adno1939 Staphyloc |
| 128 | 44.5 | 39.7 | 646 | 5 | AAU75155 | AAu75155 Modified | 201 | 43 | 38.4 | 481 | 8 | ADNO1953 | Adno1953 Staphyloc |
| 129 | 44.5 | 39.7 | 842 | 5 | ABBO6211 | Abbo6211 HIV Env 1 | 202 | 43 | 38.4 | 481 | 8 | ADNO1955 | Adno1955 Staphyloc |
| 130 | 44.5 | 39.7 | 842 | 6 | ABU66565 | Abu66565 Human imm | 203 | 43 | 38.4 | 481 | 8 | ADNO1946 | Adno1946 Staphyloc |
| 131 | 44.5 | 39.7 | 842 | 6 | ABRS5684 | ABrs5684 HIV IsoLa | 204 | 43 | 38.4 | 486 | 6 | ABMW1573 | ABmw1573 Staphyloc |
| 132 | 44.5 | 39.7 | 842 | 7 | ADCI3218 | ADci3218 Protein o | 205 | 43 | 38.4 | 490 | 2 | AAW89764 | AAw89764 Staphyloc |
| 133 | 44.5 | 39.7 | 842 | 3 | AAAM73868 | AAm73868 HIV-1 pol | 206 | 43 | 38.4 | 490 | 8 | ADNO1954 | Adno1954 Staphyloc |
| 134 | 44.5 | 39.7 | 847 | 8 | ADY97073 | Ady97073 Variant H | 207 | 43 | 38.4 | 510 | 8 | ADN17403 | Adn17403 Bacterial |
| 135 | 44.5 | 39.7 | 847 | 8 | ADDO5103 | Ado05103 Human imm | 208 | 43 | 38.4 | 521 | 7 | ADBO23592 | Adbo23592 Ricketsei |
| 136 | 44 | 39.3 | 114 | 2 | ADCC6973 | Adc6973 E. faeciu | 209 | 43 | 38.4 | 555 | 6 | ABU39997 | Abu39997 Protein e |
| 137 | 44 | 39.3 | 136 | 2 | AAV12478 | AAv12478 Human 5' | 210 | 43 | 38.4 | 587 | 6 | ABU29807 | ABu29807 Protein e |
| 138 | 44 | 39.3 | 138 | 4 | AAU31547 | AAu31547 Novel hum | 211 | 43 | 38.4 | 594 | 8 | ADN20584 | Adn20584 Bacterial |
| 139 | 44 | 39.3 | 143 | 2 | AAAY36077 | AAay36077 Extended | 212 | 43 | 38.4 | 597 | 7 | ADCG7426 | Adcg7426 E. faeciu |
| 140 | 44 | 39.3 | 143 | 8 | ADP19385 | Adp19385 Human sec | 213 | 43 | 38.4 | 759 | 6 | ABMT70917 | ABmt70917 Staphyloc |
| 141 | 44 | 39.3 | 157 | 8 | ADN17554 | Adn17554 Bacterial | 214 | 43 | 38.4 | 788 | 4 | ABBE1410 | ABbe1410 Drosophil |
| 142 | 44 | 39.3 | 176 | 3 | AAGS4430 | AAgs4430 Zea mays | 215 | 43 | 38.4 | 1188 | 8 | ADBO80423 | ADbo80423 Zebrafish |
| 143 | 44 | 39.3 | 206 | 5 | ABU04642 | Abj04642 Protein o | 216 | 43 | 38.4 | 1551 | 4 | AAAG5026 | AAg5026 Shrim wh |
| 144 | 44 | 39.3 | 215 | 3 | AAGS4429 | AAgs4429 Zea mays | 217 | 43 | 38.4 | 1673 | 5 | ABP69698 | ABp69698 Human pol |
| 145 | 44 | 39.3 | 273 | 8 | ADRO4184 | ADro4184 E. faeciu | 218 | 43 | 38.4 | 1690 | 5 | ABP69699 | ABp69699 Human pol |
| 146 | 44 | 39.3 | 277 | 6 | ABU29809 | ABu29809 Protein e | 219 | 43 | 38.4 | 1893 | 5 | AAU84593 | AAU84593 HIV Casse |
| 147 | 44 | 39.3 | 282 | 5 | ABP27289 | ABp27289 Streptoco | 220 | 43 | 38.4 | 1896 | 5 | AAU84590 | AAU84590 HIV Casse |
| 148 | 44 | 39.3 | 302 | 3 | ADSA4428 | ADsa4428 Zea mays | 221 | 43 | 38.4 | 3290 | 6 | ADSA4199 | ADsa4199 Actinecto |
| 149 | 44 | 39.3 | 308 | 8 | ADSA4636 | ADsa4636 Bacterial | 222 | 43 | 38.4 | 5245 | 7 | ADJ23931 | Adj23931 Streptomy |
| 150 | 44 | 39.3 | 378 | 3 | AAAG46567 | AAga6567 Arabidops | 223 | 43 | 38.4 | 5245 | 7 | ADJ23897 | Adj23897 Streptomy |
| 151 | 44 | 39.3 | 404 | 3 | AAAG46566 | AAga6566 Arabidops | 224 | 43 | 38.4 | 5746 | 5 | AAU84596 | AAu84596 HIV compl |
| 152 | 44 | 39.3 | 410 | 5 | ABP30521 | ABp30521 Streptoco | 225 | 42.5 | 37.9 | 226 | 5 | ABP40649 | ABp40649 Staphyloc |
| 153 | 44 | 39.3 | 426 | 6 | ABU11528 | Abu11528 Human WDD | 226 | 42.5 | 37.9 | 226 | 5 | ADSO7889 | ADso7889 Staphyloc |
| 154 | 44 | 39.3 | 429 | 5 | ABP26315 | ABp26315 Streptoco | 227 | 42.5 | 37.9 | 227 | 6 | ABMT2833 | ABmt2833 Staphyloc |
| 155 | 44 | 39.3 | 429 | 5 | ABP29714 | ABp29714 Streptoco | 228 | 42.5 | 37.9 | 424 | 8 | ADN17579 | Adn17579 Staphyloc |
| 156 | 44 | 39.3 | 463 | 3 | AAAG46565 | AAga6565 Arabidops | 229 | 42.5 | 37.9 | 429 | 1 | AAAP1958 | AAp1958 Peptide e |
| 157 | 44 | 39.3 | 473 | 7 | ADBS38435 | ADbs38435 Human pro | 230 | 42.5 | 37.9 | 429 | 2 | AAAS1887 | AAs1887 DAPA synt |
| 158 | 44 | 39.3 | 476 | 3 | ADBP41793 | ADbp41793 Human ova | 231 | 42.5 | 37.9 | 429 | 4 | AAU34505 | AAu34505 E. coli c |
| 159 | 44 | 39.3 | 480 | 6 | ADA48242 | Ada48242 Rice proc | 232 | 42.5 | 37.9 | 429 | 6 | ABU28561 | ABu28561 Protein e |
| 160 | 44 | 39.3 | 491 | 4 | AAU34175 | AAu34175 Staphyloc | 233 | 42.5 | 37.9 | 429 | 8 | ADFO4948 | Adfo4948 Bacterial |
| 161 | 44 | 39.3 | 504 | 4 | AAU37099 | AAu37099 Staphyloc | 234 | 42.5 | 37.9 | 429 | 7 | ADN18117 | Adn18117 Bacterial |
| 162 | 44 | 39.3 | 504 | 6 | ABMW2813 | ABmw2813 Staphyloc | 235 | 42.5 | 37.9 | 431 | 2 | AAU73903 | AAu73903 E. coli D |
| 163 | 44 | 39.3 | 511 | 6 | ABU16504 | Abu16504 Protein e | 236 | 42.5 | 37.9 | 435 | 6 | ABU131641 | ABu131641 Protein e |
| 164 | 44 | 39.3 | 545 | 8 | AAAB19080 | AAab19080 Amino aci | 237 | 42.5 | 37.9 | 447 | 7 | ABO66770 | ABo66770 Klebsiell |
| 165 | 44 | 39.3 | 553 | 8 | ADSB28434 | ADsb28434 Bacterial | 238 | 42.5 | 37.9 | 513 | 3 | ADSB6383 | ADsb6383 Rat Prote |
| 166 | 44 | 39.3 | 560 | 6 | ABME68550 | ABme68550 Phototrab | 239 | 42.5 | 37.9 | 546 | 4 | AAU23561 | AAu23561 Novel hum |
| 167 | 44 | 39.3 | 571 | 8 | ADN17366 | ADn17366 Bacterial | 240 | 42.5 | 37.9 | 546 | 4 | AAU87604 | AAu87604 Novel cen |
| 168 | 44 | 39.3 | 584 | 4 | ABG26094 | ABg26094 Novel hum | 241 | 42.5 | 37.9 | 546 | 8 | ADIS4919 | ADis4919 Novel hum |
| 169 | 44 | 39.3 | 586 | 4 | ABBS8288 | ABbs8288 Drosophil | 242 | 42.5 | 37.9 | 568 | 8 | AAU87314 | AAu87314 Novel cen |
| 170 | 44 | 39.3 | 658 | 4 | ABBS9450 | ABbs9450 Drosophil | 243 | 42.5 | 37.9 | 568 | 8 | ADIS4629 | ADis4629 Novel hum |
| 171 | 44 | 39.3 | 765 | 7 | ADFT4168 | Adft4168 Human nov | 244 | 42.5 | 37.9 | 586 | 2 | AAK49855 | AAk49855 Sequence |

| | | | | | | | | | | | | | | | |
|-----|------|------|------|---|----------|----------|-----------|-----|------|------|-----|---|-----------|-----------|-----------|
| 245 | 42.5 | 37.9 | 624 | 4 | AU22925 | Au22925 | Novel hum | 318 | 41.5 | 37.1 | 472 | 7 | ADG33808 | Adg33808 | Actinomy |
| 246 | 42.5 | 37.9 | 846 | 3 | AAB69345 | Aab69345 | HIV-1 non | 319 | 41.5 | 37.1 | 489 | 3 | AAC53393 | Aac53393 | Arabidops |
| 247 | 42.5 | 37.9 | 883 | 4 | AAB82761 | Aab82761 | Ancestral | 320 | 41.5 | 37.1 | 489 | 5 | AAB891098 | Aab891098 | Herbicida |
| 248 | 42.5 | 37.9 | 1300 | 7 | ADBE3060 | Adbe3060 | Rat Prote | 321 | 41.5 | 37.1 | 489 | 8 | ADN73091 | Adn73091 | Thale cre |
| 249 | 42 | 37.5 | 70 | 3 | AAG12432 | Aag12432 | Zea may | 322 | 41.5 | 37.1 | 559 | 5 | AAB893132 | Aab893132 | Herbicida |
| 250 | 42 | 37.5 | 78 | 8 | AD841591 | Ad841591 | Bacterial | 323 | 41.5 | 37.1 | 561 | 5 | ABP73469 | Abp73469 | Candida a |
| 251 | 42 | 37.5 | 82 | 7 | ADCO0634 | Adco0634 | Actinobac | 324 | 41.5 | 37.1 | 639 | 5 | ABP53637 | Abp53637 | Maize cal |
| 252 | 42 | 37.5 | 115 | 6 | AD342222 | Ad342222 | Actinobac | 325 | 41.5 | 37.1 | 647 | 8 | ADN72231 | Adn72231 | Thale cre |
| 253 | 42 | 37.5 | 117 | 3 | AAG12617 | Aag12617 | Zea may | 326 | 41.5 | 37.1 | 846 | 2 | AAR08406 | Aar08406 | Sequence |
| 254 | 42 | 37.5 | 120 | 8 | AD05051 | Ad05051 | Novel hum | 327 | 41.5 | 37.1 | 854 | 8 | AD195311 | Ad195311 | Human imm |
| 255 | 42 | 37.5 | 127 | 3 | AAG12616 | Aag12616 | Zea may | 328 | 41 | 36.6 | 52 | 6 | ABP76206 | Abp76206 | Human GEN |
| 256 | 42 | 37.5 | 129 | 7 | ADH86956 | Adh86956 | Enterococ | 329 | 41 | 36.6 | 52 | 6 | ABP76053 | Abp76053 | Human GEN |
| 257 | 42 | 37.5 | 156 | 3 | AAG12615 | Aag12615 | Zea may | 330 | 41 | 36.6 | 71 | 2 | AAM09412 | Aam09412 | Human G p |
| 258 | 42 | 37.5 | 178 | 6 | ABM71384 | Abm71384 | Staphyloc | 331 | 41 | 36.6 | 71 | 4 | AAB03966 | Aab03966 | Human gen |
| 259 | 42 | 37.5 | 208 | 7 | ABO60894 | Ab060894 | Klebsiell | 332 | 41 | 36.6 | 71 | 4 | AAM39864 | Aam39864 | Human pol |
| 260 | 42 | 37.5 | 225 | 6 | ABU50105 | Abu50105 | Protein e | 333 | 41 | 36.6 | 71 | 5 | ABG73049 | Abg73049 | Human gam |
| 261 | 42 | 37.5 | 244 | 8 | ADN20298 | Adn20298 | Bacterial | 334 | 41 | 36.6 | 71 | 8 | ADM67205 | Adm67205 | Murine ad |
| 262 | 42 | 37.5 | 268 | 6 | ADA36831 | Ada36831 | Actinobac | 335 | 41 | 36.6 | 82 | 4 | AAM41650 | Aam41650 | Human pol |
| 263 | 42 | 37.5 | 306 | 6 | ABM69568 | Abm69568 | Photococ | 336 | 41 | 36.6 | 83 | 3 | AAG01243 | Aag01243 | Human sec |
| 264 | 42 | 37.5 | 307 | 2 | AAM93255 | Aam93255 | Tobacco C | 337 | 41 | 36.6 | 83 | 7 | ADP59249 | Adp59249 | Human pol |
| 265 | 42 | 37.5 | 311 | 7 | ADP59532 | Adp59532 | Human pol | 338 | 41 | 36.6 | 86 | 2 | AAV12896 | Aav12896 | Human 5' |
| 266 | 42 | 37.5 | 324 | 6 | ABU29166 | Abu29166 | Protein e | 339 | 41 | 36.6 | 99 | 5 | ABP30099 | Abp30099 | Streptoco |
| 267 | 42 | 37.5 | 324 | 6 | ADM25910 | Adm25910 | Hyperther | 340 | 41 | 36.6 | 106 | 7 | ADF07525 | Adf07525 | Bacterial |
| 268 | 42 | 37.5 | 328 | 7 | ADH86358 | Adh86358 | Enterococ | 341 | 41 | 36.6 | 140 | 2 | AAV40111 | Aav40111 | Amno aci |
| 269 | 42 | 37.5 | 341 | 8 | ADN47212 | Adn47212 | Thermococ | 342 | 41 | 36.6 | 140 | 6 | ABU49843 | Abu49843 | Protein e |
| 270 | 42 | 37.5 | 351 | 5 | ABP73534 | Abp73534 | Candida a | 343 | 41 | 36.6 | 144 | 3 | AAG07958 | Aag07958 | Arabidops |
| 271 | 42 | 37.5 | 372 | 4 | AAG81063 | Ag81063 | HIV prote | 344 | 41 | 36.6 | 144 | 3 | AAG43189 | Aag43189 | Arabidops |
| 272 | 42 | 37.5 | 423 | 8 | ADN24093 | Adn24093 | Bacterial | 345 | 41 | 36.6 | 149 | 8 | ADN19493 | Adn19493 | Bacterial |
| 273 | 42 | 37.5 | 450 | 6 | ABU41584 | Abu41584 | Protein e | 346 | 41 | 36.6 | 158 | 8 | ADU48507 | Adu48507 | Oll-aseoc |
| 274 | 42 | 37.5 | 451 | 6 | ABU39727 | Abu39727 | Protein e | 347 | 41 | 36.6 | 160 | 7 | ADM04633 | Adm04633 | Human pro |
| 275 | 42 | 37.5 | 459 | 3 | AAG29591 | Ag29591 | Arabidops | 348 | 41 | 36.6 | 160 | 8 | ADQ67105 | Adq67105 | Novel hum |
| 276 | 42 | 37.5 | 460 | 7 | ADG33874 | Adg33874 | Actinomy | 349 | 41 | 36.6 | 161 | 8 | ADS43976 | Ads43976 | Bacterial |
| 277 | 42 | 37.5 | 464 | 4 | ADN24352 | Adn24352 | Bacterial | 350 | 41 | 36.6 | 162 | 4 | AAM41792 | Aam41792 | Human pol |
| 278 | 42 | 37.5 | 467 | 3 | AAV99855 | Aay99855 | Becherich | 351 | 41 | 36.6 | 162 | 4 | AAM41793 | Aam41793 | Human pol |
| 279 | 42 | 37.5 | 467 | 3 | AAV99854 | Aay99854 | Becherich | 352 | 41 | 36.6 | 164 | 2 | AAM04866 | Aam04866 | Chicken g |
| 280 | 42 | 37.5 | 467 | 3 | AAV99853 | Aay99853 | Becherich | 353 | 41 | 36.6 | 164 | 7 | ADG31901 | Adg31901 | Chicken f |
| 281 | 42 | 37.5 | 468 | 3 | AAV99857 | Aay99857 | Becherich | 354 | 41 | 36.6 | 166 | 8 | ADM67228 | Adm67228 | Human adi |
| 282 | 42 | 37.5 | 468 | 3 | AAV99856 | Aay99856 | Becherich | 355 | 41 | 36.6 | 169 | 3 | AAG43188 | Aag43188 | Arabidops |
| 283 | 42 | 37.5 | 468 | 3 | AAV99858 | Aay99858 | Becherich | 356 | 41 | 36.6 | 169 | 3 | AAG07957 | Aag07957 | Arabidops |
| 284 | 42 | 37.5 | 474 | 4 | AU46847 | Au46847 | Propionib | 357 | 41 | 36.6 | 186 | 6 | ABM72361 | Abm72361 | Staphyloc |
| 285 | 42 | 37.5 | 474 | 6 | ABM43366 | Abm43366 | Propionib | 358 | 41 | 36.6 | 188 | 7 | ADF43564 | Adf43564 | Nocardiop |
| 286 | 42 | 37.5 | 490 | 8 | ADS27426 | Ad27426 | Bacterial | 359 | 41 | 36.6 | 188 | 8 | ADM01090 | Adm01090 | Nocardiop |
| 287 | 42 | 37.5 | 509 | 5 | AB849686 | Ab849686 | Listeria | 360 | 41 | 36.6 | 188 | 7 | ADR21480 | Adr21480 | Partial s |
| 288 | 42 | 37.5 | 529 | 3 | AAG29590 | Ag29590 | Arabidops | 361 | 41 | 36.6 | 194 | 7 | ABO66351 | Ab066351 | Klebsiell |
| 289 | 42 | 37.5 | 540 | 3 | AAV75735 | Aay75735 | Neisseria | 362 | 41 | 36.6 | 208 | 5 | ABP39604 | Abp39604 | Staphyloc |
| 290 | 42 | 37.5 | 542 | 4 | AAG29589 | Ag29589 | Arabidops | 363 | 41 | 36.6 | 208 | 8 | ADS05621 | Ad05621 | Staphyloc |
| 291 | 42 | 37.5 | 564 | 4 | AB866319 | Ab866319 | Drosophil | 364 | 41 | 36.6 | 210 | 5 | ABUS1679 | Abus1679 | Helicobac |
| 292 | 42 | 37.5 | 564 | 8 | ADQ89714 | Adq89714 | Antagonis | 365 | 41 | 36.6 | 215 | 3 | AAG43187 | Aag43187 | Arabidops |
| 293 | 42 | 37.5 | 574 | 8 | ADK70709 | Adk70709 | Collapsin | 366 | 41 | 36.6 | 215 | 3 | AAG07956 | Aag07956 | Arabidops |
| 294 | 42 | 37.5 | 608 | 6 | ABU43518 | Abu43518 | Protein e | 367 | 41 | 36.6 | 215 | 7 | ADM25823 | Adm25823 | Hyperther |
| 295 | 42 | 37.5 | 608 | 6 | ABU39109 | Abu39109 | Protein e | 368 | 41 | 36.6 | 215 | 8 | ADN73189 | Adn73189 | Thale cre |
| 296 | 42 | 37.5 | 650 | 8 | ADK70696 | Adk70696 | Chicken C | 369 | 41 | 36.6 | 264 | 8 | ADN47006 | Adn47006 | Thermococ |
| 297 | 42 | 37.5 | 659 | 5 | AB893561 | Ab893561 | Herbicida | 370 | 41 | 36.6 | 265 | 6 | ABM69559 | Abm69559 | Photococ |
| 298 | 42 | 37.5 | 684 | 6 | ABU19991 | Abu19991 | Protein e | 371 | 41 | 36.6 | 280 | 5 | AB891588 | Ab891588 | Herbicida |
| 299 | 42 | 37.5 | 688 | 8 | ADS24539 | Ad24539 | Bacterial | 372 | 41 | 36.6 | 299 | 4 | AAM40007 | Aam40007 | Human pol |
| 300 | 42 | 37.5 | 698 | 8 | ADS29165 | Ad29165 | Bacterial | 373 | 41 | 36.6 | 308 | 4 | ABG19577 | Abg19577 | Novel hum |
| 301 | 42 | 37.5 | 747 | 8 | ADR86215 | Adr86215 | Aspergill | 374 | 41 | 36.6 | 309 | 8 | ADS21870 | Ad21870 | Bacterial |
| 302 | 42 | 37.5 | 1238 | 7 | ADU70644 | Adu70644 | Human hea | 375 | 41 | 36.6 | 312 | 3 | AAB43035 | Aab43035 | Human ORF |
| 303 | 42 | 37.5 | 1269 | 7 | ABM81833 | Abm81833 | Tumour-as | 376 | 41 | 36.6 | 312 | 4 | AAM40006 | Aam40006 | Human pol |
| 304 | 42 | 37.5 | 1289 | 7 | ADG31527 | Adg31527 | Human nov | 377 | 41 | 36.6 | 312 | 7 | ADC49307 | Adc49307 | Human inh |
| 305 | 42 | 37.5 | 1297 | 7 | AAV13565 | Aay13565 | C. elegan | 378 | 41 | 36.6 | 329 | 4 | AA876662 | Aa876662 | Corynebac |
| 306 | 42 | 37.5 | 1297 | 7 | AAV08403 | Aay08403 | C. elegan | 379 | 41 | 36.6 | 352 | 4 | AAU23088 | Aau23088 | Novel hum |
| 307 | 42 | 37.5 | 1297 | 7 | ADB85337 | Adb85337 | C. elegan | 380 | 41 | 36.6 | 367 | 3 | AA843024 | Aa843024 | Human ORF |
| 308 | 42 | 37.5 | 1409 | 8 | ADN22734 | Adn22734 | Bacterial | 381 | 41 | 36.6 | 376 | 6 | ADA34663 | Ada34663 | Actinobac |
| 309 | 42 | 37.5 | 1973 | 8 | AD084852 | Ad084852 | S epidem | 382 | 41 | 36.6 | 397 | 7 | ABO73973 | Ab073973 | Pseudomon |
| 310 | 42 | 37.5 | 1973 | 8 | AD084850 | Ad084850 | S epidem | 383 | 41 | 36.6 | 399 | 3 | AAG35778 | Aag35778 | Arabidops |
| 311 | 41.5 | 37.1 | 203 | 4 | ABG24283 | Abg24283 | Novel hum | 384 | 41 | 36.6 | 401 | 5 | ABUS1332 | Abus1332 | Helicobac |
| 312 | 41.5 | 37.1 | 368 | 6 | AAE84128 | Aae84128 | An (iso) | 385 | 41 | 36.6 | 410 | 4 | ABG04922 | Abg04922 | Novel hum |
| 313 | 41.5 | 37.1 | 368 | 6 | AAE29785 | Aae29785 | Clarkia b | 386 | 41 | 36.6 | 415 | 5 | ABU52179 | Abu52179 | Helicobac |
| 314 | 41.5 | 37.1 | 368 | 6 | ADK39716 | Adk39716 | Fairy fan | 387 | 41 | 36.6 | 420 | 2 | AAI10965 | Aai10965 | H. pylori |
| 315 | 41.5 | 37.1 | 425 | 6 | ABU40737 | Abu40737 | Protein e | 388 | 41 | 36.6 | 426 | 4 | AA862035 | Aa862035 | P. furios |
| 316 | 41.5 | 37.1 | 461 | 3 | AAG53395 | Aag53395 | Arabidops | 389 | 41 | 36.6 | 421 | 2 | AAW20369 | Aaw20369 | H. pylori |
| 317 | 41.5 | 37.1 | 462 | 3 | AAG53394 | Aag53394 | Arabidops | 390 | 41 | 36.6 | 421 | 2 | AAW20835 | Aaw20835 | H. pylori |

| | | | | | | | | | | | | | | | |
|-----|----|------|-----|---|-----------|-----------|------------|-----|------|------|------|---|-----------|-----------|------------|
| 391 | 41 | 36.6 | 425 | 3 | AAG35777 | Aag35777 | Arabidops | 464 | 41 | 36.6 | 977 | 2 | AAW03942 | Aaw03942 | LKT-GnRH |
| 392 | 41 | 36.6 | 430 | 7 | ADB70157 | Adb70157 | C. neofor | 465 | 41 | 36.6 | 977 | 2 | AAW79569 | Aaw79569 | LKT-GnRH |
| 393 | 41 | 36.6 | 433 | 7 | ABR65475 | Abbr65475 | Drosophill | 466 | 41 | 36.6 | 1069 | 2 | AAW52748 | Aaw52748 | Bovine IF |
| 394 | 41 | 36.6 | 441 | 5 | ABR48633 | Abbr48633 | Listeria | 467 | 41 | 36.6 | 1069 | 2 | AAW13867 | Aaw13867 | Chimeric |
| 395 | 41 | 36.6 | 448 | 6 | ABM68700 | Abm68700 | Phototrab | 468 | 41 | 36.6 | 1069 | 2 | AAW21074 | Aaw21074 | Bovine ga |
| 396 | 41 | 36.6 | 451 | 7 | ADL55455 | Adl55455 | C. glutam | 469 | 41 | 36.6 | 1068 | 2 | AAW22103 | Aaw22103 | Bovine IL |
| 397 | 41 | 36.6 | 455 | 8 | ADS29127 | Ads29127 | Bacterial | 470 | 41 | 36.6 | 1098 | 2 | AAW32747 | Aaw32747 | Bovine IL |
| 398 | 41 | 36.6 | 459 | 4 | AAW76660 | Aaw76660 | Corynebac | 471 | 41 | 36.6 | 1098 | 2 | AAW13866 | Aaw13866 | Chimeric |
| 399 | 41 | 36.6 | 465 | 6 | ABU38244 | Abu38244 | Protein e | 472 | 41 | 36.6 | 1098 | 3 | AAW1073 | Aaw1073 | Bovine IL |
| 400 | 41 | 36.6 | 469 | 7 | ABO79123 | Abot79123 | Pseudomon | 473 | 41 | 36.6 | 1100 | 8 | ADP99064 | Adp99064 | C. albica |
| 401 | 41 | 36.6 | 477 | 2 | AAI10993 | Aai10993 | H. pylori | 474 | 41 | 36.6 | 1133 | 3 | AAW38913 | Aaw38913 | Arabidops |
| 402 | 41 | 36.6 | 479 | 4 | AAG90011 | Aag90011 | C. glutami | 475 | 41 | 36.6 | 1193 | 3 | AAW38913 | Aaw38913 | Arabidops |
| 403 | 41 | 36.6 | 479 | 7 | ABM73851 | Abm73851 | DNA clone | 476 | 41 | 36.6 | 1256 | 4 | ABW64133 | Abw64133 | Drosophill |
| 404 | 41 | 36.6 | 489 | 6 | ABU17356 | Abu17356 | Protein e | 477 | 41 | 36.6 | 1411 | 6 | ABW3378 | Abw3378 | Disease t |
| 405 | 41 | 36.6 | 490 | 2 | AAW33929 | Aaw33929 | Leukotoxi | 478 | 41 | 36.6 | 1411 | 7 | ADK63342 | Adk63342 | Disease t |
| 406 | 41 | 36.6 | 490 | 6 | ADA28694 | Ada28694 | Plasmid p | 479 | 41 | 36.6 | 1566 | 4 | ABW64864 | Abw64864 | Drosophila |
| 407 | 41 | 36.6 | 494 | 4 | ABW68783 | Abw68783 | Drosophill | 480 | 41 | 36.6 | 2188 | 6 | ADA36476 | Ada36476 | Acinetoba |
| 408 | 41 | 36.6 | 495 | 5 | AAW48000 | Aaw48000 | Arabidops | 481 | 41 | 36.6 | 3196 | 5 | ABU1611 | Abu1611 | Protein e |
| 409 | 41 | 36.6 | 495 | 8 | ADN23982 | Adn23982 | Bacterial | 482 | 40.5 | 36.2 | 96 | 3 | AAW62753 | Aaw62753 | Zea mays |
| 410 | 41 | 36.6 | 501 | 3 | AAG35776 | Aag35776 | Arabidops | 483 | 40.5 | 36.2 | 100 | 7 | ADH66104 | Adh66104 | Enterococ |
| 411 | 41 | 36.6 | 501 | 5 | AAW48001 | Aaw48001 | Arabidops | 484 | 40.5 | 36.2 | 163 | 3 | AAW62752 | Aaw62752 | Zea mays |
| 412 | 41 | 36.6 | 505 | 6 | ABU18461 | Abu18461 | Protein e | 485 | 40.5 | 36.2 | 213 | 4 | ABW11455 | Abw11455 | Drosophill |
| 413 | 41 | 36.6 | 510 | 2 | AAW88360 | Aaw88360 | Caenorhab | 486 | 40.5 | 36.2 | 243 | 6 | ABW78956 | Abw78956 | N. gonorr |
| 414 | 41 | 36.6 | 514 | 2 | AAW03943 | Aaw03943 | LKT-GnRH | 487 | 40.5 | 36.2 | 248 | 6 | ABW67960 | Abw67960 | Phototrab |
| 415 | 41 | 36.6 | 544 | 2 | AAW79570 | Aaw79570 | LKT-GnRH | 488 | 40.5 | 36.2 | 251 | 8 | ADW525182 | Adw525182 | Bacterial |
| 416 | 41 | 36.6 | 572 | 4 | ABW61834 | Abw61834 | Drosophill | 489 | 40.5 | 36.2 | 251 | 8 | ADW525911 | Adw525911 | Bacterial |
| 417 | 41 | 36.6 | 572 | 8 | ADK70707 | Adk70707 | Collapsin | 490 | 40.5 | 36.2 | 252 | 8 | ADW525556 | Adw525556 | Bacterial |
| 418 | 41 | 36.6 | 579 | 2 | AAW37874 | Aaw37874 | Alcohol a | 491 | 40.5 | 36.2 | 257 | 8 | ADW522518 | Adw522518 | Bacterial |
| 419 | 41 | 36.6 | 585 | 6 | ABU43406 | Abu43406 | Protein e | 492 | 40.5 | 36.2 | 291 | 7 | ADW6763 | Adw6763 | E. faeciu |
| 420 | 41 | 36.6 | 596 | 4 | AAU33748 | Aau33748 | Staphyloc | 493 | 40.5 | 36.2 | 413 | 6 | ABW68660 | Abw68660 | Phototrab |
| 421 | 41 | 36.6 | 604 | 4 | ABU36932 | Abu36932 | Staphyloc | 494 | 40.5 | 36.2 | 459 | 8 | ADN19683 | Adn19683 | Bacterial |
| 422 | 41 | 36.6 | 604 | 6 | ABU16053 | Abu16053 | Protein e | 495 | 40.5 | 36.2 | 459 | 8 | ADN19681 | Adn19681 | Bacterial |
| 423 | 41 | 36.6 | 604 | 6 | ABW73224 | Abw73224 | Staphyloc | 496 | 40.5 | 36.2 | 470 | 5 | ADP74741 | Adp74741 | HIV-1 iso |
| 424 | 41 | 36.6 | 608 | 4 | AAW04636 | Aaw04636 | Pasteurel | 497 | 40.5 | 36.2 | 479 | 5 | ABW91096 | Abw91096 | Herbicida |
| 425 | 41 | 36.6 | 611 | 8 | ADN22551 | Adn22551 | Bacterial | 498 | 40.5 | 36.2 | 503 | 4 | AAW83355 | Aaw83355 | HIV-1 gp1 |
| 426 | 41 | 36.6 | 630 | 5 | ABW48390 | Abw48390 | Listeria | 499 | 40.5 | 36.2 | 571 | 4 | ABW60235 | Abw60235 | Drosophill |
| 427 | 41 | 36.6 | 630 | 6 | ABU32723 | Abu32723 | Protein e | 500 | 40.5 | 36.2 | 838 | 2 | AAW49078 | Aaw49078 | Solanum t |
| 428 | 41 | 36.6 | 676 | 8 | ADK70694 | Adk70694 | Chicken C | 501 | 40.5 | 36.2 | 840 | 7 | ABO70815 | Abot70815 | Pseudomon |
| 429 | 41 | 36.6 | 695 | 2 | AAW79573 | Aaw79573 | LKT-GnRH | 502 | 40.5 | 36.2 | 3768 | 2 | AAW13753 | Aaw13753 | ACV5. 3/2 |
| 430 | 41 | 36.6 | 695 | 3 | AAW58361 | Aaw58361 | Leukotoxi | 503 | 40.5 | 36.2 | 3778 | 2 | AAW13895 | Aaw13895 | ACV synth |
| 431 | 41 | 36.6 | 695 | 3 | AAW58361 | Aaw58361 | Leukotoxi | 504 | 40.5 | 36.2 | 4644 | 8 | ADP26621 | Adp26621 | Mouse cyt |
| 432 | 41 | 36.6 | 754 | 6 | ABU38838 | Abu38838 | Protein e | 505 | 40.5 | 36.2 | 4644 | 8 | ADP26623 | Adp26623 | Mouse cyt |
| 433 | 41 | 36.6 | 754 | 8 | ADH97174 | Adh97174 | P. aerugi | 506 | 40.5 | 36.2 | 4646 | 8 | ADP26625 | Adp26625 | Human cyt |
| 434 | 41 | 36.6 | 754 | 8 | ADH97176 | Adh97176 | P. aerugi | 507 | 40.5 | 36.2 | 4646 | 8 | ADP26631 | Adp26631 | Human cyt |
| 435 | 41 | 36.6 | 780 | 7 | ABW84146 | Abw84146 | Pseudomon | 508 | 40.5 | 36.2 | 10 | 6 | ABW70338 | Abw70338 | Tryptic p |
| 436 | 41 | 36.6 | 780 | 7 | ABW84146 | Abw84146 | Pseudomon | 509 | 40.5 | 36.2 | 10 | 6 | ABW70337 | Abw70337 | Tryptic p |
| 437 | 41 | 36.6 | 786 | 3 | AAW70243 | Aaw70243 | Human RNA | 510 | 40.5 | 36.2 | 43 | 5 | ABW30629 | Abw30629 | Streptoco |
| 438 | 41 | 36.6 | 831 | 7 | ADW51486 | Adw51486 | Bacterial | 511 | 40.5 | 36.2 | 50 | 2 | AAW71093 | Aaw71093 | C. jejuni |
| 439 | 41 | 36.6 | 831 | 8 | ADW529643 | Adw529643 | Bacterial | 512 | 40.5 | 36.2 | 52 | 6 | ABW82557 | Abw82557 | Human MAN |
| 440 | 41 | 36.6 | 849 | 4 | AAW93170 | Aaw93170 | Human pro | 513 | 40.5 | 36.2 | 65 | 5 | ABW39574 | Abw39574 | Staphyloc |
| 441 | 41 | 36.6 | 883 | 6 | ABU02533 | Abu02533 | S. pneumo | 514 | 40.5 | 36.2 | 65 | 4 | ADW05543 | Adw05543 | Staphyloc |
| 442 | 41 | 36.6 | 887 | 4 | AAU37586 | Aau37586 | Streptoco | 515 | 40.5 | 36.2 | 90 | 4 | AAW74248 | Aaw74248 | Human col |
| 443 | 41 | 36.6 | 890 | 6 | ABP81476 | Abp81476 | Streptoco | 516 | 40.5 | 36.2 | 94 | 5 | ABW78867 | Abw78867 | Tumour ne |
| 444 | 41 | 36.6 | 890 | 6 | ABU46253 | Abu46253 | Protein e | 517 | 40.5 | 36.2 | 94 | 5 | ABW78866 | Abw78866 | Tumour ne |
| 445 | 41 | 36.6 | 890 | 8 | ADK48224 | Adk48224 | Streptoco | 518 | 40.5 | 36.2 | 106 | 5 | ABW30697 | Abw30697 | Streptoco |
| 446 | 41 | 36.6 | 920 | 4 | ABW29636 | Abw29636 | Novel hum | 519 | 40.5 | 36.2 | 106 | 5 | ABW30640 | Abw30640 | Streptoco |
| 447 | 41 | 36.6 | 924 | 2 | AAW10889 | Aaw10889 | Leukotoxi | 520 | 40.5 | 36.2 | 120 | 4 | AAW00976 | Aaw00976 | Human hum |
| 448 | 41 | 36.6 | 924 | 2 | AAW42378 | Aaw42378 | Recombina | 521 | 40.5 | 36.2 | 126 | 4 | AAW00976 | Aaw00976 | Human hum |
| 449 | 41 | 36.6 | 924 | 2 | AAW42380 | Aaw42380 | Recombina | 522 | 40.5 | 36.2 | 138 | 2 | AAW36920 | Aaw36920 | Amino aci |
| 450 | 41 | 36.6 | 924 | 2 | AAW42385 | Aaw42385 | Recombina | 523 | 40.5 | 36.2 | 143 | 3 | AAW36920 | Aaw36920 | Amino aci |
| 451 | 41 | 36.6 | 926 | 2 | AAW14482 | Aaw14482 | LTK352. 1 | 524 | 40.5 | 36.2 | 144 | 1 | AAW91023 | Aaw91023 | Modified |
| 452 | 41 | 36.6 | 926 | 2 | AAW34545 | Aaw34545 | Leukotoxi | 525 | 40.5 | 36.2 | 146 | 1 | AAW30676 | Aaw30676 | Modified |
| 453 | 41 | 36.6 | 926 | 2 | AAW50291 | Aaw50291 | Recombina | 526 | 40.5 | 36.2 | 147 | 1 | AAW91042 | Aaw91042 | Modified |
| 454 | 41 | 36.6 | 926 | 2 | AAW03945 | Aaw03945 | P. haemol | 527 | 40.5 | 36.2 | 147 | 1 | AAW91035 | Aaw91035 | Modified |
| 455 | 41 | 36.6 | 926 | 2 | AAW79568 | Aaw79568 | Leukotoxi | 528 | 40.5 | 36.2 | 153 | 3 | AAW40483 | Aaw40483 | Arabidops |
| 456 | 41 | 36.6 | 936 | 2 | AAW34547 | Aaw34547 | GnRH-leuk | 529 | 40.5 | 36.2 | 153 | 4 | AAW38761 | Aaw38761 | Human pol |
| 457 | 41 | 36.6 | 936 | 2 | AAW34546 | Aaw34546 | Somatosta | 530 | 40.5 | 36.2 | 154 | 3 | AAW29997 | Aaw29997 | Arabidops |
| 458 | 41 | 36.6 | 951 | 2 | AAW34548 | Aaw34548 | Rotavirius | 531 | 40.5 | 36.2 | 158 | 6 | ABW82550 | Abw82550 | Human MAN |
| 459 | 41 | 36.6 | 953 | 2 | AAW07167 | Aaw07167 | 105KD PTX | 532 | 40.5 | 36.2 | 158 | 6 | ABW82553 | Abw82553 | Mouse MAN |
| 460 | 41 | 36.6 | 953 | 2 | AAW15159 | Aaw15159 | Leukotoxi | 533 | 40.5 | 36.2 | 158 | 6 | AAW026456 | Aaw026456 | Human ch3 |
| 461 | 41 | 36.6 | 953 | 2 | AAW3865 | Aaw3865 | Leukotoxi | 534 | 40.5 | 36.2 | 159 | 6 | ABW82554 | Abw82554 | A synthet |
| 462 | 41 | 36.6 | 953 | 2 | AAW60072 | Aaw60072 | Pcxa prot | 535 | 40.5 | 36.2 | 159 | 6 | ABW82551 | Abw82551 | A synthet |
| 463 | 41 | 36.6 | 953 | 4 | AAW04638 | Aaw04638 | Pasteurel | 536 | 40.5 | 36.2 | 161 | 4 | ABW00722 | Abw00722 | Novel hum |

| | | | | | | | | | | | | | |
|-----|----|-------|-----|---|-----------|---------------------|-----|----|-------|-----|---|-----------|-----------------------|
| 537 | 40 | 35..7 | 162 | 3 | AAB43377 | Abb43377 Human ORF | 610 | 40 | 35..7 | 275 | 4 | ABG07277 | Abg07277 Novel hum |
| 538 | 40 | 35..7 | 162 | 6 | ABG99957 | ABg99957 Human nov | 611 | 40 | 35..7 | 276 | 7 | ABO63141 | Aboc63141 Klebsiell |
| 539 | 40 | 35..7 | 166 | 6 | ABP97165 | ABp97165 Human lys | 612 | 40 | 35..7 | 282 | 6 | ABU36887 | Abu36887 Protein e |
| 540 | 40 | 35..7 | 166 | 7 | ADJ70254 | Adj70254 Human hea | 613 | 40 | 35..7 | 282 | 6 | ABU34865 | Abu34865 Protein e |
| 541 | 40 | 35..7 | 179 | 4 | AAB62160 | Aab62160 Mouse arg | 614 | 40 | 35..7 | 291 | 4 | ABB36424 | Abb36424 Peptide # |
| 542 | 40 | 35..7 | 179 | 4 | AAB62159 | Aab62159 Mouse arg | 615 | 40 | 35..7 | 291 | 4 | AAW29924 | Aaw29924 Peptide # |
| 543 | 40 | 35..7 | 179 | 6 | ABB82558 | Abb82558 Bovine pr | 616 | 40 | 35..7 | 291 | 4 | ABAB31217 | Abb31217 Peptide # |
| 544 | 40 | 35..7 | 179 | 6 | ABB82552 | Abb82552 Mouse pro | 617 | 40 | 35..7 | 291 | 4 | ABBR21776 | Abbr21776 Protein # |
| 545 | 40 | 35..7 | 179 | 6 | ABB82549 | Abb82549 Human pro | 618 | 40 | 35..7 | 291 | 4 | AAW65985 | Aaw65985 Human bon |
| 546 | 40 | 35..7 | 179 | 6 | ABB82559 | Abb82559 Pig pro-M | 619 | 40 | 35..7 | 291 | 4 | AAW57183 | Aaw57183 Human bra |
| 547 | 40 | 35..7 | 179 | 6 | AAO26455 | AAo26455 Human ch3 | 620 | 40 | 35..7 | 291 | 4 | ABG51259 | Abg51259 Human liv |
| 548 | 40 | 35..7 | 182 | 4 | ABB65390 | Abb65390 Drosophi1 | 621 | 40 | 35..7 | 291 | 5 | ABG39209 | Abg39209 Human pep |
| 549 | 40 | 35..7 | 182 | 4 | ABB57808 | Abb57808 Drosophi1 | 622 | 40 | 35..7 | 294 | 5 | ABBS4169 | Abbs4169 Lactococc |
| 550 | 40 | 35..7 | 182 | 8 | ADO96544 | Ado96544 T cell ac | 623 | 40 | 35..7 | 294 | 8 | ADS29357 | Ads29357 Bacteri |
| 551 | 40 | 35..7 | 187 | 4 | AAAG65919 | AAg65919 Amino aci | 624 | 40 | 35..7 | 307 | 5 | AAW49055 | Aaw49055 Tobacc |
| 552 | 40 | 35..7 | 198 | 4 | AAAG65920 | AAg65920 Amino aci | 625 | 40 | 35..7 | 316 | 4 | AAU00818 | AAu00818 Human Imm |
| 553 | 40 | 35..7 | 199 | 6 | ABU24475 | ABu24475 Protein e | 626 | 40 | 35..7 | 319 | 7 | ADC95915 | Adc95915 E. faeciu |
| 554 | 40 | 35..7 | 201 | 4 | AAW38762 | AAw38762 Human pol | 627 | 40 | 35..7 | 324 | 6 | ADA54362 | Ada54362 Human pro |
| 555 | 40 | 35..7 | 206 | 5 | ABP51289 | ABp51289 Human MDD | 628 | 40 | 35..7 | 326 | 6 | ABU25302 | Abu25302 Protein e |
| 556 | 40 | 35..7 | 206 | 7 | ADH85557 | Adh85557 Enterococ | 629 | 40 | 35..7 | 327 | 5 | ABW49937 | Abw49937 Listeria |
| 557 | 40 | 35..7 | 207 | 2 | AAW09530 | AAw09530 Human lys | 630 | 40 | 35..7 | 330 | 7 | ABW74320 | Abw74320 DNA clone |
| 558 | 40 | 35..7 | 207 | 3 | AAAG40482 | AAg40482 Arabidops | 631 | 40 | 35..7 | 332 | 8 | ADH56074 | Adh56074 DebarYomy |
| 559 | 40 | 35..7 | 207 | 7 | ABO82593 | ABo82593 Pseudomon | 632 | 40 | 35..7 | 336 | 8 | ADU119383 | Adu119383 Pyrococcu |
| 560 | 40 | 35..7 | 209 | 3 | AAAG29996 | AAg29996 Arabidops | 633 | 40 | 35..7 | 339 | 4 | AAAB6053 | AAb6053 Putative |
| 561 | 40 | 35..7 | 214 | 3 | AAW69296 | AAw69296 A human 1 | 634 | 40 | 35..7 | 344 | 3 | AAAB56782 | AAb56782 Human pro |
| 562 | 40 | 35..7 | 214 | 3 | AAAG40481 | AAg40481 Arabidops | 635 | 40 | 35..7 | 344 | 8 | ADS27683 | Ads27683 Bacteri |
| 563 | 40 | 35..7 | 214 | 8 | ADG47876 | Adg47876 Arabidops | 636 | 40 | 35..7 | 345 | 4 | AAAB62222 | AAb62222 Putative |
| 564 | 40 | 35..7 | 214 | 8 | ADG62901 | Adg62901 Transcript | 637 | 40 | 35..7 | 345 | 5 | ABP60914 | ABp60914 Pyrococcu |
| 565 | 40 | 35..7 | 215 | 8 | ADR66301 | Adr66301 Human pro | 638 | 40 | 35..7 | 345 | 7 | ADF04255 | Adf04255 Bacteri |
| 566 | 40 | 35..7 | 215 | 8 | ADR66862 | Adr66862 Human pro | 639 | 40 | 35..7 | 347 | 4 | ABBB1186 | Abbb1186 Drosophi1 |
| 567 | 40 | 35..7 | 217 | 6 | AAE34443 | AAe34443 Human lip | 640 | 40 | 35..7 | 351 | 8 | ADS28060 | Ads28060 Bacteri |
| 568 | 40 | 35..7 | 218 | 4 | AAW25257 | AAw25257 Human pro | 641 | 40 | 35..7 | 357 | 6 | ABU24898 | Abu24898 Protein e |
| 569 | 40 | 35..7 | 219 | 4 | AAAG75019 | AAg75019 Human col | 642 | 40 | 35..7 | 358 | 6 | ADA35088 | Ada35088 Actinob |
| 570 | 40 | 35..7 | 224 | 4 | AAAG62621 | AAg62621 Human SNA | 643 | 40 | 35..7 | 359 | 7 | ADP28205 | ADp28205 Human MDD |
| 571 | 40 | 35..7 | 224 | 6 | ABU00236 | ABu00236 Human nov | 644 | 40 | 35..7 | 360 | 5 | ABP26080 | ABp26080 Streptoc |
| 572 | 40 | 35..7 | 230 | 2 | AAW09531 | AAw09531 Human lys | 645 | 40 | 35..7 | 371 | 3 | AAAG21115 | AAg21115 Arabidops |
| 573 | 40 | 35..7 | 230 | 4 | AAAB82669 | AAb82669 Human bra | 646 | 40 | 35..7 | 372 | 3 | AAAG21114 | AAg21114 Arabidops |
| 574 | 40 | 35..7 | 230 | 5 | AAUB5136 | AAuB5136 Mouse lys | 647 | 40 | 35..7 | 388 | 3 | AAAB43313 | AAb43313 Human ORF |
| 575 | 40 | 35..7 | 230 | 5 | AAUB5133 | AAuB5133 Mouse lys | 648 | 40 | 35..7 | 389 | 8 | ADP89415 | ADp89415 Chlamydia |
| 576 | 40 | 35..7 | 230 | 5 | AAUB5134 | AAuB5134 Human lys | 649 | 40 | 35..7 | 390 | 7 | ADC96041 | ADC96041 E. faeciu |
| 577 | 40 | 35..7 | 230 | 5 | AAUB5132 | AAuB5132 Human lys | 650 | 40 | 35..7 | 391 | 2 | AAW35503 | AAw35503 Chlamydia |
| 578 | 40 | 35..7 | 230 | 6 | ABP97164 | ABp97164 Human lys | 651 | 40 | 35..7 | 394 | 7 | ADW04014 | ADw04014 Human pro |
| 579 | 40 | 35..7 | 230 | 6 | ABR54196 | ABr54196 Human NOV | 652 | 40 | 35..7 | 407 | 4 | AAW93675 | AAw93675 Human pro |
| 580 | 40 | 35..7 | 230 | 6 | ABR54198 | ABr54198 Human NOV | 653 | 40 | 35..7 | 407 | 8 | ADU13531 | ADu13531 Human pro |
| 581 | 40 | 35..7 | 230 | 7 | ADBS8726 | ADbs8726 Human pro | 654 | 40 | 35..7 | 418 | 6 | ABU27547 | ABu27547 Protein e |
| 582 | 40 | 35..7 | 230 | 7 | ADH45662 | ADh45662 Human pro | 655 | 40 | 35..7 | 443 | 3 | AAAG21113 | AAg21113 Arabidops |
| 583 | 40 | 35..7 | 230 | 7 | ADH47694 | ADh47694 Human NOV | 656 | 40 | 35..7 | 444 | 5 | ABG79686 | ABg79686 Tymour ln |
| 584 | 40 | 35..7 | 230 | 8 | ABM80964 | ABm80964 Human NOV | 657 | 40 | 35..7 | 450 | 6 | ABU43672 | ABu43672 Protein e |
| 585 | 40 | 35..7 | 230 | 8 | ABM80990 | ABm80990 Tymour-as | 658 | 40 | 35..7 | 455 | 5 | ABB05727 | ABB05727 Human sig |
| 586 | 40 | 35..7 | 234 | 4 | AAAB90765 | AAaB90765 Human she | 659 | 40 | 35..7 | 463 | 3 | AAAB12529 | AAaB12529 Human Mas |
| 587 | 40 | 35..7 | 234 | 6 | ABBB2548 | ABbb2548 Human arg | 660 | 40 | 35..7 | 463 | 3 | AAAB42315 | AAaB42315 Human ORF |
| 588 | 40 | 35..7 | 234 | 6 | AAE34881 | AAe34881 Human ARP | 661 | 40 | 35..7 | 466 | 7 | ADG33792 | ADg33792 Actinomy |
| 589 | 40 | 35..7 | 234 | 8 | ADMA4586 | ADma4586 Human arg | 662 | 40 | 35..7 | 469 | 3 | AAW98040 | AAw98040 Human ets |
| 590 | 40 | 35..7 | 234 | 8 | ADNO5973 | ADno5973 Antipept | 663 | 40 | 35..7 | 469 | 3 | AAW90689 | AAw90689 Human Ets |
| 591 | 40 | 35..7 | 234 | 8 | ADOL9303 | ADol9303 Human PRO | 664 | 40 | 35..7 | 469 | 5 | ABB78349 | ABB78349 Human aci |
| 592 | 40 | 35..7 | 234 | 8 | ADOG96546 | ADoG96546 T cell ac | 665 | 40 | 35..7 | 469 | 8 | ABOB85042 | ABOb85042 Human can |
| 593 | 40 | 35..7 | 234 | 8 | ADP54366 | ADp54366 Human PRO | 666 | 40 | 35..7 | 470 | 6 | ADBO9370 | ADBo9370 Alloiococ |
| 594 | 40 | 35..7 | 234 | 8 | ADP23376 | ADp23376 PRO polyp | 667 | 40 | 35..7 | 472 | 2 | AAW86327 | AAw86327 Kidney ln |
| 595 | 40 | 35..7 | 234 | 6 | ABU11366 | ABu11366 Protein e | 668 | 40 | 35..7 | 473 | 6 | ADBO9372 | ADBo9372 Alloiococ |
| 596 | 40 | 35..7 | 238 | 4 | ABG07040 | ABg07040 Novel hum | 669 | 40 | 35..7 | 476 | 4 | ABG08740 | ABg08740 Novel hum |
| 597 | 40 | 35..7 | 247 | 8 | ADN17795 | ADn17795 Bacterial | 670 | 40 | 35..7 | 478 | 6 | ABU36344 | ABu36344 Protein e |
| 598 | 40 | 35..7 | 248 | 2 | AAW84050 | AAw84050 Rice OsMA | 671 | 40 | 35..7 | 484 | 6 | ABU24912 | ABu24912 Protein e |
| 599 | 40 | 35..7 | 248 | 3 | AAO14278 | AAo14278 Plant flo | 672 | 40 | 35..7 | 486 | 7 | ABO70890 | ABo70890 Pseudomon |
| 600 | 40 | 35..7 | 248 | 8 | ADQ37091 | ADq37091 Cell prol | 673 | 40 | 35..7 | 490 | 8 | ADM72386 | ADm72386 A. thaila |
| 601 | 40 | 35..7 | 250 | 1 | AAW70498 | AAw70498 Aspergill | 674 | 40 | 35..7 | 491 | 6 | ABU20497 | ABu20497 Protein e |
| 602 | 40 | 35..7 | 250 | 4 | ABBB60023 | ABbb60023 Drosophi1 | 675 | 40 | 35..7 | 505 | 6 | ADBO9374 | ADBo9374 Alloiococ |
| 603 | 40 | 35..7 | 250 | 6 | ABU41029 | ABu41029 Protein e | 676 | 40 | 35..7 | 509 | 6 | AAE30011 | AAe30011 Tobacc |
| 604 | 40 | 35..7 | 252 | 7 | ABOB82067 | ABOb82067 Pseudomon | 677 | 40 | 35..7 | 513 | 6 | ABW72116 | ABw72116 Staphyloc |
| 605 | 40 | 35..7 | 254 | 8 | ADG42533 | ADg42533 Bacteri | 678 | 40 | 35..7 | 535 | 4 | AAAG74327 | AAg74327 Human col |
| 606 | 40 | 35..7 | 258 | 2 | AAW37099 | AAw37099 Amino aci | 679 | 40 | 35..7 | 541 | 6 | ABU49123 | ABu49123 Protein e |
| 607 | 40 | 35..7 | 263 | 3 | AAAB53451 | AAaB53451 Human col | 680 | 40 | 35..7 | 544 | 2 | AAAR13337 | AAaR13337 HyPB prot |
| 608 | 40 | 35..7 | 272 | 7 | ADFO4631 | ADfo4631 Bacterial | 681 | 40 | 35..7 | 544 | 2 | AAAR67383 | AAaR67383 C. psittaci |
| 609 | 40 | 35..7 | 273 | 8 | ADBS23832 | ADbs23832 Bacterial | 682 | 40 | 35..7 | 544 | 2 | AAW10975 | AAw10975 Chlamydia |

| | | | | | | | | | | | | | |
|-----|----|------|------|---|-----------|---------------------|-----|------|------|------|---|-----------|---------------------|
| 683 | 40 | 35.7 | 544 | 2 | AAW11863 | Aw11863 Polypepti | 756 | 40 | 35.7 | 1231 | 7 | ADC95523 | Adc95523 E. faeciu |
| 684 | 40 | 35.7 | 544 | 2 | AAy34735 | Aay34735 Amino ac | 757 | 40 | 35.7 | 1253 | 6 | ABO07127 | AbO07127 Novel hum |
| 685 | 40 | 35.7 | 544 | 2 | AAE11757 | AAe11757 Chlamydoc | 758 | 40 | 35.7 | 1353 | 7 | ADG42170 | AdG42170 Human bra |
| 686 | 40 | 35.7 | 544 | 5 | ABB94272 | Abb94272 Chlamydia | 759 | 40 | 35.7 | 1394 | 6 | AAg79647 | AAg79647 Human pro |
| 687 | 40 | 35.7 | 544 | 5 | ABG31261 | Abg31261 Chlamydia | 760 | 40 | 35.7 | 1444 | 8 | ADN61347 | ADn61347 Penibacti |
| 688 | 40 | 35.7 | 544 | 5 | ADL97984 | Adl97984 C. psittca | 761 | 40 | 35.7 | 1444 | 8 | ADR21520 | AdR21520 Penibacti |
| 689 | 40 | 35.7 | 544 | 5 | ADL97987 | Adl97987 C. tiracho | 762 | 40 | 35.7 | 1518 | 7 | ADD93660 | AdD93660 Streptoco |
| 690 | 40 | 35.7 | 544 | 6 | ABU26931 | Abu26931 Protein e | 763 | 40 | 35.7 | 1600 | 4 | ABG20004 | ABg20004 Novel hum |
| 691 | 40 | 35.7 | 544 | 6 | ABU27237 | Abu27237 Protein e | 764 | 40 | 35.7 | 1600 | 4 | ABG09417 | ABg09417 Novel hum |
| 692 | 40 | 35.7 | 549 | 8 | ADI45327 | Adi45327 Rice isop | 765 | 40 | 35.7 | 1600 | 4 | ABG09423 | ABg09423 Novel hum |
| 693 | 40 | 35.7 | 551 | 8 | ADS29961 | Ads29961 Bacterial | 766 | 40 | 35.7 | 1600 | 4 | ABG12275 | ABg12275 Novel hum |
| 694 | 40 | 35.7 | 551 | 8 | ADS29961 | Ads29961 Bacterial | 767 | 40 | 35.7 | 1600 | 4 | ADP60439 | AdP60439 Novel hum |
| 695 | 40 | 35.7 | 551 | 8 | ADS29961 | Ads29961 Bacterial | 768 | 40 | 35.7 | 1600 | 7 | ADP60402 | AdP60402 Human con |
| 696 | 40 | 35.7 | 561 | 5 | ABB92269 | Abb92269 Herbicida | 769 | 40 | 35.7 | 1941 | 5 | ABP65509 | ABp65509 Bifidobac |
| 697 | 40 | 35.7 | 572 | 2 | AAW68487 | AAw68487 Mouse Utl1 | 770 | 40 | 35.7 | 1987 | 7 | ABU63358 | ABu63358 Human sin |
| 698 | 40 | 35.7 | 572 | 5 | AAU85553 | Aau85553 Clone #50 | 771 | 40 | 35.7 | 2000 | 8 | ADN04333 | ADn04333 Antipsoxi |
| 699 | 40 | 35.7 | 572 | 5 | ABR42050 | AbR42050 Human col | 772 | 40 | 35.7 | 2000 | 8 | ADP24104 | ADp24104 PRO Polyv |
| 700 | 40 | 35.7 | 572 | 6 | ABU69525 | Abu69525 Human lun | 773 | 40 | 35.7 | 2013 | 4 | ABE62322 | ABe62322 Drosophi1 |
| 701 | 40 | 35.7 | 572 | 6 | ABU66428 | Abu66428 Lung canc | 774 | 40 | 35.7 | 2013 | 7 | ABU63356 | ABu63356 Human sin |
| 702 | 40 | 35.7 | 572 | 6 | ABP97909 | Abp97909 Amino aci | 775 | 40 | 35.7 | 2014 | 7 | AAE67395 | AAe67395 Amino aci |
| 703 | 40 | 35.7 | 572 | 7 | ADES9435 | Ades9435 Rat Prote | 776 | 40 | 35.7 | 2014 | 5 | AAE24137 | AAe24137 Human kin |
| 704 | 40 | 35.7 | 572 | 7 | ADES9437 | Ades9437 Rat Prote | 777 | 40 | 35.7 | 2014 | 6 | ABP60434 | ABp60434 Human ste |
| 705 | 40 | 35.7 | 572 | 7 | ADH47334 | Adh47334 Human lun | 778 | 40 | 35.7 | 2014 | 7 | ABU63359 | ABu63359 Human sin |
| 706 | 40 | 35.7 | 572 | 7 | ADN95176 | Adn95176 Human BGC | 779 | 40 | 35.7 | 2040 | 7 | ABU63357 | ABu63357 Human sin |
| 707 | 40 | 35.7 | 572 | 8 | ADK70705 | AdK70705 Col1a6sin | 780 | 40 | 35.7 | 2041 | 6 | ABP60435 | ABp60435 Human ste |
| 708 | 40 | 35.7 | 572 | 8 | ADJ21253 | Adj21253 Human lun | 781 | 40 | 35.7 | 2168 | 4 | ABG09420 | ABg09420 Novel hum |
| 709 | 40 | 35.7 | 572 | 8 | ABM80551 | Abm80551 Tumour-as | 782 | 40 | 35.7 | 2168 | 4 | ABG09727 | ABg09727 Novel hum |
| 710 | 40 | 35.7 | 584 | 3 | AAW42539 | Aaw42539 Human ORF | 783 | 40 | 35.7 | 2176 | 4 | ABG12287 | ABg12287 Novel hum |
| 711 | 40 | 35.7 | 584 | 6 | ABU00948 | Abu00948 S. pneumo | 784 | 40 | 35.7 | 2176 | 4 | ABG20022 | ABg20022 Novel hum |
| 712 | 40 | 35.7 | 589 | 4 | AAW39712 | Aaw39712 Human pol | 785 | 40 | 35.7 | 2176 | 7 | ADP60184 | ADp60184 Human con |
| 713 | 40 | 35.7 | 607 | 5 | ABR52408 | ABr52408 Protein r | 786 | 40 | 35.7 | 2472 | 7 | ADBS5353 | ADe55353 Human pro |
| 714 | 40 | 35.7 | 609 | 7 | ADM05286 | Adm05286 Human pro | 787 | 40 | 35.7 | 2472 | 7 | ADBS5351 | ADe55351 Rat Prote |
| 715 | 40 | 35.7 | 622 | 5 | ABBA8075 | Abba8075 Listeria e | 788 | 40 | 35.7 | 2477 | 7 | ABR84742 | ABr84742 Human spe |
| 716 | 40 | 35.7 | 622 | 6 | ABU32903 | Abu32903 Protein e | 789 | 40 | 35.7 | 2477 | 7 | ADJ68432 | ADj68432 Human hea |
| 717 | 40 | 35.7 | 629 | 6 | ABJ25441 | Abj25441 Aspergill1 | 790 | 40 | 35.7 | 2509 | 7 | ABO67896 | ABo67896 Pseudomon |
| 718 | 40 | 35.7 | 629 | 8 | ADJ75404 | Adj75404 Marker ge | 791 | 40 | 35.7 | 2541 | 3 | AAW41087 | AAw41087 Human ORF |
| 719 | 40 | 35.7 | 631 | 8 | ADH88290 | Adh88290 Enterococ | 792 | 40 | 35.7 | 2541 | 3 | ABW81459 | ABw81459 Human Tal |
| 720 | 40 | 35.7 | 647 | 8 | ADS44610 | Ads44610 Bacterial | 793 | 40 | 35.7 | 2541 | 5 | ADG90450 | ADg90450 Human tal |
| 721 | 40 | 35.7 | 650 | 8 | ADJ76381 | Adj76381 Marker ge | 794 | 40 | 35.7 | 2541 | 6 | ABR47614 | ABr47614 Breast ca |
| 722 | 40 | 35.7 | 651 | 5 | ABP65617 | Abp65617 Human pol | 795 | 40 | 35.7 | 2541 | 7 | ADDA5522 | ADd45522 Human pro |
| 723 | 40 | 35.7 | 651 | 5 | ADJ69772 | Adj69772 Human hea | 796 | 40 | 35.7 | 2541 | 7 | ADDS5868 | ADd58686 Human pro |
| 724 | 40 | 35.7 | 662 | 5 | ABR52423 | ABr52423 Protein r | 797 | 40 | 35.7 | 2541 | 7 | ADP65318 | ADp65318 Human tal |
| 725 | 40 | 35.7 | 666 | 4 | AAW41498 | Aaw41498 Human pol | 798 | 40 | 35.7 | 2541 | 8 | ADP65745 | ADp65745 Human Tal |
| 726 | 40 | 35.7 | 683 | 8 | ADK70692 | AdK70692 Chicken C | 799 | 40 | 35.7 | 2541 | 8 | ABW81037 | ABw81037 Tumour-as |
| 727 | 40 | 35.7 | 684 | 4 | ABB69330 | Abb69330 Drosophi1 | 800 | 40 | 35.7 | 2636 | 7 | ABO77007 | ABo77007 Pseudomon |
| 728 | 40 | 35.7 | 685 | 6 | ABJ26041 | Abj26041 Aspergill1 | 801 | 40 | 35.7 | 2652 | 5 | ABG31321 | ABg31321 Predicted |
| 729 | 40 | 35.7 | 698 | 5 | ABRS2422 | ABr52422 Protein r | 802 | 40 | 35.7 | 2652 | 8 | ADL02250 | ADl02250 Human OCP |
| 730 | 40 | 35.7 | 703 | 6 | ABJ26648 | Abj26648 Human pro | 803 | 40 | 35.7 | 2727 | 4 | ABW61674 | ABw61674 Drosophi1 |
| 731 | 40 | 35.7 | 703 | 7 | ADC39232 | Adc39232 Novel hum | 804 | 40 | 35.7 | 2828 | 5 | ABG11332 | ABg11332 Human adl |
| 732 | 40 | 35.7 | 704 | 2 | AAW10976 | Aaw10976 Dihydrofo | 805 | 40 | 35.7 | 2828 | 5 | ABG31319 | ABg31319 Human adl |
| 733 | 40 | 35.7 | 704 | 2 | AAW11864 | AAw11864 DHFR/Poly | 806 | 40 | 35.7 | 2828 | 5 | ABG32897 | ABg32897 Human adl |
| 734 | 40 | 35.7 | 747 | 5 | ABR52421 | ABr52421 Protein r | 807 | 40 | 35.7 | 2828 | 5 | ADJ17071 | ADj17071 Human NOV |
| 735 | 40 | 35.7 | 749 | 7 | ADJ22754 | Adj22754 Human dis | 808 | 40 | 35.7 | 2828 | 5 | ADJ17072 | ADj17072 Human NOV |
| 736 | 40 | 35.7 | 774 | 1 | AAPE60616 | AAp60616 Cephalosp | 809 | 40 | 35.7 | 2828 | 6 | ABJ37051 | ABj37051 Human bre |
| 737 | 40 | 35.7 | 806 | 5 | ABRS2420 | ABr52420 Protein r | 810 | 40 | 35.7 | 2828 | 6 | ABU56609 | ABu56609 Lung canc |
| 738 | 40 | 35.7 | 806 | 5 | ADBS27497 | ADbs27497 Bacterial | 811 | 40 | 35.7 | 2828 | 6 | ABR47439 | ABr47439 Breast ca |
| 739 | 40 | 35.7 | 811 | 6 | ABU17849 | Abu17849 Protein e | 812 | 40 | 35.7 | 2828 | 7 | ADJ83135 | ADj83135 Human adl |
| 740 | 40 | 35.7 | 822 | 8 | ADBR39827 | ADbr39827 Rat NRC 1 | 813 | 40 | 35.7 | 2828 | 7 | ADN39857 | ADn39857 Cancer/an |
| 741 | 40 | 35.7 | 829 | 3 | AAW58894 | Aaw58894 Breast an | 814 | 40 | 35.7 | 2828 | 8 | ADN38740 | ADn38740 Cancer/an |
| 742 | 40 | 35.7 | 904 | 8 | ADG57715 | ADg57715 Novel hum | 815 | 40 | 35.7 | 2828 | 8 | ADN02241 | ADn02241 Human OCP |
| 743 | 40 | 35.7 | 1002 | 3 | AAW38741 | AAw38741 Arabidops | 816 | 40 | 35.7 | 2828 | 8 | ADQ17737 | ADq17737 Human sof |
| 744 | 40 | 35.7 | 1002 | 5 | ABW92602 | ABw92602 Herbicida | 817 | 40 | 35.7 | 2828 | 8 | ADP67221 | ADp67221 Human bla |
| 745 | 40 | 35.7 | 1019 | 7 | ADP04162 | ADp04162 Bacterial | 818 | 40 | 35.7 | 2845 | 8 | ABP70049 | ABp70049 Human NOV |
| 746 | 40 | 35.7 | 1024 | 5 | ABBO4821 | ABbo4821 LDL recep | 819 | 40 | 35.7 | 3432 | 6 | ABU41925 | ABu41925 Protein e |
| 747 | 40 | 35.7 | 1024 | 5 | ABBO4818 | ABbo4818 LDL recep | 820 | 40 | 35.7 | 3432 | 6 | ABU15709 | ABu15709 Protein e |
| 748 | 40 | 35.7 | 1048 | 8 | ABO84803 | ABo84803 Murine ca | 821 | 40 | 35.7 | 5266 | 4 | ABG080551 | ABg080551 Novel hum |
| 749 | 40 | 35.7 | 1052 | 3 | AAW26846 | AAw26846 Human WAS | 822 | 40 | 35.7 | 5385 | 4 | ABG66467 | ABg66467 Drosophi1 |
| 750 | 40 | 35.7 | 1052 | 3 | AAW26389 | AAw26389 Human ORF | 823 | 40 | 35.7 | 5496 | 4 | ABW67161 | ABw67161 Drosophi1 |
| 751 | 40 | 35.7 | 1052 | 8 | ADJ75547 | ADj75547 Marker ge | 824 | 40 | 35.7 | 8805 | 4 | ABW67112 | ABw67112 Drosophi1 |
| 752 | 40 | 35.7 | 1052 | 8 | ADJ75508 | ADj75508 Marker ge | 825 | 39.5 | 35.3 | 90 | 4 | ABG26817 | ABg26817 Novel hum |
| 753 | 40 | 35.7 | 1052 | 8 | ABO84804 | ABo84804 Human can | 826 | 39.5 | 35.3 | 112 | 4 | AAW78889 | AAw78889 C. glutam |
| 754 | 40 | 35.7 | 1053 | 8 | ADN05216 | ADn05216 Antipsoxi | 827 | 39.5 | 35.3 | 173 | 8 | ADG45861 | ADg45861 Staphyloc |
| 755 | 40 | 35.7 | 1093 | 8 | ADO20339 | ADo20339 Human PRO | 828 | 39.5 | 35.3 | 202 | 3 | AAW90336 | AAw90336 B. subtili |

| | | | | | | | | | | | | | |
|-----|------|------|------|---|----------|----------------------|-----|----|------|-----|---|----------|---------------------|
| 829 | 39.5 | 35.3 | 203 | 3 | AAB39147 | Aab39147 Human sec | 902 | 39 | 34.8 | 64 | 4 | AAW29753 | Aam29753 Peptide # |
| 830 | 39.5 | 35.3 | 205 | 3 | AAB39146 | Aab39146 Human sec | 903 | 39 | 34.8 | 64 | 4 | ABR31068 | Abb31068 Peptide # |
| 831 | 39.5 | 35.3 | 234 | 3 | AAG58926 | Aag58926 Arachidop | 904 | 39 | 34.8 | 64 | 4 | ABR21630 | Abb21630 Protein # |
| 832 | 39.5 | 35.3 | 247 | 3 | ADA34361 | Ada34361 Actinotoba | 905 | 39 | 34.8 | 64 | 4 | AAW69422 | Aam69422 Human bon |
| 833 | 39.5 | 35.3 | 272 | 8 | ADS24473 | Ad24473 Bacterial | 906 | 39 | 34.8 | 64 | 4 | AAW57032 | Aam57032 Human bon |
| 834 | 39.5 | 35.3 | 278 | 6 | ABU43379 | Abu43379 Protein e | 907 | 39 | 34.8 | 64 | 4 | ABG51096 | Abg51096 Human liv |
| 835 | 39.5 | 35.3 | 281 | 8 | ADN17501 | Adn17501 Bacterial | 908 | 39 | 34.8 | 64 | 4 | AAW04947 | Aam04947 Human liv |
| 836 | 39.5 | 35.3 | 329 | 2 | AAV05304 | Aav05304 S. aureus | 909 | 39 | 34.8 | 64 | 5 | ABG39042 | Abg39042 Human pep |
| 837 | 39.5 | 35.3 | 329 | 6 | ABM71215 | Abm71215 Stephyloc | 910 | 39 | 34.8 | 66 | 5 | ABP35526 | Abp35526 Human ORF |
| 838 | 39.5 | 35.3 | 340 | 6 | ABR47442 | Ab47442 Breast ca | 911 | 39 | 34.8 | 79 | 6 | ABW73464 | Abw73464 Stephyloc |
| 839 | 39.5 | 35.3 | 344 | 8 | ADJ35104 | Adj35104 Xylanase | 912 | 39 | 34.8 | 88 | 5 | ABP34686 | Abp34686 Human ORF |
| 840 | 39.5 | 35.3 | 376 | 6 | ABU07702 | Abu07702 Viral coa | 913 | 39 | 34.8 | 93 | 8 | ADR94497 | Adr94497 Novel S. |
| 841 | 39.5 | 35.3 | 474 | 8 | ADP74742 | Adp74742 HIV-1 iso | 914 | 39 | 34.8 | 100 | 8 | ADL88961 | Adl88961 Human mod |
| 842 | 39.5 | 35.3 | 481 | 5 | ABB91095 | Abb91095 Herbidicida | 915 | 39 | 34.8 | 100 | 8 | ADL88965 | Adl88965 Human mod |
| 843 | 39.5 | 35.3 | 483 | 4 | ABG67447 | Abg67447 Amino ac1 | 916 | 39 | 34.8 | 100 | 8 | ADL88956 | Adl88956 Human mod |
| 844 | 39.5 | 35.3 | 506 | 6 | ABU07703 | Abu07703 Viral coa | 917 | 39 | 34.8 | 103 | 4 | AAW33022 | Aaw33022 Human pro |
| 845 | 39.5 | 35.3 | 506 | 6 | ABU07700 | Abu07700 Viral coa | 918 | 39 | 34.8 | 105 | 5 | ABB54361 | Abb54361 Lactococc |
| 846 | 39.5 | 35.3 | 528 | 6 | AAE39562 | Aae39562 HIV SP120 | 919 | 39 | 34.8 | 107 | 4 | ABR17941 | Abbr17941 Human ner |
| 847 | 39.5 | 35.3 | 528 | 8 | ADK19375 | Adk19375 HIV SP120 | 920 | 39 | 34.8 | 108 | 5 | ABP07717 | Abp07717 Human ORF |
| 848 | 39.5 | 35.3 | 552 | 5 | ABB57060 | Abb57060 Mouse isc | 921 | 39 | 34.8 | 119 | 7 | AAU17072 | Aau17072 Novel sig |
| 849 | 39.5 | 35.3 | 554 | 4 | AAW92446 | Aaw92446 Human pro | 922 | 39 | 34.8 | 119 | 4 | AAW43643 | Aaw43643 Human pol |
| 850 | 39.5 | 35.3 | 554 | 5 | ABB97251 | Abb97251 Novel hum | 923 | 39 | 34.8 | 119 | 4 | AAW87634 | Aaw87634 Novel cen |
| 851 | 39.5 | 35.3 | 554 | 8 | ADF89891 | Adf89891 Human can | 924 | 39 | 34.8 | 119 | 4 | ABR17239 | Abbr17239 Human ner |
| 852 | 39.5 | 35.3 | 556 | 6 | ABU07696 | Abu07696 Viral coa | 925 | 39 | 34.8 | 119 | 6 | ABO27195 | Ab027195 Human sig |
| 853 | 39.5 | 35.3 | 578 | 6 | AAE39560 | Aae39560 HIV SP120 | 926 | 39 | 34.8 | 119 | 7 | ADB93780 | Adb93780 Human nov |
| 854 | 39.5 | 35.3 | 579 | 2 | AAW37068 | Aaw37068 HIV-1 gp1 | 927 | 39 | 34.8 | 119 | 8 | ADL54949 | Adl54949 Novel hum |
| 855 | 39.5 | 35.3 | 587 | 2 | AAV29900 | Aav29900 Human MDC | 928 | 39 | 34.8 | 119 | 8 | ADM24664 | Adm24664 Human PRO |
| 856 | 39.5 | 35.3 | 590 | 6 | ABU07697 | Abu07697 Viral coa | 929 | 39 | 34.8 | 120 | 5 | ABP00580 | Abp00580 Human ORF |
| 857 | 39.5 | 35.3 | 595 | 2 | AAV29902 | Aav29902 Human MCP | 930 | 39 | 34.8 | 121 | 6 | ABU21032 | Abu21032 Protein e |
| 858 | 39.5 | 35.3 | 601 | 2 | AAV29901 | Aav29901 Human IP- | 931 | 39 | 34.8 | 122 | 2 | AAE5908 | Aae5908 Protein f |
| 859 | 39.5 | 35.3 | 608 | 4 | AAW88888 | Aaw88888 C. glutam | 932 | 39 | 34.8 | 122 | 3 | AAW35810 | Aaw35810 Rice chlo |
| 860 | 39.5 | 35.3 | 608 | 4 | AAW88885 | Aaw88885 C. glutam | 933 | 39 | 34.8 | 122 | 5 | ABP60740 | Abp60740 Oryza sat |
| 861 | 39.5 | 35.3 | 618 | 7 | ABR63526 | Ab63526 C. glutam | 934 | 39 | 34.8 | 122 | 7 | ADW59274 | Adw59274 Rice thio |
| 862 | 39.5 | 35.3 | 618 | 7 | ADD13252 | Ad13252 C. glutam | 935 | 39 | 34.8 | 124 | 6 | ABU45547 | Abu45547 Protein e |
| 863 | 39.5 | 35.3 | 618 | 7 | ADL65915 | Adl65915 C. glutam | 936 | 39 | 34.8 | 137 | 1 | AAW70101 | Aaw70101 Sequence |
| 864 | 39.5 | 35.3 | 625 | 8 | ADS30749 | Ads30749 Bacterial | 937 | 39 | 34.8 | 147 | 4 | AAW61340 | Aaw61340 Human AFP |
| 865 | 39.5 | 35.3 | 657 | 4 | AAU33784 | Aau33784 Stephyloc | 938 | 39 | 34.8 | 147 | 6 | ABW70029 | Abw70029 Photorhab |
| 866 | 39.5 | 35.3 | 662 | 3 | AAW80632 | Aaw80632 Amino ac1 | 939 | 39 | 34.8 | 151 | 4 | ABW68804 | Abw68804 Drosophill |
| 867 | 39.5 | 35.3 | 662 | 4 | AAU36547 | Aau36547 Stephyloc | 940 | 39 | 34.8 | 151 | 5 | ABW52093 | Abw52093 Helicobac |
| 868 | 39.5 | 35.3 | 662 | 6 | ABU15918 | Abu15918 Protein e | 941 | 39 | 34.8 | 156 | 3 | AAW82525 | Aaw82525 Human ade |
| 869 | 39.5 | 35.3 | 662 | 6 | ABU43213 | Abu43213 Protein e | 942 | 39 | 34.8 | 156 | 6 | AAW9865 | Aaw9865 Phycomit |
| 870 | 39.5 | 35.3 | 662 | 6 | ABW71307 | Abw71307 Stephyloc | 943 | 39 | 34.8 | 156 | 5 | ADG79580 | Adg79580 Human sec |
| 871 | 39.5 | 35.3 | 669 | 6 | ABU20985 | Abu20985 Protein e | 944 | 39 | 34.8 | 163 | 6 | AAO26451 | Aao26451 Human chl |
| 872 | 39.5 | 35.3 | 687 | 6 | ADA89613 | Ada89613 Stephyloc | 945 | 39 | 34.8 | 169 | 6 | ABU16898 | Abu16898 Protein e |
| 873 | 39.5 | 35.3 | 720 | 6 | ABU07694 | Abu07694 Viral coa | 946 | 39 | 34.8 | 170 | 7 | ADH66871 | Adh66871 Enterococ |
| 874 | 39.5 | 35.3 | 720 | 6 | ABU07695 | Abu07695 Viral coa | 947 | 39 | 34.8 | 171 | 6 | ADA33496 | Ada33496 Actinotoba |
| 875 | 39.5 | 35.3 | 722 | 8 | ADN22998 | Adn22998 Bacterial | 948 | 39 | 34.8 | 182 | 4 | ABE61187 | Abb61187 Drosophill |
| 876 | 39.5 | 35.3 | 732 | 2 | AAW11056 | Aaw11056 Acylamino | 949 | 39 | 34.8 | 184 | 6 | ABU62886 | Abu62886 Rab-Famil |
| 877 | 39.5 | 35.3 | 748 | 6 | ABU20785 | Abu20785 Protein e | 950 | 39 | 34.8 | 184 | 7 | ADE59010 | Ad59010 Rat Prote |
| 878 | 39.5 | 35.3 | 751 | 8 | ADW29971 | Adw29971 Bacterial | 951 | 39 | 34.8 | 184 | 7 | ADE59012 | Ad59012 Human pro |
| 879 | 39.5 | 35.3 | 753 | 1 | AAW94265 | Aaw94265 Sequence | 952 | 39 | 34.8 | 184 | 7 | ADG31704 | Adg31704 Human pro |
| 880 | 39.5 | 35.3 | 844 | 5 | AAE18308 | Aae18308 Human imm | 953 | 39 | 34.8 | 184 | 8 | ADW55215 | Adw55215 Human Rab |
| 881 | 39.5 | 35.3 | 854 | 5 | AAW48950 | Aaw48950 HIV-1 sub | 954 | 39 | 34.8 | 184 | 8 | ABW60954 | Abw60954 Tumour-ab |
| 882 | 39.5 | 35.3 | 855 | 2 | AAW41905 | Aaw41905 HIV-1 BA- | 955 | 39 | 34.8 | 184 | 8 | ADP23197 | Adp23197 PRO polyp |
| 883 | 39.5 | 35.3 | 855 | 2 | AAW11581 | Aaw11581 Human imm | 956 | 39 | 34.8 | 185 | 8 | ADW21857 | Adw21857 Human ves |
| 884 | 39.5 | 35.3 | 855 | 2 | AAW88113 | Aaw88113 Env prote | 957 | 39 | 34.8 | 187 | 5 | ABP66967 | Abp66967 Human pol |
| 885 | 39.5 | 35.3 | 855 | 3 | AAW89351 | Aaw89351 HIV-1 non | 958 | 39 | 34.8 | 187 | 5 | ADG79397 | Adg79397 Human sec |
| 886 | 39.5 | 35.3 | 858 | 3 | AAW48951 | Aaw48951 HIV-1 sub | 959 | 39 | 34.8 | 187 | 5 | ADG79480 | Adg79480 Human sec |
| 887 | 39.5 | 35.3 | 858 | 4 | ABW60145 | Abw60145 Drosophill | 960 | 39 | 34.8 | 187 | 6 | AAO26450 | Aao26450 Human chl |
| 888 | 39.5 | 35.3 | 1330 | 7 | ADW61063 | Adw61063 Rat Prote | 961 | 39 | 34.8 | 187 | 6 | ADW44585 | Adw44585 Novel hum |
| 889 | 39.5 | 35.3 | 1332 | 7 | ADP09883 | Adp09883 CDK1P1 c | 962 | 39 | 34.8 | 190 | 5 | ABP73450 | Abp73450 Candida a |
| 890 | 39.5 | 35.3 | 14 | 3 | AAW60978 | Aaw60978 Bovine 63 | 963 | 39 | 34.8 | 194 | 5 | ADP94728 | Adp94728 Hepaticac |
| 891 | 39.5 | 35.3 | 14 | 3 | ABU58717 | Abu58717 Bovine br | 964 | 39 | 34.8 | 205 | 5 | ABU50891 | Abu50891 Helicobac |
| 892 | 39.5 | 35.3 | 14 | 8 | ADQ94948 | Adq94948 Bovine 63 | 965 | 39 | 34.8 | 208 | 4 | AAW31549 | Aaw31549 Novel hum |
| 893 | 39.5 | 35.3 | 46 | 1 | AAW80509 | Aaw80509 Polypept1 | 966 | 39 | 34.8 | 210 | 2 | AAW31641 | Aaw31641 Human tra |
| 894 | 39.5 | 35.3 | 46 | 6 | AAO26454 | Aao26454 Human chl | 967 | 39 | 34.8 | 210 | 8 | ADW23725 | Adw23725 COP1 coat |
| 895 | 39.5 | 35.3 | 48 | 6 | AAO26465 | Aao26465 Human chl | 968 | 39 | 34.8 | 214 | 4 | AAW43569 | Aaw43569 Human pol |
| 896 | 39.5 | 35.3 | 52 | 4 | AAW92022 | Aaw92022 Human dig | 969 | 39 | 34.8 | 214 | 4 | AAW87352 | Aaw87352 Novel cen |
| 897 | 39.5 | 35.3 | 52 | 4 | AAU20000 | Aau20000 Human liv | 970 | 39 | 34.8 | 214 | 8 | ADW54667 | Adw54667 Novel hum |
| 898 | 39.5 | 35.3 | 52 | 4 | ABP40861 | Abp40861 Human liv | 971 | 39 | 34.8 | 214 | 8 | ADM24550 | Adm24550 Human PRO |
| 899 | 39.5 | 35.3 | 52 | 7 | ADJ14979 | Adj14979 Human liv | 972 | 39 | 34.8 | 215 | 4 | ABW63850 | Abw63850 Drosophill |
| 900 | 39.5 | 35.3 | 64 | 4 | AAW17258 | Aaw17258 Peptide # | 973 | 39 | 34.8 | 216 | 5 | ABU51709 | Abu51709 Helicobac |
| 901 | 39.5 | 35.3 | 64 | 4 | ABW36257 | Abw36257 Peptide # | 974 | 39 | 34.8 | 230 | 3 | AAW96099 | Aaw96099 Human ald |

| | | | | | | | |
|------|----|------|-----|---|----------|----------|-----------|
| 975 | 39 | 34.8 | 230 | 3 | AAV90353 | hag90353 | Human gly |
| 976 | 39 | 34.8 | 230 | 4 | AA84681 | hah84681 | Amino aci |
| 977 | 39 | 34.8 | 230 | 5 | ABP65425 | abp65425 | Bifidobac |
| 978 | 39 | 34.8 | 230 | 6 | AA026544 | aa026544 | Human ald |
| 979 | 39 | 34.8 | 238 | 6 | ABU5159 | abu5159 | Protein e |
| 980 | 39 | 34.8 | 239 | 8 | ADS42137 | ads42137 | Bacterial |
| 981 | 39 | 34.8 | 241 | 5 | ABU52152 | abu52152 | Helicobac |
| 982 | 39 | 34.8 | 242 | 2 | AA45020 | aa45020 | Staphyloc |
| 983 | 39 | 34.8 | 242 | 4 | AA67347 | aa67347 | Staphyloc |
| 984 | 39 | 34.8 | 242 | 5 | AB876243 | ab876243 | Staphyloc |
| 985 | 39 | 34.8 | 242 | 8 | ABM83829 | abm83829 | Human dia |
| 986 | 39 | 34.8 | 244 | 4 | AA681950 | aa681950 | S. epider |
| 987 | 39 | 34.8 | 256 | 3 | AA642482 | aa642482 | Arabidops |
| 988 | 39 | 34.8 | 256 | 3 | AA644055 | aa644055 | Arabidops |
| 989 | 39 | 34.8 | 256 | 6 | ABM69042 | abm69042 | Phototrab |
| 990 | 39 | 34.8 | 260 | 3 | AA642130 | aa642130 | Arabidops |
| 991 | 39 | 34.8 | 260 | 5 | AA616385 | aa616385 | Human deo |
| 992 | 39 | 34.8 | 260 | 6 | AA026448 | aa026448 | Deoxycytl |
| 993 | 39 | 34.8 | 260 | 6 | AA026449 | aa026449 | Deoxycytl |
| 994 | 39 | 34.8 | 260 | 6 | AA026446 | aa026446 | Deoxycytl |
| 995 | 39 | 34.8 | 260 | 6 | ABU48008 | abu48008 | Protein e |
| 996 | 39 | 34.8 | 260 | 7 | ADJ68602 | adj68602 | Human hea |
| 997 | 39 | 34.8 | 260 | 7 | ADN95414 | adn95414 | Human BEC |
| 998 | 39 | 34.8 | 260 | 8 | ADR73958 | adr73958 | Human deo |
| 999 | 39 | 34.8 | 260 | 8 | ADR73958 | adr73958 | Human deo |
| 1000 | 39 | 34.8 | 260 | 8 | ADR73962 | adr73962 | Human deo |

ALIGNMENTS

RESULT 1
AD195325
ID AD195325 standard; protein; 221 AA.

AC AD195325;

DT 04-NOV-2004 (first entry)

XX OSPF-related SARS coronavirus matrix protein.

XX immune response; overlapping synthetic peptide formulation; OSPF;
KM immunostimulant; virucide; antibacterial; antiparasitic; cytostatic;
KW vaccine; viral; bacterial; parasitic infection; prion disease;
KM neoplastic; toxin; matrix.

OS SARS coronavirus.

PN WO2004002415-A2.

PD 08-JAN-2004.

PF 27-JUN-2003; 2003WO-US020322.

PR 27-JUN-2002; 2002US-0392718P.

PA (DAND) DANA FARBER CANCER INST INC.

PI Ruprecht RM, Jiang S;

DR WPI; 2004-082868/08.

XX Modulating an immune response, useful for treating immune disorders, e.g.,
PT viral, bacterial and parasitic infections, prion diseases, or neoplastic
PT diseases, administering to a subject an overlapping synthetic peptide
PT formulation.

XX Claim 13; SEQ ID NO 233; 175bp; English.

XX The invention relates to a novel method for modulating an immune response
CC comprising administering to a subject an overlapping synthetic peptide
CC formulation (OSPF) which comprises a combination of single chain peptides
CC corresponding to the amino acid sequence of a protein of interest. The

CC method of the invention has immunostimulant, virucide, antibacterial,
CC antiparasitic and cytostatic applications and may be useful during
CC vaccine production and for treating immune disorders including viral,
CC bacterial and parasitic infections, prion diseases, neoplastic diseases,
CC as well as providing protection against toxins. The current sequence is
CC that of the OSPF-related SARS coronavirus matrix protein of the
CC invention.

XX Sequence 221 AA;

SQ Query Match 100.0%; Score 112; DB 8; Length 221;
Best Local Similarity 100.0%; Pred.No.2.7e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MADNGTITVEELKQLEQNNLV 22
1 MADNGTITVEELKQLEQNNLV 22

Db 1 MADNGTITVEELKQLEQNNLV 22
ABM67171
ID ABM67171 standard; protein; 16368 AA.

AC ABM67171;

XX 20-NOV-2003 (first entry)

XX Photorhabdus luminescens protein sequence #268.

DE Photorhabdus luminescens protein sequence #268.
XX Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;
KM detection; food; gene expression; plant; animal; microorganism; toxin;
KW antibiotic; bioplasticide; virulence factor; disease model; plague;
KM whooping cough.

XX Photorhabdus luminescens.

OS Photorhabdus luminescens.

PN WO200294867-A2.

PD 28-NOV-2002.

PF 07-FEB-2002; 2002WO-1B003040.

PR 07-FEB-2001; 2001FR-00001659.

PA (INSP) INST PASTEUR.

PI (CNRS) CNRS CENT NAT RECH SCI.

PN Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst F, Danchin A;

PT Buchrieser C;

DR WPI; 2003-148459/14.

PF Genomic sequence of Photorhabdus luminescens and encoded polypeptides,
PT useful e.g. as therapeutic antimicrobials and agricultural pesticides.

PA Claim 2; SEQ ID NO 268; 1205bp; French.

XX The invention relates to the isolation of genes and their encoded
CC proteins from Photorhabdus luminescens. The isolated sequences are
CC sources of probes and primers for detecting the genome of P. luminescens
CC and related species; to study polymorphisms; for gene analysis and for
CC detection/amplification of the genes. Antibodies (Ab) raised against the
CC polypeptides encoded by the genes are used for detection/identification
CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that
CC carry a gene-containing vector are used to select compounds that
CC modulate, regulate, induce or inhibit expression of the genes in plants,
CC animals or microorganisms other than P. luminescens and are able to alter
CC response or sensitivity to toxins and antibiotics produced by P.
CC luminescens. Cells transformed to express the genes are useful for
CC recombinant production of the proteins, particularly toxins and
CC antibacterials useful as insecticides, bactericides and fungicides. The
CC genes, proteins, vectors containing the genes and Ab are also useful
CC therapeutically (to treat microbial infection by bacteria or fungi that

CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as
 CC biopesticides. Other uses of the genes and the proteins are as virulence
 CC factors and for identifying targets of human diseases for which P.
 CC luminescens is a model (particularly plague and whooping cough). This
 CC sequence represents one of the isolated P. luminescens proteins
 XX

SQ Sequence 16368 AA;

Query Match 46.4%; Score 52; DB 6; Length 16368;
 Best Local Similarity 71.4%; Pred. No. 4.5e+03;
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 7 ITVEELKQLLEQWN 20
 :|||:|
 Db 14404 LTVERKLLLESWN 14417

RESULT 3

AA19303
 ID AAM19303 standard; protein; 54 AA.

AC AAM19303;

DT 12-OCT-2001 (first entry)

DE Peptide #5737 encoded by probe for measuring cervical gene expression.

KW Probe; human; microarray; gene expression; cervical epithelial cell;
 cervical cancer.

OS Homo sapiens.

PN WO200157278-A2.

XX 09-AUG-2001.

PD 30-JAN-2001; 2001WO-US000670.

PF 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

PA Penn SG, Hanzel DK, Chen W, Rank DR;

PI WPI; 2001-488901/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

PT gene expression in human cervical epithelial cells.

XX Claim 27; SEQ ID NO 24129; 487pp; English.

CC The present invention relates to human single exon nucleic acid probes
 CC (SENPs; see AAM10068-AA128459). The present sequence is a peptide encoded
 CC by one such probe. The SENPs are derived from human HeLa cells. The SENPs
 CC can be used to produce a single exon microarray, which can be used for
 CC measuring human gene expression in a sample derived from human cervical
 CC epithelial cells. By measuring gene expression, the probes are therefore
 CC useful in grading and/or staging of diseases of the cervix, notably
 CC cervical cancer. Note: The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX

SO Sequence 54 AA;

Query Match 45.5%; Score 51; DB 4; Length 54;
 Best Local Similarity 42.9%; Pred. No. 15;
 Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MADNGITVEELKQLLEQWNL 21
 :|||:|
 Db 23 LEDKQVSVFEAKNRARQMNIV 43

RESULT 4

ABB38595
 ID ABB38595 standard; peptide; 54 AA.

AC ABB38595;

DT 04-FEB-2002 (first entry)

DE Peptide #6101 encoded by human foetal liver single exon probe.

KW Human; foetal liver; gene expression; single exon nucleic acid probe.

OS Homo sapiens.

PN WO200157277-A2.

XX 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US000669.

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

PA Penn SG, Hanzel DK, Chen W, Rank DR;

PI WPI; 2001-483447/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

PT gene expression in human fetal liver.

XX Claim 27; SEQ ID NO 31230; 639pp + Sequence Listing; English.

CC The invention relates to a single exon nucleic acid probe for measuring
 CC human gene expression in a sample derived from human foetal liver. The
 CC single exon nucleic acid probes may be used for predicting, measuring and
 CC displaying gene expression in samples derived from human fetal liver. The
 CC present sequence is a peptide encoded by a single exon nucleic acid probe
 CC of the invention. Note: The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX

SO Sequence 54 AA;

Query Match 45.5%; Score 51; DB 4; Length 54;
 Best Local Similarity 42.9%; Pred. No. 15;
 Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MADNGITVEELKQLLEQWNL 21
 :|||:|
 Db 23 LEDKQVSVFEAKNRARQMNIV 43

RESULT 5
 AAM32049
 ID AAM32049 standard; protein; 54 AA.

AC AAM32049;

DT 17-OCT-2001 (first entry)

XX

DE Peptide #6086 encoded by probe for measuring placental gene expression.
XX
XX Probe; microarray; human; placenta; antenatal diagnosis;
KM genetic disorder.
XX
OS Homo sapiens.
XX
XX WO200157272-A2.
XX
XX PD 09-AUG-2001.
XX
XX PF 30-JAN-2001; 2001WO-US000663.
XX
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488897/53.
XX
XX DR WPI; 2001-488897/53.
XX
XX PT Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human placenta.
XX
XX PS Claim 27; SEQ ID NO 32318; 654pp; English.
XX
XX CC The present invention relates to single exon nucleic acid probes (SENP;
XX see AAI31315-AA157546). The present sequence is a peptide encoded by one
XX such probe. The probes are useful for producing a microarray for
XX predicting, measuring and displaying gene expression in samples derived
XX from human placenta. The probes are useful for antenatal diagnosis of
XX human genetic disorders
XX
XX SQ Sequence 54 AA;

Query Match 45.5%; Score 51; DB 4; Length 54;
Best Local Similarity 42.9%; Pred. No. 15;
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 MADNGTIVBELKQLEQNL 21
DB 23 LEDKQVSVBEAKNRAQNMV 43

RESULT 6
ABB23710
ID ABB23710 standard; protein; 54 AA.
XX
XX AC ABB23710;
XX
XX DT 23-JAN-2002 (first entry)
XX
XX DE Protein #5709 encoded by probe for measuring heart cell gene expression.
XX
XX KW Human; gene expression; heart; microarray; vascular system;
XX cardiovascular disease; hypertension; cardiac arrhythmia;
XX congenital heart disease.
XX
XX OS Homo sapiens.
XX
XX PN WO200157274-A2.
XX
XX PD 09-AUG-2001.
XX
XX PF 30-JAN-2001; 2001WO-US000666.
XX
XX PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488899/53.
XX
XX DR WPI; 2001-488899/53.
XX
XX PT Single exon nucleic acid probes for analyzing gene expression in human
XX hearts.
XX
XX PS Claim 15; SEQ ID NO 25480; 530pp; English.
XX
XX CC The present invention relates to single exon nucleic acid probes for
XX measuring human gene expression in a sample derived from human heart (see
XX ABA21535-ABA41305). The present sequence is a protein encoded by one such
XX probe. The probes may be used for predicting, measuring and displaying
XX gene expression in samples derived from the human heart via microarrays.
XX CC By measuring gene expression, the probes are useful for predicting,
XX diagnosing, grading, staging, monitoring and prognosing diseases of the
XX human heart and vascular system e.g. cardiovascular disease,
XX hypertension, cardiac arrhythmias and congenital heart disease. Note: The
XX sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 54 AA;

Query Match 45.5%; Score 51; DB 4; Length 54;
Best Local Similarity 42.9%; Pred. No. 15;
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 MADNGTIVBELKQLEQNL 21
DB 23 LEDKQVSVBEAKNRAQNMV 43

RESULT 7
AAM71757
ID AAM71757 standard; protein; 54 AA.
XX
XX AC AAM71757;
XX
XX DT 06-NOV-2001 (first entry)
XX
XX DE Human bone marrow expressed probe encoded protein SEQ ID NO: 32063.
XX
XX KW Human; bone marrow expressed exon; gene expression analysis; probe;
XX microarray; cancer; leukemia; lymphoma; myeloma.
XX
XX OS Homo sapiens.
XX
XX PN WO200157276-A2.
XX
XX PD 09-AUG-2001.
XX
XX PF 30-JAN-2001; 2001WO-US000668.
XX
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX
XX PA (MOLE-) MOLECULAR DYNAMICS INC.

| | |
|-----------------------|---|
| PI | Penn SG, Hanzel DK, Chen W, Rank DR; |
| XX | |
| DR | WPI; 2001-488900/53. |
| XX | |
| PT | Human genome-derived single exon nucleic acid probes useful for analyzing |
| PT | gene expression in human bone marrow. |
| XX | |
| PS | Example 4; SEQ ID NO 32063; 658bp + Sequence Listing; English. |
| XX | |
| CC | The present invention provides a number of single exon nucleic acid |
| CC | probes which are derived from genomic sequences expressed in the human |
| CC | bone marrow. They can be used to measure gene expression in bone marrow |
| CC | samples, which may enable the improved diagnosis and treatment of cancers |
| CC | such as lymphoma, leukemia and myeloma. The present sequence is a |
| CC | protein encoded by one of the probes of the invention |
| XX | |
| SO | Sequence 54 AA; |
| | |
| Query Match | 45.5%; Score 51; DB 4; Length 54; |
| Best Local Similarity | 42.9%; Pred. No. 15; |
| Matches | 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0 |
| | |
| Oy | 1 MADNGTVEELKOLEQONTL 21 |
| | : : : : : : : : |
| Db | 23 LEDKKQVSVSEAKRAEQMNV 43 |
| | |
| RESULT 8 | |
| AAM59222 | |
| ID | AAM59222 standard; protein; 54 AA. |
| XX | |
| AC | AAM59222; |
| XX | |
| DT | 05-NOV-2001 (first entry) |
| XX | |
| DE | Human brain expressed single exon probe encoded protein SEQ ID NO: 31327. |
| XX | |
| XX | Human; brain expressed exon; gene expression analysis; probe; microarray; |
| KM | Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer. |
| XX | |
| OS | Homo sapiens. |
| XX | |
| FN | WO200157275-A2. |
| XX | |
| PD | 09-AUG-2001. |
| XX | |
| PF | 30-JAN-2001; 2001WO-US000667. |
| XX | |
| PR | 04-FEB-2000; 2000US-0180312P. |
| PR | 26-MAY-2000; 2000US-0207456P. |
| PR | 30-JUN-2000; 2000US-00608408. |
| PR | 03-AUG-2000; 2000US-00632366. |
| PR | 21-SEP-2000; 2000US-0234687P. |
| PR | 27-SEP-2000; 2000US-0236359P. |
| PR | 04-OCT-2000; 2000GB-00024263. |
| XX | |
| PA | (MOLE-) MOLECULAR DYNAMICS INC. |
| XX | |
| PI | Penn SG, Hanzel DK, Chen W, Rank DR; |
| XX | |
| DR | WPI; 2001-483446/52. |
| XX | |
| PT | Single exon nucleic acid probes for analyzing gene expression in human |
| PT | brains. |
| XX | |
| PS | Example 4; SEQ ID NO 31327; 650bp + Sequence Listing; English. |
| XX | |
| CC | The present invention provides a number of single exon nucleic acid |
| CC | probes which are derived from genomic sequences expressed in the human |
| CC | brain. They can be used to measure gene expression in brain cell samples, |
| CC | which may enable the diagnosis and improved treatment of nervous system |
| CC | diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, |
| CC | epilepsy and cancers. The present sequence is a protein encoded by one of |

| | |
|-----------------------|---|
| CC | the probes of the invention |
| SQ | Sequence 54 AA; |
| Query Match | 45.5%; Score 51; DB 4; Length 54; |
| Best Local Similarity | 42.9%; Pred. No. 15; |
| Matches | 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0; |
| Dn | 1 MADNGITVEELKQLLEQWNL 21 :: : :: 23 LEDRGVSVSEAKRAEQMNIV 43 |
| RESULT 9 | |
| ABG53442 | ID |
| ABG53442 | standard; peptide; 54 AA. |
| XX | ABG53442; |
| AC | |
| XX | 25-FEB-2003 (first entry) |
| DT | |
| XX | Human liver peptide, SEQ ID NO 32090. |
| DE | |
| XX | Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia; KM hypercholesterolaemia; coronary heart disease. XX OS Homo sapiens. XX PN WO200157273-A2. XX PD 09-AUG-2001. XX PF 30-JAN-2001; 2001WO-US000664. XX PR 04-FEB-2000; 2000US-0180312P. PR 26-MAY-2000; 2000US-0207456P. PR 30-JUN-2000; 2000US-00608408. PR 03-AUG-2000; 2000US-0063236P. PR 21-SEP-2000; 2000US-0234687P. PR 27-SEP-2000; 2000US-0236359P. PR 04-OCT-2000; 2000GB-00024263. XX PA (MOLE-) MOLECULAR DYNAMICS INC. XX PI Penn SG, Hanzel DK, Chen W, Rank DR; DR WPI; 2001-488898/53. PT Human genome-derived single exon nucleic acid probes useful for analyzing PT gene expression in human adult liver. XX PS Claim 27; SEQ ID NO 32090; 658bp; English. CC The invention relates to a single exon nucleic acid probe (SEN) (I) for CC measuring human gene expression in a sample derived from human adult CC liver, comprising one of 13109 defined nucleotide sequences given in the CC specification (or complements/ fragments). The probe hybridises at high CC stringency to a nucleic acid molecule expressed in the human adult liver. CC (I) may be used for predicting, measuring and displaying gene expression CC in samples derived from human adult liver. The genes identified may be CC involved in genetic liver diseases such as cirrhosis, CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is CC associated with coronary heart disease. ABG47348-ABG59930 represent human CC liver single exon encoded peptides of the invention. Note: The sequence CC information for this patent does not appear in the printed specification CC but was obtained in electronic format directly from WIPO at CC ftp.wipo.int/pub/published_pct_sequences SQ Sequence 54 AA; |
| Query Match | 45.5%; Score 51; DB 4; Length 54; |
| Best Local Similarity | 42.9%; Pred. No. 15; |
| Matches | 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0; |

OY 1 MADNCTIVEELKOLLEQONL 21
 : : : : :
 DB 23 LEDKROVSVEAKNRAEDQMN 43
 RESULT 10
 ID ABG41571
 ABG41571 standard; peptide; 54 AA.
 AC
 XX ABG41571;
 XX
 DT 19-AUG-2002 (first entry)
 DE
 XX Human peptide encoded by genome-derived single exon probe SEQ ID 31236.
 KW Human; single exon probe; asthma; lung cancer; COPD; ILD;
 KW chronic obstructive pulmonary disease; interstitial lung disease;
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
 KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
 KW Heremansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karsagen's syndrome;
 KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
 KW primary ciliary dyskinesia; pulmonary hypertension;
 KW hyaline membrane disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200186003-A2.
 XX
 PD 15-NOV-2001.
 XX
 PF 30-JAN-2001; 2001WO-US000665.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0235359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2002-114183/15.
 XX
 PT Spatially-addressable set of single exon nucleic acid probes, used to
 PT measure gene expression in human lung samples.
 XX
 PS Claim 27; SEQ ID NO 31236; 634pp; English.
 CC
 CC The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human lung comprising single exon nucleic acid probes having one of
 CC 12614 nucleic acid sequences mentioned in the specification, or their
 CC complements or the 12387 open reading frames derived from the 12614
 CC probes. Also included are a microarray comprising the novel set of probes
 CC; the novel set of probes which hybridise at high stringency to a nucleic
 CC acid expressed in the human lung; measuring gene expression in a sample
 CC derived from human lung, comprising (a) contacting the array with a
 CC collection of detectably labeled nucleic acids derived from human lung
 CC mRNA, and (b) measuring the label detectably bound to each probe of the
 CC array; identifying exons in a eukaryotic genome, comprising (a)
 CC algorithmically predicting at least one exon from genomic sequences of
 CC the eukaryote; and (b) detecting specific hybridisation to a nucleic
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
 CC having a fragment identical to the predicted exon, the probe is included
 CC in the above mentioned microarray; assigning exons to a single gene,
 CC comprising (a) identifying exons from genomic sequence by the method
 CC above and (b) measuring the expression of each of the exons in several
 CC tissues and/or cell types using hybridisation to a single exon

| | |
|-----------------------|---|
| CC | microarrays having a probe with the exon, where a common pattern of |
| CC | expression of the exons in the tissues and/or cell types indicates that |
| CC | the exons should be assigned to a single gene; a peptide comprising one |
| CC | of 12011 sequences, mentioned in the specification, or encoded by the |
| CC | probes/open reading frames (ORF). The probes are used for gene expression |
| CC | analysis and for identifying exons in a gene, particularly using human |
| CC | lung derived mRNA and for the study of lung diseases such as asthma, lung |
| CC | cancer, chronic obstructive pulmonary disease (COPD), interstitial lung |
| CC | disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis, |
| CC | tuberosus sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky- |
| CC | Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary |
| CC | histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis, |
| CC | Karagenen syndrome, fibrocystic pulmonary dysplasia, primary ciliary |
| CC | dyskinesia, pulmonary hypertension and hyaline membrane disease. The |
| CC | present sequence is a peptide/protein encoded by a single exon probe of |
| CC | the invention. Note: The sequence data for this patent did not form part |
| CC | of the printed specification, but was obtained in electronic format |
| CC | directly from WIPO at ftp.wipo.int/pub/published_pct_sequences |
| SQ | |
| SQ | Sequence 54 AA; |
| Query Match | 45.5%; Score 51; DB 5; Length 54; |
| Best Local Similarity | 42.9%; Pred. No. 15; |
| Matches | 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0 |
| OY | 1 MADNGTTTVEELKQLLEQWNL 21 : :: 23 LEDKROYSVBEAKNRAREQWNV 43 |
| Db | |
| ABU03494 | standard; protein; 206 AA. |
| ID | |
| XX | ABU03494 |
| AC | ABU03494; |
| XX | |
| DT | 21-JAN-2003 (first entry) |
| XX | |
| DE | Angiogenesis-associated human protein sequence #39. |
| XX | |
| KW | Human; angiogenesis-associated transcript; angiogenesis; angiogenesis-associated disease; cancer; cyrostatic. |
| OS | Homo sapiens. |
| XX | |
| PN | WO200279492-A2. |
| XX | |
| PD | 10-OCT-2002. |
| XX | |
| PF | 14-FEB-2002; 2002WO-US004915. |
| XX | |
| PR | 14-FEB-2001; 2001US-00784356. PR 22-FEB-2001; 2001US-00791390. ER 19-APR-2001; 2001US-0285475P. PR 03-AUG-2001; 2001US-0310025P. PR 13-NOV-2001; 2001US-0350666P. PR 29-NOV-2001; 2001US-0334244P. |
| XX | |
| PA | (EOSB-) EOS BIOTECHNOLOGY INC. |
| P1 | Murray R, Glynn R, Watson SR, Aziz N; |
| XX | |
| DR | WI: 2003-040681/03. |
| XX | |
| DR | N-PSDB; ABX08778. |
| XX | |
| FT | Detecting angiogenesis-associated transcript in a cell for diagnosing and |
| PT | treating cancer by contacting a sample with a polynucleotide that |
| XX | exhibits changes in expression level as a function of time in tissue |
| XX | undergoing angiogenesis. |
| XX | |
| XX | Example 2; Page 217; 29pp; English. |
| XX | |
| CC | The present invention relates to methods and compositions for detecting |

| | | | |
|----|---|--|-------------------------|
| DT | 02-DEC-2004 | (first entry) | |
| XX | | | |
| DE | POSH | protein associated | protein #53. |
| XX | | | |
| KW | cytostatic; | neurotropic; | neuroprotective; |
| KW | antiviral; | neuroleptic; | central nervous system; |
| KW | POSH-associated | protein; | POSH-AP; |
| KW | antiviral agent; | anti-apoptotic agent; | anti-cancer agent; |
| KW | secretory pathway | trafficking | inhibitor; |
| KW | neurological disorder | progression | disorder; |
| KW | Parkinson's disease; | Huntington's disease; | schizophrenia; |
| XX | Niemann-Pick's | disease. | |
| OS | Homo sapiens. | | |
| XX | | | |
| PN | WO2004078130-A2. | | |
| XX | | | |
| PD | 16-SEP-2004. | | |
| XX | | | |
| PP | 02-MAR-2004; | 2004WO-US006308. | |
| XX | | | |
| PR | 03-MAR-2003; | 2003US-0451437P. | |
| PR | 05-MAR-2003; | 2003US-0452284P. | |
| PR | 19-MAR-2003; | 2003US-0455760P. | |
| PR | 20-MAR-2003; | 2003US-0456640P. | |
| PR | 03-APR-2003; | 2003US-0460526P. | |
| PR | 04-APR-2003; | 2003US-0460792P. | |
| PR | 21-APR-2003; | 2003US-0464285P. | |
| PR | 09-MAY-2003; | 2003US-0469462P. | |
| PR | 15-MAY-2003; | 2003US-0471378P. | |
| PR | 20-MAY-2003; | 2003US-0472327P. | |
| PR | 30-MAY-2003; | 2003US-0474706P. | |
| PR | 03-JUN-2003; | 2003US-0475825P. | |
| PR | 17-JUN-2003; | 2003US-0479317P. | |
| PR | 19-JUN-2003; | 2003US-0480215P. | |
| PR | 19-JUN-2003; | 2003US-0480376P. | |
| PR | 08-AUG-2003; | 2003US-0493860P. | |
| PR | 28-AUG-2003; | 2003US-0498634P. | |
| PR | 16-SEP-2003; | 2003US-0503931P. | |
| PR | 10-NOV-2003; | 2003WO-US035712. | |
| PR | 05-FEB-2004; | 2004WO-US003600. | |
| PR | 02-MAR-2004; | 2004US-0549896P. | |
| XX | | | |
| PA | (PROT-) PROTEOLOGICS INC. | | |
| XX | | | |
| PI | Taglicht DN, Alroy I., | Reiss Y, Yaar L, Ben-Avraham D, Tuvia S; | |
| PI | Greener T; | | |
| XX | | | |
| DR | WPI; 2004-662346/64. | | |
| XX | | | |
| PT | Isolated, purified or recombinant complex, useful for identifying an | | |
| PT | antiviral, anti-apoptotic or anti-cancer, comprising POSH polypeptide and | | |
| PT | POSH-associated protein (POSH-AP). | | |
| XX | | | |
| PS | Disclosure; SEQ ID NO 253; 374DP; English. | | |
| XX | | | |
| CC | The invention relates to an isolated, purified or recombinant complex (I) | | |
| CC | comprising a POSH polypeptide and a POSH-associated protein (POSH-AP) (a) | | |
| CC | or HERPUDI and a ubiquitin ligase (b). Methods using (I), (a) or (b) are | | |
| CC | useful for identifying an agent that modulates an activity of a POSH | | |
| CC | polypeptide or POSH-AP, for identifying an antiviral agent, an anti- | | |
| CC | apoptotic agent, an anti-cancer agent, an agent that inhibits trafficking | | |
| CC | of a protein through the secretory pathway, an agent that inhibits the | | |
| CC | progression of a neurological disorder, an agent that modulates a POSH | | |
| CC | function, an agent that modulates a HERPUDI function. The methods can be | | |
| CC | used for creating a viral infection, for inhibiting an activity of a POSH | | |
| CC | -AP in a cell, for treating a POSH-associated disease in a subject. The | | |
| CC | POSH-associated disease is viral infection, POSH-associated cancer or | | |
| CC | POSH-associated neurological disorder. The methods are useful for | | |
| CC | treating or preventing POSH-associated neurological disorder in a subject | | |
| CC | e.g. Alzheimer's disease, Parkinson's disease, Huntington's disease, | | |
| CC | schizophrenia, Niemann-Pick's disease. This sequence corresponds to a | | |
| CC | protein of the invention. | | |

[illegible]

CC genetic profiles which aid in treating diseases and disorders (e.g.
CC cancer) based on patient response at a molecular level. The present
CC sequence is used in the exemplification of the present invention.
XX

Sequence 209 AA:

Query Match 45.5%; Score 51; DB 7; Length 209;
Best Local Similarity 42.9%; Pred. No. 62;
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 MADNGTIVBELKQLEQNMNL 21
134 LEDKQVSYVEAKNRABQNMNV 154

RESULT 18
ADP24705
ID ADP24705 standard; protein; 209 AA.

AC ADP24705;

DT 18-NOV-2004 (first entry)

DE PRO polypeptide SEQ ID NO:1883.

XX PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;
XX osteopathic; antidiabetic; dermatological; antiporiatic; antiallergic;
XX antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.

OS Unidentified.

PN WO2004041170-A2.

PD 21-MAY-2004.

PF 30-OCT-2003; 2003WO-US034312.

PR 01-NOV-2002; 2002US-0423394P.

XX (GETH) GENENTECH INC.

PI Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;

DR N-PSDB; ADP24704.

XX WPI; 2004-419628/39.

PT New PRO polypeptides and polynucleotides, useful for treating e.g.
PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
PT renal disease, or demyelinating diseases of the central or peripheral
PT nervous system.

XX Claim 7; SEQ ID NO 1883; 2940bp; English.

XX The invention relates to a novel isolated nucleic acid and the PRO
CC polypeptide encoded by it. A protein of the invention has
CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,
CC osteopathic, antidiabetic, dermatological, antiporiatic, antiallergic,
CC antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide
CC of the invention may have a use in gene therapy. The PRO polypeptide, its
CC agonist, antagonist, or antibody that specifically binds to the
CC polypeptide is useful for treating an immune related disorder such as
CC systemic lupus erythematous, rheumatoid arthritis, osteoarthritis,
CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
CC thrombocytopenia, thyroditis, diabetes mellitus, immune-mediated renal
CC disease, a demyelinating disease of the central or peripheral nervous
CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
CC disease, infectious or autoimmune chronic active hepatitis, primary
CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's

CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
CC disease, asthma, allergic rhinitis, atopic dermatitis, food
CC hypersensitivity, urticaria, an immunologic disease of the lung,
CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
CC pneumonitis, a transplantation associated disease, graft rejection or
CC graft-versus-host disease. The present sequence represents a PRO protein
CC of the invention.

Sequence 209 AA:

Query Match 45.5%; Score 51; DB 8; Length 209;
Best Local Similarity 42.9%; Pred. No. 62;
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 MADNGTIVBELKQLEQNMNL 21
134 LEDKQVSYVEAKNRABQNMNV 154

RESULT 19
ADS34490
ID ADS34490 standard; protein; 209 AA.

AC ADS34490;

DT 02-DEC-2004 (first entry)

DE POSH protein associated protein #54.

XX cytostatic; nocitropic; neuroprotective; antiparkinsonian; anticonvulsant;
XX antiviral; neuroleptic; central nervous system; POSH polypeptide;
XX POSH-associated protein; POSH-AP; HERPUD1; Ubiquitin ligase;
XX antiviral agent; anti-apoptotic agent; anti-cancer agent;
XX secretory pathway trafficking inhibitor;
XX neurological disorder progression disorder; Alzheimer's disease;
XX Parkinson's disease; Huntington's disease; schizophrenia;
XX Niemann-Pick's disease.

OS Homo sapiens.

PN WO2004078130-A2.

PD 16-SEP-2004.

PF 02-MAR-2004; 2004WO-US006308.

XX 03-MAR-2003; 2003US-0451437P.

PR 05-MAR-2003; 2003US-0452284P.

PR 19-MAR-2003; 2003US-0455760P.

PR 20-MAR-2003; 2003US-0456640P.

PR 03-APR-2003; 2003US-0460526P.

PR 04-APR-2003; 2003US-0460792P.

PR 21-APR-2003; 2003US-0464285P.

PR 09-MAY-2003; 2003US-0469462P.

PR 15-MAY-2003; 2003US-0471378P.

PR 20-MAY-2003; 2003US-0472327P.

PR 30-MAY-2003; 2003US-0474706P.

PR 03-JUN-2003; 2003US-0475825P.

PR 17-JUN-2003; 2003US-0479317P.

PR 19-JUN-2003; 2003US-0480215P.

PR 19-JUN-2003; 2003US-0480376P.

PR 08-AUG-2003; 2003US-0493860P.

PR 28-AUG-2003; 2003US-0498634P.

PR 16-SEP-2003; 2003US-0503931P.

PR 10-NOV-2003; 2003WO-US035712.

PR 05-FEB-2004; 2004WO-US003600.

PR 02-MAR-2004; 2004US-0549896P.

(PROT-) PROTEOLOGICS INC.

PI Taglicht DN, Alroy I, Reiss Y, Yaar L, Ben-Avraham D, Tuvia S;
PI Greener T;

XX WPI; 2004-662346/54.
 DR Isolated, purified or recombinant complex, useful for identifying an
 XX antiviral, anti-apoptotic or anti-cancer, comprising POSH polypeptide and
 PT POSH-associated protein (POSH-AP).
 PS Disclosure; SEQ ID NO 254; 374pp; English.
 XX
 CC The invention relates to an isolated, purified or recombinant complex (1)
 CC comprising a POSH polypeptide and a POSH-associated protein (POSH-AP) (a)
 CC or HERPUD1 and a ubiquitin ligase (b). Methods using (1), (a) or (b) are
 CC useful for identifying an agent that modulates an activity of a POSH
 CC polypeptide or POSH-AP, for identifying an antiviral agent, an anti-
 CC apoptotic agent, an anti-cancer agent, an agent that inhibits trafficking
 CC of a protein through the secretory pathway, an agent that inhibits the
 CC progression of a neurological disorder, an agent that modulates a POSH
 CC function, an agent that modulates a HERPUD1 function. The methods can be
 CC used for treating a viral infection, for inhibiting an activity of a POSH
 CC -AP in a cell, for treating a POSH-associated disease in a subject. The
 CC POSH-associated disease is viral infection, POSH-associated cancer or
 CC POSH-associated neurological disorder. The methods are useful for
 CC treating or preventing POSH-associated neurological disorder in a subject
 CC e.g. Alzheimer's disease, Parkinson's disease, Huntington's disease,
 CC schizophrenia, Niemann-Pick's disease. This sequence corresponds to a
 CC protein of the invention.
 CC
 SQ Sequence 209 AA;
 Query Match 45.5%; Score 51; DB 8; Length 209;
 Best Local Similarity 42.9%; Pred. No. 62;
 Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
 QY 1 MADNGTITVEBLKQLLEQNL 21
 DB 134 LEDKQVSYVEAKNRAEQNMV 154
 RESULT 20
 AAU31548
 ID AAU31548 standard; protein; 246 AA.
 AC AAU31548;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Novel human secreted protein #2039.
 XX
 KW Human; vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200179449-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 16-APR-2001; 2001WO-US008656.
 XX
 PR 18-APR-2000; 2000US-00552929.
 PR 26-JAN-2001; 2001US-00770160.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 XX
 DR WPI; 2001-611725/70.
 XX
 PT Nucleic acids encoding a range of human polypeptides, useful in genetic
 PT vaccination, testing and therapy.
 XX
 PS Claim 20; Page 457; 765pp; English.

XX The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising the
 CC nucleic acids encoding the polypeptides and cells genetically engineered
 CC to express them are also useful for producing the proteins. The proteins
 CC are useful in genetic vaccination, testing and therapy, and can be used
 CC as nutritional supplements. They may be used to increase stem cell
 CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon
 CC and/or nerve tissue growth or regeneration; immune suppression and/or
 CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
 CC AAU2510-AAU3304 represent the amino acid sequences of novel human
 CC secreted proteins of the invention
 CC
 SQ Sequence 246 AA;
 Query Match 45.5%; Score 51; DB 4; Length 246;
 Best Local Similarity 42.9%; Pred. No. 74;
 Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
 QY 1 MADNGTITVEBLKQLLEQNL 21
 DB 136 LEDKQVSYVEAKNRAEQNMV 156
 RESULT 21
 ABU23669
 ID ABU23669 standard; protein; 351 AA.
 AC ABU23669;
 XX
 DT 19-JUN-2003 (first entry)
 XX
 DE Protein encoded by prokaryotic essential gene #9196.
 XX
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX
 OS Clostridium acetobutylicum.
 XX
 PN WO200277183-A2.
 XX
 PD 03-OCT-2002.
 XX
 PF 21-MAR-2002; 2002WO-US009107.
 XX
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Wang L, Zamudio C, Malone C, Haseelbeck R, Ohlsen KU, Zyekind JW,
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX
 DR WPI; 2003-029926/02.
 XX
 N-PSDB; ACA27539.
 XX
 PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX
 PS Claim 25; SEQ ID NO 51593; 1766pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:

CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation; or (7) identifying a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

SO Sequence 351 AA;

Query Match 45.5%; Score 51; DB 6; Length 351;
 Best Local Similarity 42.1%; Pred. No. 1.1e+02;
 Matches 8; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 4 NGTTTBEKQLLEQNNLV 22
 ||:|||||:|:|
 DB 132 NGELSTIEELKQWMDASNIY 150

RESULT 22

AAW68488 standard; protein; 572 AA.

AC AAW68488;

DT 08-DEC-1998 (first entry)

XX Mouse UIIP-4 protein.

XX Mouse; Unc-33-like phospho-protein; UIIP; rat; neoplasm; tumorigenesis;

KW neurodegenerative disorder; diagnosis.

OS Mus musculus.

PN FR2759701-A1.

PD 21-AUG-1998.

PF 19-FEB-1997; 97FR-00001961.

PR 19-FEB-1997; 97FR-00001961.

PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

PI Aguera M, Belin MF, Homnorat J, Kolatukudy P, Quach TT, Byk T;

XX Sobel A;

DR WPI; 1998-449610/39.

DR N-PSDB; AAV60817.

PT Mouse and human UIIP poly:peptide(s) - useful in detection of para-
 neoplastic neurological syndromes.

XX Claim 1; Fig 11; 90pp; French.

XX This sequence represents the mouse unc-33-like phospho-protein (UIIP)-4.
 CC The coding sequence was isolated based on similarity to the rat UIIP
 CC sequence. Proteins of the UIIP family or their corresponding nucleic
 CC acids can be used in compositions for treating neurodegenerative
 CC disorders and neoplasms, especially for para-neoplastic neurological
 CC syndromes and/or for the early diagnosis of tumorigenesis

SO Sequence 572 AA;

Query Match 45.5%; Score 51; DB 2; Length 572;
 Best Local Similarity 64.7%; Pred. No. 1.8e+02;
 Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 ADNGTTTBEKQLLEQ 18
 ||:|||||:|:|
 DB 199 AENGDIIVEEQRLLEQ 215

RESULT 23

ID ADG33790 standard; protein; 469 AA.

AC ADG33790;

DT 26-FEB-2004 (first entry)

DE Actinomycetes dual condensation/epimerisation NRPS domain protein ID 49.

KW non-ribosomal peptide synthetase; NRPS; dual condensation; epimerisation;

KW ramoplanin; complestatin; actinomycetes taxon.

OS Pseudomonas syringae pv. syringae.

PN WO2003089641-A2.

PD 30-OCT-2003.

PF 17-APR-2003; 2003WO-CA000575.

PR 17-APR-2002; 2002US-0372790P.

XX (ECOP-) ECOPIA BIOSCIENCES INC.

PI Farnet CM, Staiffa A;

DR WPI; 2003-854123/79.

DR N-PSDB; ADG33791.

PT New dual condensation/epimerization non-ribosomal peptide synthetase
 PT domain and encoding polynucleotide, useful for modifying the
 PT stereochemistry of synthesized peptides (e.g. ramoplanin or complestatin)
 PT in vitro or in vivo.

PS Claim 9; SEQ ID NO 49; 245pp; English.

XX This invention relates to novel domains of non-ribosomal peptide
 CC synthetases (NRPSs) that exhibit dual condensation and epimerisation
 CC activities. Specifically, these domains allow incorporation of non-
 CC proteinogenic substrates (e.g. D-amino acids) into peptide products.
 CC Furthermore, they can be used in vivo to modify the stereochemistry of
 CC synthesised peptides (e.g. ramoplanin or complestatin) at selected amino
 CC acid sites by the addition of non-chiral residues. The present invention
 CC describes the identification of isolated polynucleotide NRPS domains in
 CC various organisms from the actinomycetes taxon, and the encoded
 CC polypeptides thereof, as well as suitable expression vectors. This
 CC polypeptide sequence is a dual condensation/ epimerisation NRPS domain
 CC protein of the invention.

SO Sequence 469 AA;

Query Match 44.6%; Score 50; DB 7; Length 469;
 Best Local Similarity 64.3%; Pred. No. 2e+02;
 Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 7 ITVEELKOLLEQWN 20
 : | | | | | | | | | |
 Db 432 LPLNERKOLLEQWN 445

RESULT 24

ABU48797
 ID ABU48797 standard; protein; 673 AA.

XX ABU48797;
 AC

DT 19-JUN-2003 (first entry)
 XX

DE Protein encoded by Prokaryotic essential gene #34324.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX Ureaplasma urealyticum.
 OS

XX WO200277183-A2.
 PN

XX 03-OCT-2002.
 PD

XX 21-MAR-2002; 2002WO-US009107.
 PF

XX 21-MAR-2001; 2001US-00815242.
 PR

XX 06-SEP-2001; 2001US-00948993.
 PR

XX 25-OCT-2001; 2001US-0342923P.
 PR

XX 08-FEB-2002; 2002US-00072851.
 PR

XX 06-MAR-2002; 2002US-0362699P.
 PR

XX (ELITR-) ELITRA PHARM INC.
 PA

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zykkind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.
 DR

XX N-PSDB; ACAS2667.
 DR

XX New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 76721; 1766bp; English.

CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-regulated gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational

CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

SO Sequence 673 AA;

Query Match 44.6%; Score 50; DB 6; Length 673;
 Best Local Similarity 66.7%; Pred. No. 3e+02;
 Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 9 VEELKOLLEQWN 20
 : | | | | | | | | | |
 Db 8 IDELKOLLEQWN 19

RESULT 25

AAB32530
 ID AAB32530 standard; protein; 123 AA.

XX AAB32530;
 AC

DT 19-JAN-2001 (first entry)
 XX

DE *S. lavendulae* MmcQ encoded protein sequence.

XX Mitomycin; biosynthesis; mitosome ring system; antibiotic; anti-cancer;
 KW anti-inflammatory; immune-enhancer; immunosuppressant; asthma;

XX chronic obstructive pulmonary disease; respiratory inflammation;
 KW fungicide; pesticide.

XX Streptomyces lavendulae.
 OS

XX WO200053737-A2.
 PN

XX 14-SEP-2000.
 PD

XX 10-MAR-2000; 2000WO-US006394.
 PF

XX 12-MAR-1999; 99US-00266965.
 PR

XX (MINU) UNIV MINNESOTA.
 PA (SHER) SHERMAN D H.

XX (MAOY) MAO Y.
 PA (VARO) VAROGLU M.

XX (HEMM) HE M.
 PA (SHEL) SHELTON P C.

XX Sherman DH, Mao Y, Varoglu M, He M, Sheldon PC;
 PI

XX WPI; 2000-601980/57.
 DR

XX N-PSDB; AAC55831.
 DR

XX Novel nucleic acid molecule comprising mitomycin biosynthetic gene
 PT cluster useful for cloning mitomycin biosynthetic genes for elucidating
 PT the molecular basis of mitosome ring system biosynthesis.

XX Disclosure; Page 382; 399pp; English.

XX This invention relates to isolated and purified nucleic acid molecules
 CC from the mitomycin biosynthetic gene cluster. Mitomycins are a group of
 CC natural products that contain a variety of functional groups, including
 CC amino benzoguinone and aziridine ring systems. The *S. lavendulae*
 CC mitomycin biosynthetic gene cluster comprises 47 mitomycin genes spanning
 CC 55kb of DNA. The invention includes an expression cassette comprising a
 CC mitomycin biosynthetic gene operably linked to a promoter, and host cells
 CC transformed with the cassette. The nucleotide, and protein sequences and
 CC the transformed host cells of the invention result in antitastmatic,
 CC anti-inflammatory, cytostatic, immunomodulatory, and antibiotic
 CC activities. The nucleotide sequences are used to elucidate the molecular

CC basis for the biosynthesis of the mitosome ring system, as well as to
CC engineer the biosynthesis of novel natural products, e.g. antibiotics,
CC anti-inflammatory agents, anti-cancer agents, immune-enhancers,
CC immunosuppressants, agents to treat asthma, chronic obstructive pulmonary
CC disease as well as other disease involving respiratory inflammation, or
CC cholesterol-lowering agents or as crop protection agents (e.g. fungicides
CC or insecticides) as well as biopolymers, e.g., in packaging or biomedical
CC applications, or to engineer PHA monomer synthases. Sequences AAC55782-
CC C55881, AAC55815-C55849 and AAB32485-B32542 represent mitomycin
CC biosynthetic gene cluster DNA sequences and encoded proteins. Sequences
CC AAC55812-C55814, AAC55850-C55856 and AAC55862-C55863 represent PCR
CC primers used in the cloning of the mitomycin biosynthetic genes
XX

XX Sequence 123 AA;

Query Match 43.8%; Score 49; DB 3; Length 123;
Best Local Similarity 57.1%; Pred. No. 67;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
QY 4 NGTIVBELKQLE 17
|||:||||:|
Db 86 NGTVPVELREMYE 99

RESULT 26
ADE10302
ID ADE10302 standard; protein; 123 AA.
XX
AC ADE10302;
XX
DT 29-JAN-2004 (first entry)
XX
DE S. lavendulae mitomycin biosynthetic protein MmcQ.
XX
KM Mitomycin biosynthetic protein; mitomycin C; antibiotic; MC; apoptosis;
XX tumour hypoxia; cytosol; anti-tumour agent; cancer.
XX
OS Streptomyces lavendulae.
XX
PN US2003134398-A1.
XX
PD 17-JUL-2003.
XX
PF 12-SEP-2001; 2001US-00953348.
XX
PR 12-SEP-2001; 2001US-00953348.
XX

XX (SHER/) SHERMAN D H.
XX (MAOY/) MAO Y.
XX (VARO/) VAROGILU M.
XX (HEMM/) HE M.
XX (SHEL/) SHELDON P.
XX

XX Sherman DH, Mao Y, Varoglu M, He M, Sheldon P;
XX WPI; 2003-863498/80.
XX N-PSDB; ADE10250.
XX

XX New nucleic acid molecule comprising a sequence having mitomycin
XX biosynthetic gene cluster, useful for enhancing production of
XX antibiotics.
XX

XX Disclosure; SEQ ID NO 132; 308bp; English.

XX The invention relates to an isolated and purified nucleic acid molecule
XX comprising a sequence having mitomycin biosynthetic gene cluster, or its
XX variant or fragment. Also included are an expression cassette comprising
XX the novel nucleic acid molecule (operably linked to a promoter functional
XX in a host cell), a recombinant bacterial host cell in which at least a
XX portion of a nucleic acid molecule comprising mitomycin biosynthetic gene
XX cluster is disrupted (resulting in a recombinant host cell that produces
XX altered levels of mitomycin relative to a corresponding nonrecombinant
XX bacterial host cell), introducing exogenous DNA into a refractory

CC Streptomyces strain, identifying a nucleic acid molecule that is related
CC to at least a portion of a nucleic acid molecule comprising a mitomycin
CC gene cluster, preparing a compound or its salt from the recombinant host
CC cell and a product produced by the recombinant host cell. The nucleic
CC acid encodes a MitT, Mts, MitR, MitC, MitP, MitQ, MitN, MitM, MitL and/or
CC MitK, MitJ, MitH, MitG, MitF, MitE, MitD, MitC, MitB, MitA and/or
CC MmcA-MmcY. The nucleic acid is useful for enhancing production of
CC mitomycin antibiotics, which induce apoptosis and hence are useful as
CC anti-tumour (via tumour hypoxia) agents and are useful in treating
CC cancer. The gene cluster was isolated from Streptomyces lavendulae. The
CC present sequence is a mitomycin biosynthetic protein of the invention.
XX

XX Sequence 123 AA;

Query Match 43.8%; Score 49; DB 7; Length 123;
Best Local Similarity 57.1%; Pred. No. 67;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
QY 4 NGTIVBELKQLE 17
|||:||||:|
Db 86 NGTVPVELREMYE 99

RESULT 27
AAB69350
ID AAB69350 standard; protein; 842 AA.
XX
AC AAB69350;
XX
DT 12-SEP-2003 (revised)
DT 20-APR-2001 (first entry)
XX
DE HIV-1 non-subtype B clone 93BR029-4 env protein.
XX
KM HIV-1; human immunodeficiency virus; non-subtype B; gag; pol; env; vpu;
XX vif; vpr; tat; rev; nef; vaccine.
XX
OS Human immunodeficiency virus 1.
XX
PN WO200026416-A1.
XX
PD 11-MAY-2000.
XX
PF 25-OCT-1999; 99WO-US024837.
XX
PR 02-NOV-1998; 98US-00184418.
XX

XX (UABR-) UAB RES FOUND.
XX

XX Hahn BH, Shaw GM, Gao F;
XX

XX WPI; 2000-365651/31.
XX

XX Novel genomic nucleic acids of non-subtype B human immunodeficiency virus
XX type 1 useful for detecting and treating AIDS comprises a specific
XX nucleotide sequence.
XX

XX Claim 41; Fig 21; 131pp; English.

XX The present invention provides the protein and coding sequences for a
XX number of human immunodeficiency virus (HIV) type 1 non-subtype B
XX isolates. The sequences shown include the near full-length coding
XX sequences from each isolate, and the env, pol, vif, vpr, vpu, gag, tat,
XX rev and nef proteins. These can be used to detect the presence of HIV-1
XX in a sample and to produce antibodies against non-subtype B HIV-1 virus.
XX These antibodies can be used in vaccines to prevent and treat HIV
XX infection. (Updated on 12-SEP-2003 to standardise OS field)
XX

XX Sequence 842 AA;

Query Match 43.3%; Score 48.5; DB 3; Length 842;
Best Local Similarity 47.6%; Pred. No. 66+02;
Matches 10; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

```
OY      3 DNGRTTIVE-ELKQLEQNNLV 22  
       |||||:-::|||:-||  
DB      396 DNGRTITLECRIKQIVNMGEV 416
```

```
RESULT 28  
ID ADF07641  
XX ADF07641 standard; protein; 300 AA.  
AC ADF07641;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Bacterial polypeptide #3754.  
XX  
KW Proteus mirabilis infection; bacterial infection; antibacterial,  
   immunostimulant.  
OS  
XX Proteus mirabilis.  
PN US6605709-B1.  
XX  
PD 12-AUG-2003.  
XX  
PF 05-APR-2000; 2000US-00543681.  
PR 09-APR-1999; 99US-0128706P.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
XX  
PI Breton GL;  
DR WPI; 2003-895291/82.  
DR N-PSTB; ADF03469.  
XX
```

New Proteus mirabilis polypeptides and polynucleotides, useful as reagents for diagnosis of bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for plants.

Disclousure; SEQ ID NO 7926; 870pp; English.

The invention relates to new Proteus mirabilis polypeptides and polynucleotides. The invention also relates to antibodies against the polypeptides, methods for producing the polypeptides, a method of generating vaccines for immunising an individual against P. mirabilis, a method for evaluating a compound for the ability to bind a P. mirabilis polypeptide and a method for screening test compounds for anti-bacterial activity. The polypeptides and polynucleotides are useful as molecular targets for diagnosing, preventing and treating pathological conditions resulting from bacterial infection, as reagents for diagnosis of bacterial diseases, as components of antibacterial vaccines, as targets for antibacterial drugs or as bio-control agents for plants. This sequence represents a Proteus mirabilis polypeptide of the invention.

```
SO Sequence 300 AA;
```

```
OY      Query Match          42.9%; Score 48; DB 7; Length 300;  
       Best Local Similarity 45.0%; Pred.No. 2.4e+02;  
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0  
OY      1 MADNGITVEELKQLLEOWN 20  
       :|:|||:-|||:-||  
DB      60 LTDDGAILYEHAKQIILAQFN 79
```

```
RESULT 29  
ID ADS21407  
XX ADS21407 standard; protein; 401 AA.  
AC ADS21407;  
XX
```

| | | | |
|----|---|------------------------------------|---------------|
| DT | | 02-DEC-2004 | (first entry) |
| XX | Bacterial polypeptide #10440. | | |
| KW | Recombinant DNA construct; transformed plant; improved plant property; | | |
| KM | cold tolerance; heat tolerance; drought tolerance; herbicide; osmotic; | | |
| KW | pathogen tolerance; pest tolerance; plant disease resistance; | | |
| KM | cell cycle pathway modification; plant growth regulator; | | |
| KW | homologous recombination; seed oil yield; protein yield; carbohydrate; | | |
| KM | nitrogen; phosphorus; photosynthesis; lignin; galactomannan; | | |
| KX | bacterial polypeptide. | | |
| OS | Bacteria. | | |
| PV | US200323675-A1. | | |
| PD | 18-DEC-2003. | | |
| PF | 20-FEB-2003; 2003US-00369493. | | |
| PR | 21-FEB-2002; 2002US-0360039P. | | |
| PA | (CAOY/) CAO Y. | | |
| PA | (HINK/) HINKLE G J. | | |
| PA | (SLAT/) SLATER S C. | | |
| PA | (CHEN/) CHEN X. | | |
| PA | (GOLD/) GOLDMAN B S. | | |
| PI | Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS; | | |
| DR | WPI; 2004-061375/06. | | |
| XX | New recombinant DNA construct comprising a promoter positioned to provide | | |
| PT | for expression of a polynucleotide encoding a polypeptide from a | | |
| PT | microbial source, useful for producing plants with improved properties. | | |
| PS | Claim 1; SEQ ID NO 10440; 122bp; English. | | |
| CC | The invention relates to a recombinant DNA construct comprising a | | |
| CC | promoter functional in a plant cell, where the promoter is positioned to | | |
| CC | provide for expression of a polynucleotide encoding a polypeptide from a | | |
| CC | microbial source. The invention also relates to a transformed plant | | |
| CC | transforming the recombinant DNA construct and a method of producing a | | |
| CC | such as maize or soybean. The method of producing a transformed plant | | |
| CC | having an improved property comprises transforming a plant with the | | |
| CC | recombinant DNA construct and growing the transforming plant, where the | | |
| CC | polynucleotide or polypeptide is useful for improving plant properties. | | |
| CC | The recombinant DNA construct is useful for producing plants with | | |
| CC | improved plant properties, e.g. improved cold, heat or drought tolerance, | | |
| CC | tolerance to herbicides, extreme osmotic conditions, pathogens or pests, | | |
| CC | increased resistance to plant disease, better growth rate by modification | | |
| CC | of the cell cycle pathway with plant growth regulators, increased rate of | | |
| CC | homologous recombination, modified seed oil or protein yield and/or | | |
| CC | content, improved yield by modification of carbohydrate, nitrogen or | | |
| CC | phosphorus use and/or uptake, by modification of photosynthesis or by | | |
| CC | providing improved plant growth and development under at least one stress | | |
| CC | condition, improved lignin production or improved galactomannan | | |
| CC | production. This sequence represents a bacterial polypeptide used in the | | |
| CC | scope of the invention. Note: The sequence data for this patent did not | | |
| CC | form part of the printed specification but was obtained in electronic | | |
| CC | format from USPTO at seqdata.uspto.gov/sequence.html. | | |
| SQ | Sequence 401 AA: | | |
| QY | Query Match | 42.9%; Score 48; DB 8; Length 401; | |
| | Best Local Similarity | 46.7%; Pred. No. 3.2e+02; | |
| | Matches | 7; Conservative | 6; Mismatches |
| | | 2; Indels | 0; Gaps |
| | | | 0; |
| DB | 5 GTTVEELKQLLBEOW 19 ::: :: :: 184 GNVTLEOVKKSEKM 198 | | |

RESULT 30
ABU1384
ID ABU1384 standard; protein; 4437 AA.
AC ABU1384;
XX
XX 11-FEB-2003 (first entry)
DE Protein encoded by S. atroolivaceus leinamycin gene cluster ORF lmi1.
XX
XX leinamycin biosynthesis gene cluster; lmi, open reading frame; ORF;
XX anti-tumour antibiotic; broad spectrum antimicrobial activity;
XX Gram-positive; Gram-negative bacteria; chemical modification; metabolite;
XX apo-carrier protein; holo-carrier protein; tumour; polyketide;
XX hybrid polyketide/polyketide metabolite; lmi production; cytostatic.
XX Streptomyces atroolivaceus.
XX MO20027179-A2.
XX
XX 03-OCT-2002.
XX
XX 22-MAR-2002; 2002MO-US008937.
XX
XX 26-MAR-2001; 2001US-0278935P.
XX
XX (REGC) UNITV CALIFORNIA.
XX (KYOM) KYOMA HAKKO KOGYO KK.
XX
XX Shen B, Cheng Y, Tang G;
XX
XX WPI; 2003-018907/01.
XX N-PSDB; ABX34289.
XX
XX Novel gene cluster responsible for synthesis of leinamycin in
XX Streptomyces atroolivaceus useful for making various peptide and/or
XX polyketide, and/or hybrid polyketide/polyketide metabolites.
XX
XX Claim 13; Page 143-145; 185pp; English.
XX
XX The present invention relates to the isolation of the Streptomyces
XX atroolivaceus leinamycin (lmi) biosynthesis gene cluster containing 71
XX open reading frames (ORFs) (ORFs -35 through -1, ORFs lmiA through lmiZ,
XX and ORFs +1 through +9). Leinamycin is a novel anti-tumour antibiotic
XX produced by several Streptomyces species. It exhibits broad spectrum
XX antimicrobial activity against Gram-positive and Gram-negative bacteria,
XX but not against fungi. The polypeptides encoded by the lmi biosynthesis
XX gene cluster ORFs are useful for chemically modifying a molecule in a
XX host cell. The host cell is a bacterium or eukaryotic cell, including a
XX mammalian, yeast, plant, fungal, or insect cell. The molecule is an
XX endogenous metabolite produced by the host cell or exogenously supplied
XX metabolite, or an amino acid, and the polypeptide is a peptide synthetase
XX or amino transferase. The polypeptides encoded by the lmi gene cluster
XX are useful for converting an apo-carrier protein to a holo-carrier
XX protein. lmi shows potent antitumour activity in tumour models in vivo.
XX The lmi gene cluster modules and/or catalytic domains are useful for
XX making various peptide and/or polyketide, and/or hybrid
XX polyketide/polyketide metabolites. The proteins encoded by the ORFs are
XX useful alone, or in combination with other active domains to modify
XX various target substrates. The lmi gene cluster is useful to upregulate
XX endogenous lmi production to permit lmi production in cells and/or to
XX make various lmi modified lmi. lmi, its analogue, or other polyketide,
XX peptide or hybrid polyketide/polyketide metabolites are useful as
XX therapeutic agents, to treat a number of disorders, depending upon the
XX type of metabolites. ABU1341-ABU1411 represent the proteins encoded by
XX ORFs of the S. atroolivaceus leinamycin biosynthesis gene cluster
XX
XX Sequence 4437 AA;

Query Match 42.9%; Score 48; DB 6; Length 4437;
Best Local Similarity 42.1%; Pred. No. 4.1e+03;
Matches 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 2 ADNGITVEELKQLEQWN 20
||| : ||| : |||
DB 949 ADGEVGAELHKLHEWN 967

RESULT 31
ADI3885
ID ADI3885 standard; protein; 159 AA.
AC ADI3885;
XX
XX 15-APR-2004 (first entry)
DE Glucosamine-6-phosphate acetyltransferase, GNA1, SEQ ID 30.
XX
XX Glucosamine; N-acetylglucosamine; fermentation;
XX glucosamine-6-phosphate acetyltransferase;
XX glucosamine-6-phosphate synthase; glucosamine-6-phosphate deaminase;
XX glucosamine-1-phosphate N-acetyltransferase; glucosamine-6-phosphate;
XX glucosamine-1-phosphate; N-acetylglucosamine-1-phosphate;
XX N-acetylglucosamine-6-phosphate; enzyme.
XX
XX Saccharomyces cerevisiae.
XX
XX MO2004003175-A2.
XX
XX 08-JAN-2004.
XX
XX 01-JUL-2003; 2003MO-US020925.
XX
XX 01-JUL-2002; 2002US-0393348P.
XX
XX (ARKI-) ARKION LIFE SCI LLC.
XX
XX Deng M, Angerer JD, Cyron D, Grund AD, Terrell TA, Leanna C;
XX Mathre O, Rosson R, Running J, Severson D, Song L, Wassink S;
XX
XX WPI; 2004-203380/19.
XX N-PSDB; ADI38884.
XX
XX Producing glucosamine or N-acetylglucosamine by fermentation involves
XX culturing microorganism comprising glucosamine-6-phosphate
XX acetyltransferase, in fermentation medium, and collecting product.
XX
XX Claim 5; SEQ ID NO 30; 327pp; English.
XX
XX The present invention relates to a method (M1) for producing glucosamine
XX and N-acetylglucosamine by fermentation. The method comprises (a)
XX culturing in a fermentation medium a microorganism (I) which comprises
XX endogenous glucosamine-6-phosphate acetyltransferase (II) and a genetic
XX modification that increases the activity of (II), glucosamine-6-phosphate
XX synthase (III) or glucosamine-6-phosphate deaminase (IV), or decreases
XX the activity of (IV) and increases the activity of glucosamine-1
XX phosphate N-acetyltransferase (V), and (b) and collecting the product,
XX which is chosen from the group consisting of glucosamine-6-phosphate,
XX glucosamine, glucosamine-1-phosphate, N-acetylglucosamine-1-phosphate, N-
XX acetylglucosamine-6-phosphate, and N-acetylglucosamine. The present
XX sequence was used to illustrate the method of the invention.
XX
XX Sequence 159 AA;

Query Match 42.0%; Score 47; DB 8; Length 159;
Best Local Similarity 50.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 5 GTITVEELKQLEQWN 20
||| : ||| : |||
DB 31 GTITPESFSLIKIYWN 46

RESULT 32
ADJ64176

ID ADJ64176 standard; protein; 159 AA.
 XX
 AC ADJ64176;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE S. cerevisiae glucosamine phosphate N-acetyltransferase.
 XX
 KM Hexosamine; arthritis; osteoarthritis; rheumatoid arthritis; pain;
 KM inflammation; articular joint disease; spondyloarthritis;
 KM gouty arthritis; systemic lupus erythematosus; juvenile arthritis;
 KM tendinitis; bursitis; connective tissue injury; psoriasis; eczema; burn;
 KM dermatitis; transgenic plant; glucosamine phosphate N-acetyltransferase;
 KM yeast; enzyme; EC 2.3.1.4.
 XX
 OS Saccharomyces cerevisiae.
 XX
 PN US2004003432-A1.
 XX
 PD 01-JAN-2004.
 XX
 PP 05-MAY-2003; 2003US-00429812.
 XX
 PR 06-MAY-2002; 2002US-0378297P.
 XX
 PA (PHAA) PHARMACIA CORP.
 XX
 PI Obukowicz MG;
 XX
 DR WPI; 2004-061704/06.
 DR N-PSDB; ADJ64175.
 XX
 PT Producing hexosamine useful for treating arthritis by culturing cell
 PT comprising heterologous polynucleotide sequences which encode for enzymes
 PT required for biosynthetic pathway capable of synthesizing hexosamine.
 XX
 PS Disclosure; SEQ ID NO 4; 35pp; English.
 XX
 CC The invention relates to a method of producing a hexosamine that involves
 CC providing a cell comprising polynucleotide sequences which code for
 CC enzymes required for a biosynthetic pathway capable of synthesizing the
 CC hexosamine, where at least one of the polynucleotide sequences comprises
 CC a recombinant polynucleotide. The method involves transforming a cell
 CC with at least one heterologous polynucleotide coding for a polypeptide in
 CC a biosynthetic pathway that is capable of producing hexosamine, culturing
 CC the transformed cell under conditions that permit the cell to translate
 CC the polynucleotide into a polypeptide comprising an enzyme which is part
 CC of the biosynthetic pathway. The hexosamine produced by the method of
 CC invention is useful for treating arthritis, preferably osteoarthritis and
 CC rheumatoid arthritis in humans and pet animals. The hexosamines are also
 CC useful for treating pain, inflammation or inflammation-associated
 CC disorder. The hexosamines are also useful for treating other articular
 CC joint damage or diseases such as spondyloarthritis, gouty arthritis,
 CC systemic lupus erythematosus and juvenile arthritis and other joint
 CC damage or disease conditions such as tendinitis, bursitis, connective tissue
 CC injuries or disorders, and skin related conditions such as psoriasis,
 CC eczema, burns and dermatitis. The method provides improved production of
 CC hexosamine without compromising its clinical effectiveness and in a form
 CC that is acceptable for delivery to a broad class of patients. Consumption
 CC of edible portions of transgenic plants containing hexosamines provide a
 CC supply of hexosamine to the subject in a conventional and easily
 CC consumable form. The present sequence is Saccharomyces cerevisiae
 CC glucosamine phosphate N-acetyltransferase (EC 2.3.1.4).
 CC
 XX
 XX
 SQ Sequence 159 AA;
 XX
 Query Match 42.0%; Score 47; DB 8; Length 159;
 Best Local Similarity 50.0%; Pred. No. 1.7e+02;
 Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 QY 5 GTTVEELKQLLEQWV 20
 DB 31 GTTPESFSKLRKYN 46

RESULT 33
 ADN10653
 ID ADN10681 standard; protein; 508 AA.
 XX
 AC ADN10681;
 XX
 DT 15-JUL-2004 (first entry)
 XX
 DE Nicotiana p450 enzyme amino acid sequence SEQ ID NO:266.
 XX
 KM plant; p450; enzyme; Nicotiana; plant growth regulant; gene therapy;
 KM phenotype.
 XX
 OS Nicotiana sp.
 XX
 PN WO2004035745-A2.
 XX
 PD 29-APR-2004.
 XX
 PP 16-OCT-2003; 2003WO-US032722.
 XX
 PR 16-OCT-2002; 2002US-0418933P.
 PR 08-JUL-2003; 2003US-0485368P.
 PR 18-SEP-2003; 2003US-0503989P.
 XX
 PA (USSM-) US SMOKELESS TOBACCO CO.
 XX
 PI Xu D;
 XX
 DR WPI; 2004-348441/32.
 DR N-PSDB; ADN10680.
 XX
 PT New isolated nucleic acid molecules and encoded cytochrome P450 enzymes
 PT from Nicotiana plants, useful for altering plant phenotypes.
 XX
 PS Claim 3; SEQ ID NO 266; 198pp; English.
 XX
 CC The present invention describes a plant p450 enzyme nucleic acid molecule
 CC isolated from Nicotiana. Also described: (i) an isolated p450 protein
 CC from Nicotiana; (2) a transgenic plant comprising the nucleic acid
 CC molecule described above; (3) a method of producing the transgenic plant,
 CC comprising: (i) operably linking the above nucleic acid molecule with a
 CC promoter functional in the plant to create a plant transformational
 CC vector; (ii) transforming the plant with the vector; (iii) selecting a
 CC plant cell transformed with the transformation vector; and (iv)
 CC regenerating a transformation plant from the transformed plant cell; and
 CC (4) a method of selecting a plant containing the above nucleic acid
 CC molecule, where the plant is analysed for the presence of the above
 CC nucleic acid sequences. The p450 sequences have plant growth regulant
 CC activity, and can be used in gene therapy. Compositions and methods from
 CC the present invention are useful for altering plant phenotypes. The
 CC present sequence represents a Nicotiana p450 enzyme amino acid sequence
 CC from the present invention.
 CC
 XX
 XX
 SQ Sequence 508 AA;
 XX
 Query Match 42.0%; Score 47; DB 8; Length 508;
 Best Local Similarity 47.1%; Pred. No. 5.7e+02;
 Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
 QY 6 TTTVEELKQLLEQWV 22
 DB 196 TVRVEDLYLVDPWFLL 212
 RESULT 34
 ADN10653
 ID ADN10653 standard; protein; 508 AA.
 XX
 AC ADN10653;
 XX

[illegible][illegible]


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XX 31-OCT-2000 (first entry)
XX HIV synthetic Env containing polypeptide.
DE Gag; expression cassette; antigenic; type C; HIV Env; synthetic;
XX DNA immunization; packaging cell line; antigen presentation.
XX Human immunodeficiency virus; type C strain AF110968.
OS Synthetic.
XX MO200039304-A2.
XX 06-JUL-2000.
XX 30-DEC-1999; 99MO-US031273.
XX 31-DEC-1998; 98US-0114495P.
XX 01-SEP-1999; 99US-0152195P.
XX (CHIR ) CHIRON CORP.
XX Barnett S, Zur Megede J;
XX WPI; 2000-452401/39.
XX Polynucleotide encoding antigenic type C HIV Gag polypeptide or a HIV Env
XX polypeptide and the polypeptide useful for immunizing a mammal especially
XX human against HIV.
XX Example 1; Page 106-109, 113pp; English.
XX Expression cassettes comprising a polynucleotide encoding antigenic type
XX C human immunodeficiency virus (HIV) Gag or Env polypeptides are useful
XX in DNA immunization, generation of packaging cell lines and production of
XX Gag- and/or Env-containing proteins. Synthetic Env and Gag expression
XX cassettes exhibit increased potency for induction of cytotoxic T-
XX lymphocyte (CTL) responses by DNA immunization. Gag of HIV-1 self-
XX assemble into non-infectious virus-like particles which are used as a
XX matrix for the proper presentation of an antigen entrapped or associated
XX to the immune system of the host
XX Sequence 849 AA;
SQ
Query Match 41.5%; Score 46.5; DB 3; Length 849;
Best Local Similarity 45.0%; Pred. No. 1.1e+03;
Matches 9; Conservative 4; Mismatches 6; Indels 1; Gaps 1;
QY 4 NGTIVTE-ELKQLEQNLV 22
DB 403 NGTITTCRIKQIINMOKV 422
RESULT 39
AAG02044
ID AAG02044 standard; protein; 100 AA.
XX AAG02044;
AC AAG02044;
XX 06-OCT-2000 (first entry)
XX Human secreted protein, SEQ ID NO: 6125.
XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX gene therapy; chromosome mapping.
XX Homo sapiens.
XX EP1033401-A2.
XX 06-SEP-2000.
XX 21-FEB-2000; 2000EP-00200610.

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XX 26-FEB-1999; 99US-0122487P.
XX (GEST ) GENSET.
XX Dumas Milne Edwards J, Duclert A, Giordano J;
XX WPI; 2000-500361/45.
XX N-PSDB; AAC02050.
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
XX obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
XX diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX Claim 13; SEQ ID NO 6125; 71pp + Sequence Listing; English.
XX The present sequence is a polypeptide encoded by one of a large number of
XX 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
XX prepared from total human RNAs or polyA+ RNAs derived from 30 different
XX tissues. EST sequences usually correspond mainly to the 3' untranslated
XX region (UTR) of the mRNA because they are often obtained from oligo-dT
XX primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
XX sequences derived from the 5' ends of mRNAs and even in those cases where
XX longer cDNA sequences have been obtained, the full 5' UTR is rarely
XX included. 5' ESTs are derived from mRNAs with intact 5' ends and can
XX therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
XX are also used in diagnostic, forensic, gene therapy and chromosome
XX mapping procedures. They are used to obtain upstream regulatory sequences
XX and to design expression and secretion vectors
XX Sequence 100 AA;
SQ
Query Match 41.1%; Score 46; DB 3; Length 100;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 3 DNGTIVTEELKQLE 17
DB 47 ENGELINIEELKNLE 61
RESULT 40
ABB70970
ID ABB70970 standard; protein; 114 AA.
XX ABB70970;
AC ABB70970;
XX 26-MAR-2002 (first entry)
XX Drosophila melanogaster polypeptide SEQ ID NO 39702.
XX Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical.
XX Drosophila melanogaster.
XX WO200171042-A2.
XX 27-SEP-2001.
XX 23-MAR-2001; 2001WO-US009231.
XX 23-MAR-2000; 2000US-0191637P.
XX 11-JUL-2000; 2000US-00614150.
XX (PEKE ) PE CORP NY.
XX Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
XX N-PSDB; ABL15073.
XX New isolated nucleic acid detection reagent for detecting 1000 or more

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| | | |
|----|---|---|
| | PT | genes from Drosophila and for elucidating cell signaling and cell-cell interactions. |
| | PX | |
| | PY | Disclosure; SEQ ID NO 39702; 21pp + Sequence Listing; English. |
| | XX | The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL6176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences |
| | YY | |
| | ZZ | |
| | Sequence 114 AA: | |
| | Query Match | 41.1%; Score 46; DB 4; Length 114; |
| | Best Local Similarity | 41.2%; Pred. No. 1.6e+02; |
| | Matches 7; Conservative 5; Mismatches 5; Indels 0; Gaps 0; | |
| Dy | 3 DNGTIVTELKQLLEQW 19 | |
| Db | : : : : | |
| | 57 NKGTISARQLRNLDNW 73 | |
| | RESULT 41 | |
| | ABG59978 | |
| Xx | ID ABG59978 standard; protein; 189 AA. | |
| Xx | AC ABG59978; | |
| Xx | DT 30-JUL-2002 (first entry) | |
| Xx | Human DTTHP polypeptide #36. | |
| KM | Human; DTTHP; diagnostic and therapeutic polypeptide; bone; testis; skin; cell proliferative disorder; cancer; tumour; autoimmune disorder; brain; inflammatory disorder; viral infection; bacterial infection; seizure; fungal infection; parasitic infections; developmental disorder; breast; endocrine disorder; metabolic disorder; neurological disorder; cervix; gastrointestinal disorder; transport disorder; gene therapy; kidney; adrenal gland; bone marrow; lung; ovary; pancreas; prostate; spleen; thymus. | |
| OS | Homo sapiens. | |
| XX | WO200220754-A2. | |
| PN | 14-MAR-2002. | |
| PD | 29-AUG-2001; 2001WO-US027127. | |
| Pf | 05-SEP-2000; 2000US-0229747P. | |
| Px | 05-SEP-2000; 2000US-0229748P. | |
| Px | 05-SEP-2000; 2000US-0229749P. | |
| Pr | 05-SEP-2000; 2000US-0229750P. | |
| Pr | 05-SEP-2000; 2000US-0229751P. | |
| Pr | 05-SEP-2000; 2000US-0230581P. | |
| Pr | 06-SEP-2000; 2000US-0230514P. | |
| Pr | 06-SEP-2000; 2000US-0230515P. | |
| Pr | 06-SEP-2000; 2000US-0230517P. | |
| Pr | 06-SEP-2000; 2000US-0230518P. | |
| Pr | 06-SEP-2000; 2000US-0230519P. | |
| Pr | 06-SEP-2000; 2000US-0230595P. | |
| Pr | 06-SEP-2000; 2000US-0230597P. | |
| Pr | 06-SEP-2000; 2000US-0230598P. | |
| Pr | 06-SEP-2000; 2000US-0230599P. | |
| Pr | 06-SEP-2000; 2000US-0230610P. | |
| Pr | 06-SEP-2000; 2000US-0230865P. | |
| Pr | 06-SEP-2000; 2000US-0230988P. | |

| | | |
|-----------------------|---|----------------------|
| PR | 07-SEP-2000; | 2000US-0230951P. |
| PR | 07-SEP-2000; | 2000US-0231163P. |
| PR | 07-SEP-2000; | 2000US-0231167P. |
| XX | | |
| XX | (INCY-) | INCYTE GENOMICS INC. |
| PI | Stuart J, Lincoln SE, Altus CM, Dufour GE, Chalup MS, Hillman JL; | |
| PI | Jones AL, Yu JY, Wright RJ, Gietzen D, Liu TF, Yap PE, Dahl CR; | |
| PI | Moniymma MG, Bradley DL, Rohatgi SD, Harris B, Roseberry AM; | |
| PI | Gerstein EH, Peralta CH, David MH, Panzer SR, Flores V, Daffo A; | |
| PI | Marwaha R, Chen AJ, Chang SC, Au AP, Iman RR; | |
| DR | WPI: 2002-363054/41. | |
| DR | N-PSDB; ABK71570. | |
| XX | | |
| XX | An isolated polynucleotide useful in diagnostics and therapeutics. | |
| XX | | |
| PS | Claim 29; Page 553; 686pp; English. | |
| XX | | |
| CC | The invention relates to human diagnostic and therapeutic (ditnp) | |
| CC | polynucleotides and their associated polypeptides (DITNP polypeptides). | |
| CC | The sequences of the invention are used in the treatment and diagnosis of | |
| CC | cell proliferative disorders (e.g. atherosclerosis, cirrhosis), cancers | |
| CC | (e.g. tumours of the adrenal gland, bone, bone marrow, brain, breast, | |
| CC | cervix, kidney, lung, ovary, pancreas, prostate, skin, spleen, testis or | |
| CC | thyroid), autoimmune/inflammatory disorders (e.g. asthma, bronchitis, | |
| CC | psoriasis, osteoporosis), viral infections, bacterial infections, fungal | |
| CC | infections, parasitic infections, developmental disorders (e.g. anaemia, | |
| CC | epilepsy), seizure disorders (e.g. cerebral palsy, spina bifida), | |
| CC | endocrine disorders (e.g. thrombosis, aneurysm), metabolic disorders | |
| CC | (e.g. obesity, diabetes), neurological disorders (e.g. stroke, | |
| CC | amyotrophic lateral sclerosis, multiple sclerosis), gastrointestinal | |
| CC | disorders (e.g. ulcerative colitis, lysinuria) and transport disorders | |
| CC | (e.g. myoclonic dystrophy, catatonica, peripheral neuropathy). Sequences | |
| CC | AB059943-AB060220 represent human DITNP polypeptides of the invention | |
| SO | | |
| XX | Sequence 189 AA; | |
| XX | | |
| Query Match | 41.1%; Score 46; DB 5; Length 189; | |
| Best Local Similarity | 50.0%; Pred. No. 2.7e+02; | |
| Matches | 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0. | |
| OY | 4 NGTTTBEKQLLEQNNL 21 | |
| | : :: :: :: :: | |
| DB | 113 SGFTIDELSGACEQFGL 130 | |
| XX | | |
| RESULT 42 | | |
| XX | AA082765 | |
| ID | AA082765 standard; protein; 216 AA. | |
| XX | | |
| AC | AA082765; | |
| XX | | |
| OT | 03-SEP-2001 (first entry) | |
| XX | | |
| DE | S. epidermidis open reading frame protein sequence SEQ ID NO:2624. | |
| XX | | |
| KW | Staphylococcus epidermidis SRI strain; infection; diagnosis; vaccination; | |
| XX | endocarditis. | |
| OS | Staphylococcus epidermidis. | |
| XX | | |
| PN | WO200134809-A2. | |
| PD | | |
| PD | 17-MAY-2001. | |
| XX | | |
| PF | 09-NOV-2000; 2000WO-US030782. | |
| XX | | |
| PR | 09-NOV-1999; 99US-0164258P. | |
| XX | | |
| PA | (GLAXO) GLAXO GROUP LTD. | |
| XX | | |
| PI | Kimmerly WJ; | |

XX WPI; 2001-316495/33.
DR N-PSDB; AAH53615.
XX
XX Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
PT useful for vaccinating against infections, e.g. endocarditis.
PS Claim 18; Page 688; 2188pp; English.
XX
XX AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
CC (II), given in AAG61454 to AAG63120, from Staphylococcus epidermidis. (I)
CC and (II) can have antibacterial activity and therefore can be used in
CC vaccination. The nucleic acids (I) may be used to produce the S.
CC epidermidis polypeptides (II) via the production of vectors containing
CC them which are used to produce host cells which express the
CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
CC used to vaccinate subjects and to raise antibodies against the bacteria.
CC The polypeptides may also be used to assay for other inhibitors of their
CC activity and therefore identify compounds that may be used for the
CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
CC AAH55090 represent specifically claimed S. epidermidis genomic DNA
CC polynucleotide sequences from the present invention. AAH55091 to AAH55098
CC represent oligonucleotide sequences and primers which are used in the
CC exemplification of the present invention. N.B. The present invention
CC specifically claims all the polynucleotide sequences given in the
CC sequence listing of the present specification, however the sequence
CC listing only goes up to SEQ ID NO:4454 so even though sequences are given
CC in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present
CC for SEQ ID NO:4455 to 4464
XX
SQ Sequence 216 AA;
Query Match 41.1%; Score 46; DB 4; Length 216;
Best Local Similarity 60.0%; Pred. No. 3.1e+02;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 4 NGTIVBELKQLLEQ 18
DB 59 NGMTLEAKYQLE 73
RESULT 43
ABJ19037
ID ABJ19037 standard; protein; 216 AA.
AC
XX ABJ19037;
XX
DT 06-MAR-2003 (first entry)
XX
DE Pathogen specific antigen related staphylococcal protein SEQ ID No 286.
XX
XX Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV;
XX hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen;
XX auto-immunity; vaccine; staphylococcal infection; antibody; cancer;
XX autoimmune disease; HIV; hepatitis.
XX
OS Staphylococcus sp.
XX
XX WO200259148-A2.
XX
PN 01-AUG-2002.
XX
PD 21-JAN-2002; 2002WO-EP000546.
XX
PF 21-JAN-2002; 2002WO-EP000546.
XX
PR 26-JAN-2001; 2001AT-00000130.
XX
XX (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
XX
XX Meinke A, Nagy E, Von Ahesen U, Klade C, Henics T, Zauner W;
PI Minke DB, Vytvytska O, Etz H, Dryla A, Weichart T, Hafner M;
PI Tempelmeier B;
XX
DR WPI; 2003-075410/07.

XX identifying, isolating and producing hyperimmune serum-reactive antigens
PT from a pathogen, for preparing vaccine or medicament for treating or
PT preventing e.g. staphylococcal infections, comprises providing antibody
PT preparation.
XX
PS Example 7; Page 201; 252pp; English.
XX
XX The invention relates to a novel method for identifying, isolating and
CC producing hyperimmune serum-reactive antigens from a pathogen, tumour,
CC allergen, a tissue or host prone to auto-immunity, where the antigens are
CC used in a vaccine, comprises providing antibody preparation from a plasma
CC pool of a type of animal, or individual sera with antibodies against the
CC specific pathogen, tumour, allergen, tissue or host prone to auto-
CC immunity. The hyperimmune serum-reactive antigens comprising any of the
CC 62 sequences of 53-2261 amino acids fully defined in the specification,
CC or their hyperimmune fragments are useful for the manufacture of a
CC pharmaceutical preparation, particularly a vaccine against staphylococcal
CC infections or colonisation against S. aureus or S. epidermidis. The
CC preparation of antibodies is useful for the manufacture of a medicament
CC for treating or preventing staphylococcal infections or colonisation
CC against S. aureus or S. epidermidis. The antibody preparations may also
CC be used for diagnostic and imaging purposes. Other conditions that can be
CC treated include cancer, autoimmune diseases or infections caused by viral
CC (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This
CC sequence represents a staphylococcal protein relating to the method for
CC identifying and producing pathogen specific antigens of the invention
XX
SQ Sequence 216 AA;
Query Match 41.1%; Score 46; DB 6; Length 216;
Best Local Similarity 60.0%; Pred. No. 3.1e+02;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 4 NGTIVBELKQLLEQ 18
DB 59 NGMTLEAKYQLE 73
RESULT 44
ADQ37007
ID ADQ37007 standard; protein; 253 AA.
AC
XX ADQ37007;
XX
DT 07-OCT-2004 (first entry)
XX
DE Cell proliferation-related polypeptide #81.
XX
XX cell proliferation related polypeptide; cell proliferation; senescence;
XX differentiation; stress response.
XX
OS Oryza sativa.
XX
XX WO2004061122-A2.
XX
XX 22-JUL-2004.
XX
PD 23-DEC-2003; 2003WO-US041200.
XX
PF 26-DEC-2002; 2002US-0436565P.
XX
PR (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
XX Cooper B;
XX
XX WPI; 2004-534389/51.
XX
XX New nucleic acid molecule encoding a cell proliferation-related
PT polypeptide, useful for modulating cell proliferation, senescence,
PT differentiation, development, and stress response in plants, and for
PT producing enhanced food crops.
XX

PS Claim 28; SEQ ID NO 166; 408bp; English.
XX
CC The present invention relates to an isolated nucleic acid molecule
CC encoding a cell proliferation-related polypeptide. The nucleic acid
CC molecule and the encoded polypeptide, and methods are useful for
CC modulating cell proliferation, senescence, differentiation, development,
CC and stress response in plants, and for producing enhanced food crops. The
CC present sequence represents a cell proliferation-related polypeptide. The
CC present sequence is published separately from the main body of the
CC specification as EPO data.
XX
SQ Sequence 253 AA;
XX
QY 4 NGTITVEELKQLLEQWNL 21
DB 186 SGRTITDELSQLACEQFGL 203
XX
Query Match 41.1%; Score 46; DB 8; Length 253;
Best Local Similarity 50.0%; Pred. No. 3.7e+02;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
XX
RESULT 45
ADQ15677
ID ADQ15677 standard; protein; 253 AA.
XX
XX ADQ15677;
XX
DT 07-OCT-2004 (first entry)
XX
XX Rice stress-related protein #43.
XX
XX Rice, stress-related protein; plant maturation; plant development;
XX plant proliferation; plant senescence; plant disease-resistance;
XX plant stress response; transgenic plant; pest tolerance;
XX herbicide tolerance; biotic stress tolerance; abiotic stress tolerance;
XX improved nutritional value; increased yield; increased proliferation.
XX
XX Oryza sativa.
XX
XX WO2004061080-A2.
XX
XX 22-JUL-2004.
XX
XX 23-DEC-2003; 2003MO-US041098.
XX
XX 26-DEC-2002; 2002US-0436564P.
XX
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
XX Cooper B;
XX
XX MPI; 2004-534374/51.
XX
XX N-PSDB; ADQ15676.
XX
XX New isolated nucleic acids and proteins, useful for producing transgenic
XX plants having improved properties, e.g. tolerance to pests, herbicides,
XX or biotic or abiotic stresses, improved nutritional value, or increased
XX yield or proliferation.
XX
XX Claim 28; SEQ ID NO 86; 551pp; English.
XX
XX The invention comprises the amino acid and coding sequences of rice
XX stress-related proteins. The DNA and protein sequences of the invention
XX are useful for regulating and controlling plant maturation and
XX development, including proliferation, senescence, disease-resistance, or
XX stress response. They are also useful for producing transgenic plants
XX having improved properties, e.g. tolerance to pests, herbicides, or
XX biotic or abiotic stresses, improved nutritional value, increased yield
XX or proliferation, or improved structure causing less loss from lodging or
XX shattering. The present amino acid sequence represents a rice stress-
XX related protein of the invention.

SQ Sequence 253 AA;
XX
QY 4 NGTITVEELKQLLEQWNL 21
DB 186 SGRTITDELSQLACEQFGL 203
XX
Query Match 41.1%; Score 46; DB 8; Length 253;
Best Local Similarity 50.0%; Pred. No. 3.7e+02;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
XX
RESULT 46
ABP40434
ID ABP40434 standard; protein; 274 AA.
XX
XX ABP40434;
XX
XX 24-JUL-2002 (first entry)
XX
XX Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5279.
XX
XX Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
XX antimicrobial; gene therapy.
XX
XX Staphylococcus epidermidis.
XX
XX US6380370-B1.
XX
XX 30-APR-2002.
XX
XX 13-AUG-1998; 98US-00134001.
XX
XX 14-AUG-1997; 97US-0055779P.
XX
XX 08-NOV-1997; 97US-0064964P.
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
XX
XX Doucette-Stamm LA, Bush D;
XX
XX MPI; 2002-381255/41.
XX
XX N-PSDB; ABN92979.
XX
XX Novel isolated nucleic acid encoding a Staphylococcus epidermis
XX polypeptide, useful for diagnosing and treating bacterial infections.
XX
XX Disclosure; SEQ ID NO 5279; 267pp; English.
XX
XX ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading
XX frame (ORF) nucleic acid sequences which encode the amino acid sequences
XX given in ABP35124 to ABP37960. The S. epidermidis sequences have
XX antibacterial activity and can be used in gene therapy. The sequences can
XX also be used in the diagnosis and treatment of bacterial infections,
XX particularly S. epidermidis infections. The sequences can be used to
XX screen for compounds able to interfere with the S. epidermidis life cycle
XX or inhibit S. epidermidis infection. N.B. The sequence data for this
XX patent did not form part of the printed specification, but was obtained
XX in electronic format directly from the USPTO web site
XX
SQ Sequence 274 AA;
XX
QY 4 NGTITVEELKQLLEQ 18
DB 117 NGMTLEBAKYGQEE 131
XX
RESULT 47
ADS05966
ID ADS05966 standard; protein; 274 AA.
XX

| | |
|-----------------------|--|
| AC | ADS05966; |
| XX | |
| DT | 04-NOV-2004 (first entry) |
| XX | |
| DE | Staphylococcus epidermis polypeptide seqid 5261. |
| XX | |
| KW | antibacterial; vaccine; antisense therapy; Staphylococcus epidermidis; recombinant expression vector; infection; computer readable medium; |
| KM | computer based system. |
| XX | |
| OS | Staphylococcus epidermidis. |
| XX | |
| PN | US2004147734-A1. |
| XX | |
| PD | 29-JUL-2004. |
| XX | |
| PF | 01-DEC-2003; 2003US-00724972. |
| PR | 08-NOV-1997; 97US-0064964P. 13-AUG-1998; 98US-00134001. 29-NOV-1999; 99US-00450969. |
| PR | |
| PA | (DOUC/) DOUCETTE-STAMM L. (BUSH/) BUSH D. |
| XX | |
| PI | Doucette-Stamm L, Bush D; |
| XX | |
| DR | WPI, 2004-580138/56. N-PSDB; ADS02194. |
| XX | |
| PT | New isolated polypeptide and encoding nucleic acid derived from Staphylococcus epidermidis, useful for diagnosing, preventing and/or treating an S. epidermidis bacterial infection. |
| XX | |
| PS | Claim 17, SEQ ID NO 5261; 741bp; English. |
| XX | |
| CC | The invention describes an isolated nucleic acid comprising a nucleotide sequence with any of 3772 fully defined nucleotide sequences (SEQ ID NO: 1-3772) and encoding an Staphylococcus epidermidis polypeptide with any of 3772 fully defined amino acid sequences (SEQ ID NO: 3772-7544) as given in the specification. Also described are: a recombinant expression vector; a cell comprising a recombinant expression vector of (1); producing an S. epidermidis polypeptide; an isolated nucleic acid comprising a nucleotide sequence of at least 8 nucleotides in length; a vaccine composition for prevention or treatment of an S. epidermidis infection, comprising a nucleic acid cited above and a carrier; treating a subject for S. epidermidis infection; a recombinant or substantially pure preparation of an S. epidermidis polypeptide or its fragment; a vaccine composition for prevention or treatment of an S. epidermidis infection; detecting the presence of a Staphylococcus nucleic acid in a sample; a computer readable medium having recorded in it the nucleotide sequences with SEQ ID NO: 1-3772 or its fragments; a computer based system for identifying fragments of the Staphylococcus genome of commercial importance; a computer based system for identifying fragments of the Staphylococcus plasmids of commercial importance; identifying commercially important nucleic acid fragments of the Staphylococcus genome and/or plasmids; and identifying an expression modulating fragment of the Staphylococcus genome and/or plasmids. The methods and compositions of the present invention are useful for the diagnosis, prevention and/or treatment of an Staphylococcal epidermidis bacterial infection. This is the amino acid sequence of a S. epidermis protein of the invention. |
| CC | |
| CC | |
| CC | |
| XX | Sequence 274 AA; |
| SQ | |
| Query Match | 41.1%; Score 46; DB 8; Length 274; |
| Best Local Similarity | 60.0%; Pred. No. 4e+02; |
| Matches | 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0; |
| b3 | NGTITVEELKQLSQ 18 :-: : 117 NGTITVEELAKYQLSE 131 |

[illegible]

XX Acinetobacter sp. caprolactone hydrolase.
DE Adipic acid, nylon-6,6; lubricant; plasticizer; food acidulant; enzyme;
XX caprolactone hydrolase.
KW Acinetobacter sp.
XX US2003087403-A1.
PN 08-MAY-2003.
PD 16-OCT-2002; 2002US-00272419.
PF 19-FEB-1999; 99US-00252553.
PR 14-JUL-1999; 99US-00648004.
XX (CHEN/) CHENG Q.
PA (NAGA/) NAGARAJAN V.
PA (THOM/) THOMAS S M.
PI Cheng Q, Nagarajan V, Thomas SM;
XX WPI; 2003-755145/71.
DR N-PSDB; AAD59830.
XX New nucleic acid fragment encoding an adipic acid synthesizing enzyme,
PT useful for producing nylon-6,6, lubricants and plasticizers, or as food
XX acidulant.
PS Claim 4; Page 31-32; 45pp; English.
XX The present invention provides novel nucleic acid molecules derived from
CC Acinetobacter sp. encoding adipic acid synthesizing enzymes, useful for
CC producing nylon-6,6, lubricants and plasticizers. The invention is also
CC useful as food acidulant. The present sequence is Acinetobacter sp.
CC caprolactone hydrolase enzyme. This enzyme is involved in the synthesis
CC of adipic acid
SQ Sequence 300 AA;
QY Query Match 41.1%; Score 46; DB 7; Length 300;
Best Local Similarity 25.0%; Pred. No. 4.5e+02;
Matches 5; Conservative 9; Mismatches 6; Indels 0; Gaps 0;
Db 1 MADNGTTVEELKQLEQWN 20
22 MQENPMNTIEDFRSMFDEWH 41
RESULT 50
AAG34981
ID AAG34981 standard; protein; 385 AA.
XX AAG34981;
AC 18-OCT-2000 (first entry)
DT Arabidopsis thaliana protein fragment SEQ ID NO: 42658.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 42658.
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridization assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX Arabidopsis thaliana.
OS EP1033405-A2.
PN 06-SEP-2000.
PD 25-FEB-2000; 2000EP-00301439.
PF 25-FEB-1999; 99US-0121825P.
XX

PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
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PR 28-APR-1999; 99US-0130891P.
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PR 30-APR-1999; 99US-0132048P.
PR 04-MAY-1999; 99US-0132407P.
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PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
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PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 08-JUN-1999; 99US-0137724P.
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PR 28-OCT-1999; 99US-0161920P.
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PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 41.1%; Score 46; DB 3; Length 385;
Best Local Similarity 44.4%; Pred. No. 5.8e+02;
Matches 12; Conservative 3; Mismatches 4; Indels 8; Gaps 1;
Qy 2 ADNGTIT-----VEELKOLLEQWN 20
Db 92 SDNGTIEDIVENDLHLLQLEEVGN 118

Search completed: May 11, 2005, 21:22:33
Job time : 160.489 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 11, 2005, 21:13:34 : Search time 22 Seconds
(without alignments)
96.217 Million cell updates/sec

Title: US-10-712-812-5

Perfect score: 112
Sequence: 1 MADNGTITVEELKQLEQNNLV 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 58 | 51.8 | 376 | 2 | TS1170 |
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| 3 | 51 | 45.5 | 344 | 2 | D83894 |
| 4 | 51 | 45.5 | 351 | 2 | E97225 |
| 5 | 50 | 44.6 | 323 | 2 | C64087 |
| 6 | 50 | 44.6 | 673 | 2 | P82930 |
| 7 | 50 | 44.6 | 882 | 2 | S41034 |
| 8 | 49 | 43.8 | 218 | 2 | S50566 |
| 9 | 49 | 43.8 | 462 | 2 | B32840 |
| 10 | 48 | 42.9 | 206 | 1 | TVGJRA |
| 11 | 48 | 42.9 | 206 | 2 | JN0622 |
| 12 | 48 | 42.9 | 309 | 2 | T23021 |
| 13 | 48 | 42.9 | 462 | 2 | S52528 |
| 14 | 47.5 | 42.4 | 294 | 2 | S60545 |
| 15 | 47.5 | 42.4 | 294 | 2 | S60524 |
| 16 | 47 | 42.0 | 159 | 1 | S56237 |
| 17 | 47 | 42.0 | 312 | 2 | AC0897 |
| 18 | 47 | 42.0 | 335 | 2 | AG2311 |
| 19 | 47 | 42.0 | 627 | 2 | B83692 |
| 20 | 47 | 42.0 | 659 | 2 | S74435 |
| 21 | 47 | 42.0 | 1067 | 2 | T06312 |
| 22 | 46.5 | 41.5 | 201 | 2 | E97339 |
| 23 | 46.5 | 41.5 | 428 | 2 | G82338 |
| 24 | 46 | 41.1 | 438 | 2 | E90178 |
| 25 | 46 | 41.1 | 340 | 2 | E69527 |
| 26 | 46 | 41.1 | 420 | 2 | C71407 |
| 27 | 46 | 41.1 | 472 | 2 | H90563 |
| 28 | 46 | 41.1 | 474 | 2 | H72403 |
| 29 | 46 | 41.1 | 506 | 2 | AC0845 |

| | | | | | | |
|-----|------|------|------|---|--------|---------------------|
| 30 | 46 | 41.1 | 529 | 2 | A65051 | YgaA protein - Ec |
| 31 | 46 | 41.1 | 529 | 2 | E91074 | probable 2-compone |
| 32 | 46 | 41.1 | 529 | 2 | D85919 | probable 2-compone |
| 33 | 46 | 41.1 | 536 | 1 | JC6129 | 3',5'-cyclic-nucle |
| 34 | 46 | 41.1 | 545 | 2 | G81328 | 60 kD chaperonin (|
| 35 | 46 | 41.1 | 594 | 2 | A82913 | hypothetical prote |
| 36 | 45.5 | 40.6 | 88 | 2 | A82591 | conserved hypothet |
| 37 | 45.5 | 40.6 | 88 | 2 | B97373 | hypothetical prote |
| 38 | 45.5 | 40.6 | 422 | 2 | AD0141 | adenosylmethionine |
| 39 | 45 | 40.2 | 104 | 2 | P90183 | hypothetical prote |
| 40 | 45 | 40.2 | 128 | 2 | C63183 | hypothetical prote |
| 41 | 45 | 40.2 | 226 | 2 | S37434 | membrane glycoprot |
| 42 | 45 | 40.2 | 226 | 2 | D49591 | membrane protein M |
| 43 | 45 | 40.2 | 264 | 2 | T38795 | conserved uncharac |
| 44 | 45 | 40.2 | 318 | 2 | T43492 | hypothetical prote |
| 45 | 45 | 40.2 | 335 | 2 | P72404 | flagellar motor sw |
| 46 | 45 | 40.2 | 335 | 2 | F82012 | hypothetical prote |
| 47 | 45 | 40.2 | 418 | 2 | F82012 | hypothetical prote |
| 48 | 45 | 40.2 | 534 | 1 | A44162 | calcium-dependent |
| 49 | 45 | 40.2 | 535 | 1 | A44161 | 3',5'-cyclic-nucle |
| 50 | 45 | 40.2 | 535 | 1 | A46378 | 3',5'-cyclic-nucle |
| 51 | 45 | 40.2 | 626 | 2 | AC1619 | DNA primase [import |
| 52 | 45 | 40.2 | 626 | 2 | AG1256 | DNA primase [import |
| 53 | 45 | 40.2 | 643 | 2 | H64119 | threonine-tRNA lig |
| 54 | 45 | 40.2 | 644 | 2 | T02366 | hypothetical prote |
| 55 | 45 | 40.2 | 755 | 2 | T47806 | hypothetical prote |
| 56 | 45 | 40.2 | 897 | 2 | AC2001 | hypothetical prote |
| 57 | 45 | 40.2 | 1052 | 2 | T17093 | intraluminal subu |
| 58 | 45 | 40.2 | 1696 | 2 | T00057 | hypothetical prote |
| 59 | 44.5 | 39.7 | 146 | 2 | G90201 | conserved hypothet |
| 60 | 44.5 | 39.7 | 536 | 2 | T05500 | calcium-dependent |
| 61 | 44.5 | 39.7 | 852 | 2 | T12016 | envelope glycoprot |
| 62 | 44 | 39.3 | 100 | 2 | T49043 | hypothetical prote |
| 63 | 44 | 39.3 | 258 | 2 | A53963 | ubiquinol-cytochro |
| 64 | 44 | 39.3 | 308 | 1 | F69752 | 5-dehydro-4-deoxyg |
| 65 | 44 | 39.3 | 401 | 2 | E72213 | probable 2,3-bisph |
| 66 | 44 | 39.3 | 447 | 2 | F90248 | hypothetical prote |
| 67 | 44 | 39.3 | 511 | 2 | H89758 | histidine ammonia- |
| 68 | 44 | 39.3 | 553 | 2 | D84133 | exo-alpha-1,4-gluc |
| 69 | 44 | 39.3 | 571 | 2 | C70353 | succinate dehydrog |
| 70 | 44 | 39.3 | 603 | 2 | G82738 | gamma-glutamyltran |
| 71 | 44 | 39.3 | 750 | 2 | S34683 | hypothetical prote |
| 72 | 44 | 39.3 | 919 | 2 | E83212 | probable sensor/re |
| 73 | 44 | 39.3 | 1019 | 2 | F70342 | cation efflux syst |
| 74 | 44 | 39.3 | 1577 | 2 | T30858 | glucosyltransferas |
| 75 | 44 | 39.3 | 1505 | 2 | E15553 | Plexin - African c |
| 76 | 44 | 39.3 | 5369 | 2 | T44807 | mycobubillin synth |
| 77 | 43.5 | 38.8 | 209 | 2 | H69901 | general stress pro |
| 78 | 43.5 | 38.8 | 355 | 2 | S74678 | hypothetical prote |
| 79 | 43.5 | 38.8 | 429 | 1 | JC5005 | adenosylmethionine |
| 80 | 43.5 | 38.8 | 429 | 2 | AG0596 | adenosylmethionine |
| 81 | 43.5 | 38.8 | 571 | 2 | T00835 | calcium-dependent |
| 82 | 43 | 38.4 | 80 | 2 | B82267 | exodeoxyribonuclea |
| 83 | 43 | 38.4 | 145 | 2 | A56085 | regulatory protein |
| 84 | 43 | 38.4 | 178 | 2 | AG0049 | hypothetical prote |
| 85 | 43 | 38.4 | 199 | 2 | A44033 | ubiquinol-cytochro |
| 86 | 43 | 38.4 | 206 | 1 | E64317 | hypothetical prote |
| 87 | 43 | 38.4 | 237 | 2 | D97801 | hypothetical prote |
| 88 | 43 | 38.4 | 267 | 2 | H69373 | hypothetical prote |
| 89 | 43 | 38.4 | 278 | 2 | T24444 | hypothetical prote |
| 90 | 43 | 38.4 | 279 | 2 | B72255 | dimethyladenosine |
| 91 | 43 | 38.4 | 292 | 2 | D85863 | probable regulator |
| 92 | 43 | 38.4 | 292 | 2 | B91019 | probable transcrip |
| 93 | 43 | 38.4 | 322 | 2 | S52032 | triose-phosphate 1 |
| 94 | 43 | 38.4 | 336 | 2 | S74424 | sphx protein - Syn |
| 95 | 43 | 38.4 | 353 | 2 | T15429 | hypothetical prote |
| 96 | 43 | 38.4 | 420 | 2 | AH2225 | two-component sens |
| 97 | 43 | 38.4 | 429 | 2 | D70763 | threonine ammonia- |
| 98 | 43 | 38.4 | 469 | 2 | A72377 | 6-phosphogluconate |
| 99 | 43 | 38.4 | 481 | 2 | UQ1147 | N-acetylmutamoyl-L |
| 100 | 43 | 38.4 | 490 | 2 | T08873 | calcium-dependent |
| 101 | 43 | 38.4 | 499 | 2 | AH0485 | probable insulinas |
| 102 | 43 | 38.4 | 500 | 2 | A71874 | hypothetical prote |

| | | | | | | | | | | | | | |
|-----|------|------|------|---|--------|---------------------|-----|------|------|-----|---|--------|---------------------|
| 103 | 43 | 38.4 | 510 | 2 | B70368 | L-aspartate oxidase | 176 | 41.5 | 37.1 | 236 | 2 | A86075 | probable transcrip |
| 104 | 43 | 38.4 | 521 | 2 | B71717 | hypothetical prote | 177 | 41.5 | 37.1 | 236 | 2 | S40817 | hypothetical prote |
| 105 | 43 | 38.4 | 532 | 2 | S22362 | transcription fact | 178 | 41.5 | 37.1 | 236 | 2 | B91228 | probable transcrip |
| 106 | 43 | 38.4 | 577 | 2 | T51264 | calcium-dependent | 179 | 41.5 | 37.1 | 239 | 2 | D70359 | conserved hypothet |
| 107 | 43 | 38.4 | 602 | 2 | S60052 | calcium-dependent | 180 | 41.5 | 37.1 | 239 | 2 | B84964 | adenosylmethionine |
| 108 | 43 | 38.4 | 642 | 2 | C81345 | hypothetical prote | 181 | 41.5 | 37.1 | 450 | 2 | D86356 | hypothetical prote |
| 109 | 43 | 38.4 | 759 | 2 | D89946 | protein-export mem | 182 | 41.5 | 37.1 | 589 | 2 | H86356 | probable UDP-gluc |
| 110 | 43 | 38.4 | 1245 | 2 | G88104 | protein F40B12.2 [| 183 | 41.5 | 37.1 | 559 | 2 | T09038 | NADH dehydrogenase |
| 111 | 43 | 38.4 | 1245 | 2 | T31953 | hypothetical prote | 184 | 41.5 | 37.1 | 639 | 1 | T02784 | calcium-dependent |
| 112 | 43 | 38.4 | 1495 | 2 | S61023 | hypothetical prote | 185 | 41.5 | 37.1 | 678 | 2 | S56284 | hypothetical prote |
| 113 | 42.5 | 37.9 | 224 | 2 | D89836 | hypothetical prote | 186 | 41.5 | 37.1 | 846 | 1 | VCLJND | env. polyprotein pr |
| 114 | 42.5 | 37.9 | 321 | 2 | A69088 | conserved hypothet | 187 | 41.5 | 37.1 | 886 | 1 | F83862 | penicillin-binding |
| 115 | 42.5 | 37.9 | 340 | 2 | PH0217 | reverse transcript | 188 | 41 | 36.6 | 71 | 1 | RGBOG2 | GRP-binding regula |
| 116 | 42.5 | 37.9 | 428 | 2 | S09134 | gene ND4L, intron 1 | 189 | 41 | 36.6 | 71 | 2 | UC7290 | guanine nucleotide |
| 117 | 42.5 | 37.9 | 429 | 1 | XNECDP | adenosylmethionine | 190 | 41 | 36.6 | 118 | 2 | G70478 | hypothetical prote |
| 118 | 42.5 | 37.9 | 429 | 2 | E85585 | 7,8-diaminopelargo | 191 | 41 | 36.6 | 138 | 2 | H90461 | hypothetical prote |
| 119 | 42.5 | 37.9 | 429 | 2 | D90735 | 7,8-diaminopelargo | 192 | 41 | 36.6 | 140 | 2 | A10114 | conserved hypothet |
| 120 | 42.5 | 37.9 | 513 | 2 | S21976 | probable RNA-dir | 193 | 41 | 36.6 | 147 | 2 | A23910 | myosin calcium-bdn |
| 121 | 42.5 | 37.9 | 556 | 2 | S21347 | hypothetical prote | 194 | 41 | 36.6 | 150 | 1 | MC2P | caldmodulin - fibri |
| 122 | 42.5 | 37.9 | 666 | 2 | S71032 | flagellar hook-ass | 195 | 41 | 36.6 | 150 | 2 | S18394 | crotonin C isoform |
| 123 | 42.5 | 37.9 | 685 | 2 | S16783 | probable RNA-dir | 196 | 41 | 36.6 | 152 | 2 | A11018 | SoxR protein (limp |
| 124 | 42.5 | 37.9 | 821 | 2 | T24728 | hypothetical prote | 197 | 41 | 36.6 | 154 | 2 | E91259 | SoxR protein (limp |
| 125 | 42.5 | 37.9 | 932 | 2 | H86325 | hypothetical prote | 198 | 41 | 36.6 | 154 | 2 | A86100 | redox-sensing acti |
| 126 | 42.5 | 37.9 | 1601 | 2 | AE2011 | hypothetical prote | 199 | 41 | 36.6 | 154 | 2 | US0577 | soxR protein - Esc |
| 127 | 42 | 37.5 | 58 | 2 | T04616 | hypothetical prote | 200 | 41 | 36.6 | 156 | 2 | T32236 | hypothetical prote |
| 128 | 42 | 37.5 | 82 | 2 | A99836 | hypothetical prote | 201 | 41 | 36.6 | 159 | 2 | T32233 | hypothetical prote |
| 129 | 42 | 37.5 | 82 | 2 | C85694 | unknown protein en | 202 | 41 | 36.6 | 161 | 2 | S47549 | cell division cont |
| 130 | 42 | 37.5 | 103 | 2 | P69110 | hypothetical prote | 203 | 41 | 36.6 | 169 | 2 | D84864 | probable calcium b |
| 131 | 42 | 37.5 | 134 | 2 | AE2496 | transposase alt714 | 204 | 41 | 36.6 | 169 | 2 | H75387 | hypothetical prote |
| 132 | 42 | 37.5 | 135 | 2 | T29428 | hypothetical prote | 205 | 41 | 36.6 | 186 | 2 | F89831 | hypothetical prote |
| 133 | 42 | 37.5 | 158 | 2 | A72562 | hypothetical prote | 206 | 41 | 36.6 | 207 | 2 | A69349 | conserved hypothet |
| 134 | 42 | 37.5 | 172 | 2 | G69087 | conserved hypothet | 207 | 41 | 36.6 | 211 | 2 | T32591 | hypothetical prote |
| 135 | 42 | 37.5 | 186 | 2 | F82508 | hypothetical prote | 208 | 41 | 36.6 | 240 | 2 | T22210 | hypothetical prote |
| 136 | 42 | 37.5 | 189 | 2 | B69044 | conserved hypothet | 209 | 41 | 36.6 | 280 | 2 | F66768 | hypothetical prote |
| 137 | 42 | 37.5 | 191 | 2 | T10620 | probable calcium-b | 210 | 41 | 36.6 | 292 | 2 | AC0791 | probable transcrip |
| 138 | 42 | 37.5 | 225 | 2 | AF0219 | basal-body rod mod | 211 | 41 | 36.6 | 307 | 2 | B69837 | hypothetical prote |
| 139 | 42 | 37.5 | 229 | 1 | B43685 | nonstructural prot | 212 | 41 | 36.6 | 312 | 1 | QDECRG | tdcA protein - Bac |
| 140 | 42 | 37.5 | 244 | 2 | E72364 | ABC transporter, A | 213 | 41 | 36.6 | 312 | 2 | E85973 | transcription acti |
| 141 | 42 | 37.5 | 314 | 2 | G70750 | DNA-methyltransfer | 214 | 41 | 36.6 | 312 | 2 | F91128 | transcription acti |
| 142 | 42 | 37.5 | 368 | 2 | B97198 | probable enzyme wi | 215 | 41 | 36.6 | 325 | 2 | T32838 | hypothetical prote |
| 143 | 42 | 37.5 | 377 | 2 | A38862 | crRNA-splicing endo | 216 | 41 | 36.6 | 325 | 2 | E83165 | hypothetical prote |
| 144 | 42 | 37.5 | 389 | 1 | A48329 | histidinol-phospha | 217 | 41 | 36.6 | 338 | 2 | G71220 | hypothetical prote |
| 145 | 42 | 37.5 | 399 | 1 | A43685 | polymerase-associ | 218 | 41 | 36.6 | 344 | 2 | G75260 | response regulator |
| 146 | 42 | 37.5 | 423 | 2 | T29549 | hypothetical prote | 219 | 41 | 36.6 | 344 | 2 | T48827 | hypothetical prote |
| 147 | 42 | 37.5 | 427 | 2 | C87060 | threonine deaminase | 220 | 41 | 36.6 | 407 | 2 | S27774 | transforming prote |
| 148 | 42 | 37.5 | 451 | 2 | S56717 | calcium-dependent | 221 | 41 | 36.6 | 408 | 2 | AG1745 | amino transferase h |
| 149 | 42 | 37.5 | 464 | 2 | T22087 | hypothetical prote | 222 | 41 | 36.6 | 416 | 2 | F71869 | hypothetical prote |
| 150 | 42 | 37.5 | 468 | 2 | D85828 | gluconate-6-phosph | 223 | 41 | 36.6 | 420 | 2 | T43932 | cell division cont |
| 151 | 42 | 37.5 | 468 | 2 | F90982 | gluconate-6-phosph | 224 | 41 | 36.6 | 441 | 2 | AB1290 | ATP-dependent RNA |
| 152 | 42 | 37.5 | 482 | 2 | T01659 | phosphogluconate d | 225 | 41 | 36.6 | 442 | 2 | AH1661 | ATP-dependent RNA |
| 153 | 42 | 37.5 | 484 | 2 | T01658 | phosphogluconate d | 226 | 41 | 36.6 | 455 | 2 | H71028 | hypothetical prote |
| 154 | 42 | 37.5 | 509 | 2 | AB1295 | Bifunctional phosph | 227 | 41 | 36.6 | 461 | 2 | S50864 | avermectin-sensiti |
| 155 | 42 | 37.5 | 509 | 2 | AC1667 | Bifunctional phosph | 228 | 41 | 36.6 | 465 | 2 | D83598 | probable zinc prot |
| 156 | 42 | 37.5 | 521 | 2 | G96543 | calcium-dependent | 229 | 41 | 36.6 | 472 | 1 | B53236 | transcription fact |
| 157 | 42 | 37.5 | 529 | 1 | S71774 | calcium-dependent | 230 | 41 | 36.6 | 472 | 2 | AD1889 | adenylate cyclase |
| 158 | 42 | 37.5 | 540 | 2 | D81192 | hypothetical prote | 231 | 41 | 36.6 | 477 | 2 | E64595 | hypothetical prote |
| 159 | 42 | 37.5 | 553 | 1 | T02139 | calcium-dependent | 232 | 41 | 36.6 | 477 | 2 | F71918 | hypothetical prote |
| 160 | 42 | 37.5 | 554 | 1 | T03263 | calcium-dependent | 233 | 41 | 36.6 | 486 | 2 | S57786 | phosphogluconate d |
| 161 | 42 | 37.5 | 601 | 2 | C81044 | hypothetical prote | 234 | 41 | 36.6 | 492 | 2 | S50554 | hypothetical prote |
| 162 | 42 | 37.5 | 674 | 2 | S74506 | ribonuclease E - S | 235 | 41 | 36.6 | 494 | 2 | S75398 | lysine-tRNA ligase |
| 163 | 42 | 37.5 | 750 | 2 | AG3008 | polyketide synthet | 236 | 41 | 36.6 | 495 | 1 | S46284 | calcium-dependent |
| 164 | 42 | 37.5 | 779 | 2 | F98275 | saframycin mxi syn | 237 | 41 | 36.6 | 495 | 2 | T20754 | hypothetical prote |
| 165 | 42 | 37.5 | 970 | 2 | E72236 | clostridial-relate | 238 | 41 | 36.6 | 501 | 2 | G85097 | hypothetical prote |
| 166 | 42 | 37.5 | 1125 | 2 | T30298 | dysome heavy chain | 239 | 41 | 36.6 | 510 | 2 | JC7886 | cytochrome P450 92 |
| 167 | 42 | 37.5 | 1203 | 2 | B55094 | chromosomal protel | 240 | 41 | 36.6 | 520 | 2 | C84774 | probable calcium-d |
| 168 | 42 | 37.5 | 1268 | 2 | A49674 | flighless-I homol | 241 | 41 | 36.6 | 526 | 2 | E86149 | Tlnc.20 protein - |
| 169 | 42 | 37.5 | 1286 | 2 | A88396 | sax-3 protein - Ca | 242 | 41 | 36.6 | 534 | 2 | H82244 | sensor histidine k |
| 170 | 42 | 37.5 | 1386 | 1 | RNLWC2 | protein M01E10.2 [| 243 | 41 | 36.6 | 538 | 2 | A70485 | single-strand-DNA- |
| 171 | 42 | 37.5 | 1409 | 2 | T29594 | DNA-directed RNA p | 244 | 41 | 36.6 | 546 | 2 | S35311 | heat shock cognate |
| 172 | 42 | 37.5 | 1415 | 2 | C86438 | hypothetical prote | 245 | 41 | 36.6 | 557 | 2 | AC1317 | ABC transporter AT |
| 173 | 42 | 37.5 | 1733 | 2 | D70887 | hypothetical prote | 246 | 41 | 36.6 | 572 | 2 | S58889 | collapsin response |
| 174 | 42 | 37.5 | 4488 | 1 | RR1HM2 | probable polyketid | 247 | 41 | 36.6 | 604 | 2 | G89864 | hypothetical prote |
| 175 | 42 | 37.5 | 4488 | 1 | RR1HM2 | genome polyprotein | 248 | 41 | 36.6 | 611 | 2 | T21747 | hypothetical prote |

| | | | | | | | | | | | | |
|-----|------|------|------|---|-------------------------|-----|----|------|-----|---|--------|---------------------|
| 249 | 41 | 36.6 | 627 | 2 | C98148 | 322 | 40 | 35.7 | 188 | 2 | E82370 | Sua5/Ycd10/Yrdc Fam |
| 250 | 41 | 36.6 | 627 | 2 | transcription regu | 323 | 40 | 35.7 | 190 | 2 | A90354 | conserved hypochet |
| 251 | 41 | 36.6 | 630 | 2 | transcription ABC trans | 324 | 40 | 35.7 | 192 | 2 | T17331 | hypothetical prote |
| 252 | 41 | 36.6 | 654 | 2 | hypothetical prote | 325 | 40 | 35.7 | 198 | 2 | T20305 | hypothetical prote |
| 253 | 41 | 36.6 | 692 | 1 | phosphotransferase | 326 | 40 | 35.7 | 214 | 2 | T00879 | MADS-box protein A |
| 254 | 41 | 36.6 | 695 | 2 | probable tail-host | 327 | 40 | 35.7 | 226 | 1 | H69474 | conserved hypochet |
| 255 | 41 | 36.6 | 712 | 1 | ribonucleoside-tri | 328 | 40 | 35.7 | 229 | 1 | D43685 | nonstructural prot |
| 256 | 41 | 36.6 | 712 | 1 | AC1058 | 329 | 40 | 35.7 | 231 | 1 | D64170 | hypothetical prote |
| 257 | 41 | 36.6 | 712 | 2 | G91280 | 330 | 40 | 35.7 | 231 | 2 | B81057 | hypothetical prote |
| 258 | 41 | 36.6 | 712 | 2 | G86121 | 331 | 40 | 35.7 | 231 | 2 | B81060 | hypothetical prote |
| 259 | 41 | 36.6 | 712 | 2 | G86121 | 332 | 40 | 35.7 | 234 | 2 | S27956 | arginine-rich prot |
| 260 | 41 | 36.6 | 754 | 2 | topoisomerase IV s | 333 | 40 | 35.7 | 235 | 2 | AB1515 | probable phosphopr |
| 261 | 41 | 36.6 | 785 | 2 | chemotaxis protein | 334 | 40 | 35.7 | 248 | 2 | T04170 | MADS box protein - |
| 262 | 41 | 36.6 | 812 | 2 | H83904 | 335 | 40 | 35.7 | 250 | 2 | G81365 | probable ABC-type |
| 263 | 41 | 36.6 | 821 | 2 | H84600 | 336 | 40 | 35.7 | 260 | 2 | A90330 | hypothetical prote |
| 264 | 41 | 36.6 | 831 | 2 | H84368 | 337 | 40 | 35.7 | 270 | 2 | A42882 | molality protein (|
| 265 | 41 | 36.6 | 831 | 2 | UC7880 | 338 | 40 | 35.7 | 282 | 2 | H70571 | probable oxidoredu |
| 266 | 41 | 36.6 | 843 | 2 | T13334 | 339 | 40 | 35.7 | 294 | 2 | E86731 | hypothetical prote |
| 267 | 41 | 36.6 | 847 | 2 | AG1949 | 340 | 40 | 35.7 | 307 | 2 | S16390 | auxin-induced prot |
| 268 | 41 | 36.6 | 883 | 2 | B95237 | 341 | 40 | 35.7 | 315 | 2 | AH0897 | probable carbohydr |
| 269 | 41 | 36.6 | 890 | 2 | C98101 | 342 | 40 | 35.7 | 327 | 2 | AT1422 | hypothetical prote |
| 270 | 41 | 36.6 | 953 | 1 | B30169 | 343 | 40 | 35.7 | 328 | 2 | C90196 | conserved hypochet |
| 271 | 41 | 36.6 | 1271 | 2 | T43269 | 344 | 40 | 35.7 | 332 | 2 | AF3265 | asparaginase (EC 3 |
| 272 | 41 | 36.6 | 1411 | 2 | S55123 | 345 | 40 | 35.7 | 333 | 2 | H82245 | glyceraldhyde 3-P |
| 273 | 41 | 36.6 | 1557 | 2 | T29132 | 346 | 40 | 35.7 | 336 | 2 | D71016 | probable thiooxid |
| 274 | 41 | 36.6 | 1795 | 2 | T30332 | 347 | 40 | 35.7 | 339 | 2 | H75187 | hypothetical prote |
| 275 | 41 | 36.6 | 1819 | 2 | D97033 | 348 | 40 | 35.7 | 345 | 2 | D75116 | chloroform reduct |
| 276 | 41 | 36.6 | 3026 | 2 | T28431 | 349 | 40 | 35.7 | 351 | 2 | A87716 | uroporphyrinogen d |
| 277 | 40.5 | 36.2 | 98 | 2 | D95371 | 350 | 40 | 35.7 | 367 | 1 | T44672 | H+-transporting AT |
| 278 | 40.5 | 36.2 | 243 | 2 | S43887 | 351 | 40 | 35.7 | 367 | 1 | D70395 | conserved hypochet |
| 279 | 40.5 | 36.2 | 243 | 2 | F81130 | 352 | 40 | 35.7 | 372 | 1 | S76448 | translation releas |
| 280 | 40.5 | 36.2 | 243 | 2 | H86487 | 353 | 40 | 35.7 | 374 | 2 | E70346 | mannosyltransferas |
| 281 | 40.5 | 36.2 | 261 | 2 | B97589 | 354 | 40 | 35.7 | 379 | 2 | H84398 | phosphate ABC tran |
| 282 | 40.5 | 36.2 | 261 | 2 | AG2810 | 355 | 40 | 35.7 | 379 | 2 | S42543 | hypothetical prote |
| 283 | 40.5 | 36.2 | 299 | 2 | S60521 | 356 | 40 | 35.7 | 383 | 2 | AB1567 | teichoic acid bios |
| 284 | 40.5 | 36.2 | 299 | 2 | S60551 | 357 | 40 | 35.7 | 389 | 2 | G72027 | conserved hypochet |
| 285 | 40.5 | 36.2 | 299 | 2 | S60552 | 358 | 40 | 35.7 | 389 | 2 | G86597 | CT712 hypochet |
| 286 | 40.5 | 36.2 | 299 | 2 | S60523 | 359 | 40 | 35.7 | 399 | 1 | C43685 | polymyrase-associa |
| 287 | 40.5 | 36.2 | 299 | 2 | S60554 | 360 | 40 | 35.7 | 427 | 2 | A53664 | carboxyl-terminal |
| 288 | 40.5 | 36.2 | 299 | 2 | S60553 | 361 | 40 | 35.7 | 443 | 2 | H96841 | hypothetical prote |
| 289 | 40.5 | 36.2 | 376 | 2 | T16050 | 362 | 40 | 35.7 | 445 | 2 | T36069 | hypothetical prote |
| 290 | 40.5 | 36.2 | 427 | 2 | F87465 | 363 | 40 | 35.7 | 459 | 2 | F75049 | hypothetical prote |
| 291 | 40.5 | 36.2 | 459 | 2 | S10840 | 364 | 40 | 35.7 | 462 | 2 | G96506 | hypochet |
| 292 | 40.5 | 36.2 | 459 | 2 | T39668 | 365 | 40 | 35.7 | 468 | 2 | I41250 | phosphoglucanate d |
| 293 | 40.5 | 36.2 | 479 | 2 | F86356 | 366 | 40 | 35.7 | 469 | 1 | TVHME2 | transcription fact |
| 294 | 40.5 | 36.2 | 516 | 2 | T33061 | 367 | 40 | 35.7 | 470 | 1 | S55655 | hypochet |
| 295 | 40.5 | 36.2 | 523 | 2 | C82289 | 368 | 40 | 35.7 | 470 | 2 | F91291 | probable regulator |
| 296 | 40.5 | 36.2 | 614 | 2 | T33149 | 369 | 40 | 35.7 | 473 | 2 | H86132 | probable regulator |
| 297 | 40.5 | 36.2 | 685 | 2 | S65974 | 370 | 40 | 35.7 | 473 | 2 | D83508 | two-component resp |
| 298 | 40.5 | 36.2 | 836 | 2 | B84417 | 371 | 40 | 35.7 | 478 | 1 | S73919 | pet112 protein hom |
| 299 | 40.5 | 36.2 | 836 | 2 | A40995 | 372 | 40 | 35.7 | 479 | 2 | T49871 | peroxisomal Ca-dep |
| 300 | 40.5 | 36.2 | 852 | 2 | A28459 | 373 | 40 | 35.7 | 487 | 1 | S71770 | calcium-dependent |
| 301 | 40.5 | 36.2 | 897 | 2 | G02529 | 374 | 40 | 35.7 | 490 | 1 | S71776 | calcium-dependent |
| 302 | 40.5 | 36.2 | 1481 | 2 | S78373 | 375 | 40 | 35.7 | 511 | 1 | E89775 | 2',3'-cyclic-nucle |
| 303 | 40.5 | 36.2 | 3746 | 1 | YGPV3 | 376 | 40 | 35.7 | 511 | 2 | T05363 | phosphoglucanate d |
| 304 | 40.5 | 36.2 | 3770 | 2 | A40889 | 377 | 40 | 35.7 | 513 | 1 | T02259 | calcium-dependent |
| 305 | 40.5 | 36.2 | 3791 | 1 | YGPV8 | 378 | 40 | 35.7 | 513 | 2 | S48981 | hypochet |
| 306 | 40.5 | 36.2 | 4644 | 1 | A38905 | 379 | 40 | 35.7 | 530 | 2 | S53392 | probable membrane |
| 307 | 40.5 | 36.2 | 4767 | 1 | T31345 | 380 | 40 | 35.7 | 531 | 1 | T02993 | calcium-dependent |
| 308 | 40 | 35.7 | 50 | 2 | E48518 | 381 | 40 | 35.7 | 533 | 1 | S56652 | calcium-dependent |
| 309 | 40 | 35.7 | 86 | 2 | D69774 | 382 | 40 | 35.7 | 536 | 2 | T23346 | hypochet |
| 310 | 40 | 35.7 | 105 | 2 | T22980 | 383 | 40 | 35.7 | 538 | 2 | T08874 | calcium-dependent |
| 311 | 40 | 35.7 | 126 | 2 | E82184 | 384 | 40 | 35.7 | 540 | 1 | T01989 | calcium-dependent |
| 312 | 40 | 35.7 | 134 | 2 | T22275 | 385 | 40 | 35.7 | 541 | 2 | A82320 | methyl-accepting c |
| 313 | 40 | 35.7 | 134 | 2 | F72638 | 386 | 40 | 35.7 | 543 | 2 | S70013 | chaperonin-like pr |
| 314 | 40 | 35.7 | 146 | 2 | D83676 | 387 | 40 | 35.7 | 544 | 2 | I40731 | heat shock protein |
| 315 | 40 | 35.7 | 150 | 2 | H86194 | 388 | 40 | 35.7 | 544 | 2 | B41479 | 60K heat shock pro |
| 316 | 40 | 35.7 | 151 | 2 | A97008 | 389 | 40 | 35.7 | 544 | 2 | JL0117 | hybp protein - Ch1 |
| 317 | 40 | 35.7 | 154 | 2 | G85041 | 390 | 40 | 35.7 | 544 | 2 | B81556 | 60 kDa chaperonin |
| 318 | 40 | 35.7 | 155 | 2 | G83774 | 391 | 40 | 35.7 | 544 | 2 | F86507 | heat shock protein |
| 319 | 40 | 35.7 | 156 | 2 | T16066 | 392 | 40 | 35.7 | 544 | 2 | S19023 | chaperonin groEL - |
| 320 | 40 | 35.7 | 172 | 2 | G69432 | 393 | 40 | 35.7 | 544 | 2 | D81709 | 60 kDa chaperonin |
| 321 | 40 | 35.7 | 177 | 2 | H83323 | 394 | 40 | 35.7 | 544 | 2 | A71555 | probable hep-60 - |

| | | | | | | | | | | | | |
|-----|------|------|------|---|---------|-----|----|------|-----|---|--------|-----------------------|
| 395 | 40 | 35.7 | 548 | 2 | H95066 | 468 | 39 | 34.8 | 122 | 2 | A45385 | translation repres |
| 396 | 40 | 35.7 | 550 | 2 | S35309 | 469 | 39 | 34.8 | 132 | 2 | S76503 | hypothetical prote |
| 397 | 40 | 35.7 | 550 | 2 | T10393 | 470 | 39 | 34.8 | 149 | 2 | A33353 | calcium-binding pr |
| 398 | 40 | 35.7 | 554 | 2 | T25902 | 471 | 39 | 34.8 | 151 | 2 | S62426 | hypothetical prote |
| 399 | 40 | 35.7 | 560 | 2 | AB2043 | 472 | 39 | 34.8 | 158 | 2 | JC5434 | larva muscle tropo |
| 400 | 40 | 35.7 | 572 | 2 | UC5316 | 473 | 39 | 34.8 | 158 | 2 | A38397 | tropomn C-1 - gia |
| 401 | 40 | 35.7 | 573 | 2 | T40474 | 474 | 39 | 34.8 | 161 | 2 | E70381 | glycine cleavage s |
| 402 | 40 | 35.7 | 584 | 2 | T08678 | 475 | 39 | 34.8 | 167 | 2 | T43621 | hypothetical prote |
| 403 | 40 | 35.7 | 606 | 2 | B69805 | 476 | 39 | 34.8 | 178 | 2 | T22802 | hypothetical prote |
| 404 | 40 | 35.7 | 608 | 2 | H72392 | 477 | 39 | 34.8 | 184 | 2 | S41960 | ras-related GTP-bi |
| 405 | 40 | 35.7 | 622 | 2 | AC1236 | 478 | 39 | 34.8 | 184 | 2 | I55401 | Ras-related protei |
| 406 | 40 | 35.7 | 629 | 2 | AE6536 | 479 | 39 | 34.8 | 192 | 2 | S16509 | DNA-invertase - St |
| 407 | 40 | 35.7 | 642 | 2 | SS9306 | 480 | 39 | 34.8 | 197 | 2 | S11781 | DNA-invertase - St |
| 408 | 40 | 35.7 | 647 | 2 | C71534 | 481 | 39 | 34.8 | 204 | 2 | C84122 | thymidine kinase (|
| 409 | 40 | 35.7 | 650 | 2 | I49523 | 482 | 39 | 34.8 | 208 | 2 | B70208 | conserved hypotet |
| 410 | 40 | 35.7 | 680 | 2 | H90558 | 483 | 39 | 34.8 | 209 | 2 | S09885 | hypothetical prote |
| 411 | 40 | 35.7 | 757 | 2 | T24266 | 484 | 39 | 34.8 | 219 | 2 | F70474 | conserved hypotet |
| 412 | 40 | 35.7 | 774 | 2 | A28392 | 485 | 39 | 34.8 | 229 | 2 | T18629 | hypothetical prote |
| 413 | 40 | 35.7 | 777 | 2 | T21048 | 486 | 39 | 34.8 | 233 | 2 | T41263 | hypothetical prote |
| 414 | 40 | 35.7 | 819 | 2 | S61217 | 487 | 39 | 34.8 | 238 | 2 | F91221 | probable phosphata |
| 415 | 40 | 35.7 | 844 | 2 | S77383 | 488 | 39 | 34.8 | 238 | 2 | A86068 | hypothetical 27.1K |
| 416 | 40 | 35.7 | 880 | 2 | AC2108 | 489 | 39 | 34.8 | 238 | 2 | D37841 | hypothetical prote |
| 417 | 40 | 35.7 | 976 | 2 | T40697 | 490 | 39 | 34.8 | 240 | 2 | AC1921 | hypothetical prote |
| 418 | 40 | 35.7 | 1002 | 2 | T46033 | 491 | 39 | 34.8 | 247 | 2 | C71229 | hypothetical prote |
| 419 | 40 | 35.7 | 1013 | 2 | A69426 | 492 | 39 | 34.8 | 248 | 2 | T20027 | hypothetical prote |
| 420 | 40 | 35.7 | 1021 | 2 | AC2202 | 493 | 39 | 34.8 | 248 | 2 | E90295 | hypothetical prote |
| 421 | 40 | 35.7 | 1030 | 2 | A32612 | 494 | 39 | 34.8 | 249 | 2 | C90468 | hypothetical prote |
| 422 | 40 | 35.7 | 1054 | 2 | T070425 | 495 | 39 | 34.8 | 260 | 1 | A38585 | deoxycytidine kina |
| 423 | 40 | 35.7 | 1097 | 2 | AD2572 | 496 | 39 | 34.8 | 260 | 2 | A10934 | glutamate racemase |
| 424 | 40 | 35.7 | 1154 | 2 | S69206 | 497 | 39 | 34.8 | 269 | 2 | C82080 | dihydrodipicolinat |
| 425 | 40 | 35.7 | 1247 | 2 | C89583 | 498 | 39 | 34.8 | 270 | 2 | S67389 | conserved hypotet |
| 426 | 40 | 35.7 | 1335 | 2 | T14790 | 499 | 39 | 34.8 | 278 | 2 | A81266 | probable biotin sy |
| 427 | 40 | 35.7 | 1441 | 1 | GNVUSV | 500 | 39 | 34.8 | 280 | 1 | PRS8EA | epidermolytic toxi |
| 428 | 40 | 35.7 | 1518 | 2 | A44811 | 501 | 39 | 34.8 | 286 | 2 | C82143 | conserved hypotet |
| 429 | 40 | 35.7 | 1569 | 2 | T35694 | 502 | 39 | 34.8 | 303 | 2 | S34966 | rfbO protein - Shi |
| 430 | 40 | 35.7 | 2339 | 2 | A45597 | 503 | 39 | 34.8 | 314 | 2 | C90038 | hypothetical prote |
| 431 | 40 | 35.7 | 2396 | 2 | T13714 | 504 | 39 | 34.8 | 315 | 2 | A84598 | probable triosepho |
| 432 | 40 | 35.7 | 2472 | 2 | A35715 | 505 | 39 | 34.8 | 316 | 2 | E90401 | hypothetical prote |
| 433 | 40 | 35.7 | 2477 | 1 | SJCHA | 506 | 39 | 34.8 | 316 | 2 | A99307 | hypothetical prote |
| 434 | 40 | 35.7 | 3228 | 2 | T21381 | 507 | 39 | 34.8 | 316 | 2 | H90426 | hypothetical prote |
| 435 | 40 | 35.7 | 5149 | 2 | P83345 | 508 | 39 | 34.8 | 325 | 2 | AC1333 | conjugated bile ac |
| 436 | 39.5 | 35.3 | 135 | 2 | A81429 | 509 | 39 | 34.8 | 334 | 2 | P86226 | hypothetical prote |
| 437 | 39.5 | 35.3 | 165 | 2 | AG2184 | 510 | 39 | 34.8 | 338 | 2 | D72327 | heat shock operon |
| 438 | 39.5 | 35.3 | 202 | 2 | H69902 | 511 | 39 | 34.8 | 340 | 2 | I51547 | probable RNA-bindl |
| 439 | 39.5 | 35.3 | 206 | 2 | AD1898 | 512 | 39 | 34.8 | 342 | 2 | S14332 | heterogeneous ribo |
| 440 | 39.5 | 35.3 | 291 | 2 | A70475 | 513 | 39 | 34.8 | 344 | 2 | B84204 | hypothetical prote |
| 441 | 39.5 | 35.3 | 301 | 2 | S60532 | 514 | 39 | 34.8 | 345 | 2 | AH3131 | male dehydrogena |
| 442 | 39.5 | 35.3 | 301 | 2 | S60531 | 515 | 39 | 34.8 | 346 | 2 | C98156 | probable L-malate |
| 443 | 39.5 | 35.3 | 314 | 2 | D89958 | 516 | 39 | 34.8 | 347 | 2 | I51546 | probable RNA-bindl |
| 444 | 39.5 | 35.3 | 368 | 2 | S54575 | 517 | 39 | 34.8 | 356 | 2 | A12317 | two-component hydr |
| 445 | 39.5 | 35.3 | 481 | 2 | E86356 | 518 | 39 | 34.8 | 369 | 2 | F81125 | glutamate 5-kinase |
| 446 | 39.5 | 35.3 | 548 | 2 | AC0871 | 519 | 39 | 34.8 | 369 | 2 | B81895 | probable glutamate |
| 447 | 39.5 | 35.3 | 552 | 2 | JC4030 | 520 | 39 | 34.8 | 371 | 2 | T02284 | hypothetical prote |
| 448 | 39.5 | 35.3 | 662 | 2 | G89909 | 521 | 39 | 34.8 | 387 | 1 | ERADY4 | 41K fiber protein |
| 449 | 39.5 | 35.3 | 707 | 2 | T42239 | 522 | 39 | 34.8 | 391 | 2 | T20752 | hypothetical prote |
| 450 | 39.5 | 35.3 | 722 | 2 | T34072 | 523 | 39 | 34.8 | 393 | 2 | S04408 | hydroxyneurospore |
| 451 | 39.5 | 35.3 | 732 | 1 | JU0132 | 524 | 39 | 34.8 | 393 | 2 | E81438 | helicase-like prot |
| 452 | 39.5 | 35.3 | 732 | 1 | S07624 | 525 | 39 | 34.8 | 394 | 2 | H97825 | acylaminoacyl-dept |
| 453 | 39.5 | 35.3 | 751 | 2 | AD2168 | 526 | 39 | 34.8 | 398 | 2 | A39371 | Ig V-region-like B |
| 454 | 39.5 | 35.3 | 877 | 2 | S76394 | 527 | 39 | 34.8 | 408 | 2 | AE0103 | probable regulator |
| 455 | 39.5 | 35.3 | 888 | 2 | S78288 | 528 | 39 | 34.8 | 413 | 2 | AE2163 | hypothetical prote |
| 456 | 39.5 | 35.3 | 1281 | 2 | I48123 | 529 | 39 | 34.8 | 417 | 2 | S58193 | adenosylhomocyste |
| 457 | 39.5 | 35.3 | 1331 | 1 | XORTDH | 530 | 39 | 34.8 | 424 | 2 | E64450 | hypothetical prote |
| 458 | 39.5 | 35.3 | 1343 | 2 | T20718 | 531 | 39 | 34.8 | 425 | 2 | S17759 | protein kinase, ca |
| 459 | 39 | 34.8 | 36 | 2 | S16552 | 532 | 39 | 34.8 | 431 | 2 | A81150 | hierarchical-RNA synt |
| 460 | 39 | 34.8 | 40 | 2 | I39944 | 533 | 39 | 34.8 | 442 | 2 | C90224 | s-adenosyl-L-homoc |
| 461 | 39 | 34.8 | 46 | 2 | A26929 | 534 | 39 | 34.8 | 445 | 2 | H64067 | hypothetical prote |
| 462 | 39 | 34.8 | 81 | 2 | F90454 | 535 | 39 | 34.8 | 446 | 2 | C64205 | signal recognition |
| 463 | 39 | 34.8 | 89 | 2 | E47758 | 536 | 39 | 34.8 | 448 | 2 | C82936 | signal recognition |
| 464 | 39 | 34.8 | 92 | 2 | E69408 | 537 | 39 | 34.8 | 452 | 2 | JC4100 | hydroxyindole O-me |
| 465 | 39 | 34.8 | 103 | 2 | D83678 | 538 | 39 | 34.8 | 453 | 2 | F82702 | conserved hypotet |
| 466 | 39 | 34.8 | 105 | 2 | E86755 | 539 | 39 | 34.8 | 465 | 1 | T03024 | calcium-dependent |
| 467 | 39 | 34.8 | 122 | 2 | T04090 | 540 | 39 | 34.8 | 468 | 1 | DDEGCG | phosphogluconate d |

| | | | | | | | | | | | | |
|-----|------|------|------|---|--------|-----|------|------|------|---|--------|--------------------|
| 541 | 39 | 34.8 | 468 | 2 | 162465 | 614 | 38.5 | 34.4 | 261 | 2 | A84128 | hypothetical prote |
| 542 | 39 | 34.8 | 468 | 2 | 162463 | 615 | 38.5 | 34.4 | 299 | 2 | S60529 | envelope polypept |
| 543 | 39 | 34.8 | 469 | 2 | B70486 | 616 | 38.5 | 34.4 | 299 | 2 | S60528 | envelope polypept |
| 544 | 39 | 34.8 | 472 | 1 | A53336 | 617 | 38.5 | 34.4 | 319 | 2 | H69043 | conserved hypochet |
| 545 | 39 | 34.8 | 472 | 2 | AH1246 | 618 | 38.5 | 34.4 | 327 | 2 | H64155 | conserved hypochet |
| 546 | 39 | 34.8 | 472 | 2 | AD1609 | 619 | 38.5 | 34.4 | 338 | 2 | S45908 | hypothetical prote |
| 547 | 39 | 34.8 | 475 | 2 | B27671 | 620 | 38.5 | 34.4 | 430 | 2 | AB2646 | flagellin protein |
| 548 | 39 | 34.8 | 485 | 2 | A84859 | 621 | 38.5 | 34.4 | 436 | 2 | A97428 | flad protein (U951 |
| 549 | 39 | 34.8 | 485 | 2 | C97022 | 622 | 38.5 | 34.4 | 443 | 2 | A13181 | selenocysteine lya |
| 550 | 39 | 34.8 | 485 | 2 | P90192 | 623 | 38.5 | 34.4 | 459 | 2 | B75165 | signal recognition |
| 551 | 39 | 34.8 | 494 | 2 | E70352 | 624 | 38.5 | 34.4 | 459 | 2 | G70672 | probable transpos |
| 552 | 39 | 34.8 | 508 | 1 | A43713 | 625 | 38.5 | 34.4 | 474 | 2 | E83392 | probable transcrip |
| 553 | 39 | 34.8 | 525 | 2 | D70747 | 626 | 38.5 | 34.4 | 502 | 1 | PIWL42 | li protein - human |
| 554 | 39 | 34.8 | 530 | 2 | D82412 | 627 | 38.5 | 34.4 | 533 | 2 | S62489 | hypothetical prote |
| 555 | 39 | 34.8 | 531 | 2 | D85059 | 628 | 38.5 | 34.4 | 563 | 2 | AH2187 | DNA mismatch repai |
| 556 | 39 | 34.8 | 532 | 2 | T14335 | 629 | 38.5 | 34.4 | 634 | 2 | T17232 | hypothetical prote |
| 557 | 39 | 34.8 | 532 | 2 | PN0108 | 630 | 38.5 | 34.4 | 650 | 2 | A11874 | ferredoxin-bulfit |
| 558 | 39 | 34.8 | 534 | 2 | T23425 | 631 | 38.5 | 34.4 | 767 | 1 | S50594 | 5-methyltetrahydro |
| 559 | 39 | 34.8 | 536 | 2 | S62110 | 632 | 38.5 | 34.4 | 855 | 1 | VCLJZR | env polypept |
| 560 | 39 | 34.8 | 545 | 2 | D69679 | 633 | 38.5 | 34.4 | 977 | 2 | E86349 | hypothetical prote |
| 561 | 39 | 34.8 | 546 | 2 | S36237 | 634 | 38.5 | 34.4 | 996 | 2 | T18717 | hypothetical prote |
| 562 | 39 | 34.8 | 546 | 2 | B71986 | 635 | 38.5 | 34.4 | 1032 | 2 | A11697 | alpha-mannosidase |
| 563 | 39 | 34.8 | 554 | 2 | T05476 | 636 | 38.5 | 34.4 | 1048 | 1 | BVESC | exonuclease (EC 3. |
| 564 | 39 | 34.8 | 554 | 2 | T43466 | 637 | 38.5 | 34.4 | 1238 | 2 | A64596 | hypothetical prote |
| 565 | 39 | 34.8 | 581 | 2 | S71597 | 638 | 38.5 | 34.4 | 1562 | 2 | T07323 | DNA-directed RNA p |
| 566 | 39 | 34.8 | 583 | 2 | H84810 | 639 | 38.5 | 34.4 | 1809 | 2 | S57329 | tuberous sclerosis |
| 567 | 39 | 34.8 | 583 | 2 | S57721 | 640 | 38.5 | 34.4 | 2374 | 2 | T21052 | hypothetical prote |
| 568 | 39 | 34.8 | 595 | 2 | G64233 | 641 | 38.5 | 33.9 | 77 | 2 | AH1947 | hypothetical prote |
| 569 | 39 | 34.8 | 595 | 2 | G73733 | 642 | 38.5 | 33.9 | 95 | 1 | LUP610 | calpactin I light |
| 570 | 39 | 34.8 | 597 | 2 | T45676 | 643 | 38.5 | 33.9 | 97 | 2 | UC1139 | calpactin I light |
| 571 | 39 | 34.8 | 601 | 2 | T46084 | 644 | 38.5 | 33.9 | 99 | 2 | B28489 | hypothetical prote |
| 572 | 39 | 34.8 | 606 | 2 | T11909 | 645 | 38.5 | 33.9 | 99 | 2 | D97747 | arsenate reductase |
| 573 | 39 | 34.8 | 611 | 1 | S62811 | 646 | 38.5 | 33.9 | 119 | 2 | E84085 | hypothetical prote |
| 574 | 39 | 34.8 | 619 | 2 | E81117 | 647 | 38.5 | 33.9 | 121 | 2 | G75604 | hypothetical prote |
| 575 | 39 | 34.8 | 619 | 2 | S67067 | 648 | 38.5 | 33.9 | 128 | 2 | S75264 | hypothetical prote |
| 576 | 39 | 34.8 | 624 | 2 | A55220 | 649 | 38.5 | 33.9 | 134 | 2 | E85629 | hypothetical prote |
| 577 | 39 | 34.8 | 633 | 2 | T47346 | 650 | 38.5 | 33.9 | 139 | 2 | B86144 | F6f3.17 protei |
| 578 | 39 | 34.8 | 633 | 2 | AH1598 | 651 | 38.5 | 33.9 | 147 | 2 | D64346 | transcription term |
| 579 | 39 | 34.8 | 633 | 2 | T33940 | 652 | 38.5 | 33.9 | 150 | 2 | S18435 | crotonin C isoform |
| 580 | 39 | 34.8 | 650 | 2 | TC7093 | 653 | 38.5 | 33.9 | 150 | 2 | S18434 | crotonin C isoform |
| 581 | 39 | 34.8 | 657 | 2 | S43415 | 654 | 38.5 | 33.9 | 150 | 2 | S22208 | hypothetical prote |
| 582 | 39 | 34.8 | 664 | 2 | B75532 | 655 | 38.5 | 33.9 | 151 | 2 | A10635 | major curlin chain |
| 583 | 39 | 34.8 | 689 | 2 | H70451 | 656 | 38.5 | 33.9 | 151 | 2 | JC6039 | fimbria protein ag |
| 584 | 39 | 34.8 | 707 | 2 | T20440 | 657 | 38.5 | 33.9 | 152 | 2 | PT0433 | progesterone 11alp |
| 585 | 39 | 34.8 | 717 | 2 | H84057 | 658 | 38.5 | 33.9 | 159 | 2 | AD2738 | conserved hypochet |
| 586 | 39 | 34.8 | 743 | 2 | A97021 | 659 | 38.5 | 33.9 | 159 | 2 | B97519 | hypothetical 17.1k |
| 587 | 39 | 34.8 | 765 | 2 | T22800 | 660 | 38.5 | 33.9 | 169 | 1 | BCRM | caltractin - Chlam |
| 588 | 39 | 34.8 | 770 | 2 | PN0105 | 661 | 38.5 | 33.9 | 174 | 2 | AB1443 | gp43 (Bacteriophag |
| 589 | 39 | 34.8 | 785 | 2 | T01025 | 662 | 38.5 | 33.9 | 175 | 2 | A71227 | probable cob(I)ala |
| 590 | 39 | 34.8 | 833 | 2 | G89007 | 663 | 38.5 | 33.9 | 177 | 2 | AC1365 | gp43 (Bacteriophag |
| 591 | 39 | 34.8 | 836 | 2 | B96716 | 664 | 38.5 | 33.9 | 179 | 2 | AC1994 | hypothetical prote |
| 592 | 39 | 34.8 | 861 | 2 | T23810 | 665 | 38.5 | 33.9 | 186 | 2 | F86379 | protein F2109.28 l |
| 593 | 39 | 34.8 | 969 | 2 | T23256 | 666 | 38.5 | 33.9 | 186 | 2 | H64031 | hypothetical prote |
| 594 | 39 | 34.8 | 977 | 2 | S53302 | 667 | 38.5 | 33.9 | 207 | 2 | E38625 | GTP-binding prote |
| 595 | 39 | 34.8 | 978 | 2 | T16948 | 668 | 38.5 | 33.9 | 219 | 2 | S32157 | RNA-directed DNA p |
| 596 | 39 | 34.8 | 984 | 2 | F81299 | 669 | 38.5 | 33.9 | 219 | 2 | S32160 | RNA-directed DNA p |
| 597 | 39 | 34.8 | 1057 | 2 | AH2198 | 670 | 38.5 | 33.9 | 219 | 2 | S32159 | RNA-directed DNA p |
| 598 | 39 | 34.8 | 1165 | 2 | S58236 | 671 | 38.5 | 33.9 | 222 | 2 | H82169 | phage shock prote |
| 599 | 39 | 34.8 | 1229 | 2 | P86155 | 672 | 38.5 | 33.9 | 228 | 1 | VG1HE1 | El membrane glycop |
| 600 | 39 | 34.8 | 1353 | 2 | T27404 | 673 | 38.5 | 33.9 | 232 | 1 | VG1HJH | El membrane glycop |
| 601 | 39 | 34.8 | 1431 | 2 | A45866 | 674 | 38.5 | 33.9 | 232 | 2 | B86698 | conserved hypochet |
| 602 | 39 | 34.8 | 1441 | 1 | GNVULC | 675 | 38.5 | 33.9 | 234 | 2 | G85098 | H+-transporting AT |
| 603 | 39 | 34.8 | 1462 | 2 | T06819 | 676 | 38.5 | 33.9 | 234 | 2 | D84075 | hypothetical prote |
| 604 | 39 | 34.8 | 1535 | 2 | T14961 | 677 | 38.5 | 33.9 | 238 | 2 | AH0918 | conserved hypochet |
| 605 | 39 | 34.8 | 1597 | 2 | F71607 | 678 | 38.5 | 33.9 | 239 | 2 | A97358 | glucose-inhibited |
| 606 | 39 | 34.8 | 2059 | 2 | D82671 | 679 | 38.5 | 33.9 | 241 | 2 | D87547 | 3-oxoacidate CoA-t |
| 607 | 39 | 34.8 | 4930 | 2 | B96679 | 680 | 38.5 | 33.9 | 241 | 2 | JX0290 | galactose-specific |
| 608 | 39 | 34.8 | 6486 | 2 | T31076 | 681 | 38.5 | 33.9 | 250 | 2 | T04167 | MADS box protein - |
| 609 | 38.5 | 34.4 | 111 | 2 | B95146 | 682 | 38.5 | 33.9 | 254 | 2 | F82151 | conserved hypochet |
| 610 | 38.5 | 34.4 | 159 | 1 | 823478 | 683 | 38.5 | 33.9 | 255 | 2 | T03408 | MADS box protein - |
| 611 | 38.5 | 34.4 | 192 | 1 | KLSSBS | 684 | 38.5 | 33.9 | 259 | 2 | A83750 | transcription regu |
| 612 | 38.5 | 34.4 | 218 | 1 | A99014 | 685 | 38.5 | 33.9 | 259 | 2 | AF1102 | conserved hypochet |
| 613 | 38.5 | 34.4 | 231 | 2 | S76204 | 686 | 38.5 | 33.9 | 264 | 2 | C84028 | sepium site-determ |

| | | | | | | | | | | | | | |
|-----|----|------|-----|---|--------|---------------------|-----|----|------|-----|---|--------|---------------------|
| 687 | 38 | 33.9 | 265 | 2 | S73334 | probable lipoprote | 760 | 38 | 33.9 | 431 | 2 | E89829 | conserved hypoteth |
| 688 | 38 | 33.9 | 265 | 2 | T26442 | hypothetical prote | 761 | 38 | 33.9 | 433 | 2 | T02157 | hypothetical prote |
| 689 | 38 | 33.9 | 269 | 2 | B97113 | protein serine/thr | 762 | 38 | 33.9 | 436 | 2 | C84743 | probable tyrosine- |
| 690 | 38 | 33.9 | 275 | 2 | B64977 | hypothetical prote | 763 | 38 | 33.9 | 440 | 1 | T06837 | protochlorophyllid |
| 691 | 38 | 33.9 | 275 | 2 | A90992 | hypothetical prote | 764 | 38 | 33.9 | 442 | 2 | G86294 | T24D18.11 protein |
| 692 | 38 | 33.9 | 275 | 2 | C85837 | hypothetical prote | 765 | 38 | 33.9 | 443 | 2 | S65963 | flavastacin (EC 3. |
| 693 | 38 | 33.9 | 276 | 2 | T43541 | putrine nucleotide | 766 | 38 | 33.9 | 449 | 2 | H81835 | probable glutamate |
| 694 | 38 | 33.9 | 283 | 2 | B81288 | hypothetical prote | 767 | 38 | 33.9 | 449 | 2 | H81128 | probable glutamate |
| 695 | 38 | 33.9 | 285 | 2 | D95095 | hypothetical prote | 768 | 38 | 33.9 | 457 | 2 | T44879 | acetyltransferase |
| 696 | 38 | 33.9 | 287 | 2 | H69067 | ATP phosphoribosyl | 769 | 38 | 33.9 | 459 | 2 | E86640 | argininosuccinate |
| 697 | 38 | 33.9 | 287 | 2 | AC0476 | probable glutamate | 770 | 38 | 33.9 | 460 | 2 | D70435 | hypothetical prote |
| 698 | 38 | 33.9 | 292 | 2 | S60950 | probable membrane | 771 | 38 | 33.9 | 461 | 2 | A32008 | site-specific DNA- |
| 699 | 38 | 33.9 | 294 | 2 | C97774 | dihydrodipicolinat | 772 | 38 | 33.9 | 465 | 2 | H90508 | cobyrlic acid synth |
| 700 | 38 | 33.9 | 294 | 2 | T25085 | hypothetical prote | 773 | 38 | 33.9 | 469 | 2 | AD1926 | hypothetical prote |
| 701 | 38 | 33.9 | 295 | 2 | H91117 | probable transcrip | 774 | 38 | 33.9 | 471 | 2 | A28568 | pneumolysin - Stre |
| 702 | 38 | 33.9 | 295 | 2 | G85962 | probable transcrip | 775 | 38 | 33.9 | 471 | 2 | F95224 | hypothetical prote |
| 703 | 38 | 33.9 | 298 | 2 | F70714 | hypothetical prote | 776 | 38 | 33.9 | 471 | 2 | A99089 | helicase (EC 3.6.1 |
| 704 | 38 | 33.9 | 299 | 2 | B83979 | 3-hydroxyisobutyla | 777 | 38 | 33.9 | 475 | 1 | Z4BPT4 | acetaldehyde dehyd |
| 705 | 38 | 33.9 | 299 | 2 | D83010 | probable binding p | 778 | 38 | 33.9 | 486 | 2 | AR1575 | acetaldehyde dehyd |
| 706 | 38 | 33.9 | 300 | 2 | S73402 | 1-phosphofructokin | 779 | 38 | 33.9 | 486 | 2 | AC1222 | hypothetical prote |
| 707 | 38 | 33.9 | 300 | 2 | AC1088 | transcription regu | 780 | 38 | 33.9 | 490 | 2 | D84592 | hypothetical prote |
| 708 | 38 | 33.9 | 300 | 2 | S60558 | envelope polypote | 781 | 38 | 33.9 | 492 | 2 | S64588 | phosphogluconate d |
| 709 | 38 | 33.9 | 300 | 2 | S60526 | envelope polypote | 782 | 38 | 33.9 | 504 | 2 | S74034 | amidase (EC 3.5.1. |
| 710 | 38 | 33.9 | 301 | 2 | A70731 | probable glycerolp | 783 | 38 | 33.9 | 505 | 1 | E69417 | probable thymidine |
| 711 | 38 | 33.9 | 304 | 2 | T22697 | hypothetical prote | 784 | 38 | 33.9 | 506 | 2 | C70468 | phosphoribosylamin |
| 712 | 38 | 33.9 | 306 | 2 | A97963 | methenyltetrahydro | 785 | 38 | 33.9 | 509 | 2 | B84643 | hypothetical prote |
| 713 | 38 | 33.9 | 309 | 2 | S46684 | killer toxin insen | 786 | 38 | 33.9 | 516 | 2 | S44191 | carboxypeptidase D |
| 714 | 38 | 33.9 | 311 | 2 | T13548 | hypothetical prote | 787 | 38 | 33.9 | 518 | 2 | AH1211 | GMP synthetase hom |
| 715 | 38 | 33.9 | 311 | 2 | C83493 | hypothetical prote | 788 | 38 | 33.9 | 518 | 2 | AH1567 | GMP synthetase hom |
| 716 | 38 | 33.9 | 312 | 2 | T20932 | hypothetical prote | 789 | 38 | 33.9 | 523 | 2 | AG1189 | ABC transporter AT |
| 717 | 38 | 33.9 | 314 | 2 | I37383 | FAS soluble protei | 790 | 38 | 33.9 | 523 | 2 | AH1547 | ABC transporter AT |
| 718 | 38 | 33.9 | 316 | 2 | F85629 | hypothetical prote | 791 | 38 | 33.9 | 525 | 2 | AF0349 | GMP synthase (glut |
| 719 | 38 | 33.9 | 317 | 2 | S54548 | hypothetical prote | 792 | 38 | 33.9 | 532 | 2 | S26877 | groEL protein - re |
| 720 | 38 | 33.9 | 322 | 2 | E71137 | hypothetical prote | 793 | 38 | 33.9 | 534 | 2 | S74322 | chaperonin groEL--2 |
| 721 | 38 | 33.9 | 323 | 2 | H69346 | tyrosyl-tRNA synth | 794 | 38 | 33.9 | 555 | 2 | AG1914 | carbon dioxide con |
| 722 | 38 | 33.9 | 323 | 2 | D86216 | protein T23G18.8 (| 795 | 38 | 33.9 | 557 | 2 | E95945 | probable urocanate |
| 723 | 38 | 33.9 | 323 | 2 | E71134 | hypothetical prote | 796 | 38 | 33.9 | 559 | 2 | B47175 | reverse transcript |
| 724 | 38 | 33.9 | 333 | 2 | S42424 | hypothetical prote | 797 | 38 | 33.9 | 560 | 1 | DOCGA | NAD-diphthamide AD |
| 725 | 38 | 33.9 | 335 | 2 | A40036 | apoptosis-mediati | 798 | 38 | 33.9 | 560 | 2 | T46189 | NAD-diphthamide AD |
| 726 | 38 | 33.9 | 335 | 2 | A40267 | interleukin-5 rece | 799 | 38 | 33.9 | 560 | 2 | F70719 | calcium-dependent |
| 727 | 38 | 33.9 | 336 | 2 | AB2525 | hypothetical prote | 800 | 38 | 33.9 | 560 | 2 | F70719 | hypothetical prote |
| 728 | 38 | 33.9 | 345 | 1 | PPPA | napsin (EC 3.4.22. | 801 | 38 | 33.9 | 564 | 2 | C84188 | glutathione-disulf |
| 729 | 38 | 33.9 | 347 | 2 | D69166 | NS,N10-methylene | 802 | 38 | 33.9 | 565 | 2 | T47625 | hypothetical prote |
| 730 | 38 | 33.9 | 350 | 2 | E81856 | probable RTX fam1 | 803 | 38 | 33.9 | 566 | 2 | T34053 | hypothetical prote |
| 731 | 38 | 33.9 | 352 | 2 | T21909 | hypothetical prote | 804 | 38 | 33.9 | 571 | 1 | RNCW7T | transcription init |
| 732 | 38 | 33.9 | 353 | 2 | I40376 | carbamoylphosphate | 805 | 38 | 33.9 | 571 | 1 | RNCW7T | transcription init |
| 733 | 38 | 33.9 | 364 | 2 | A84099 | hypothetical prote | 806 | 38 | 33.9 | 571 | 2 | I40872 | transcription init |
| 734 | 38 | 33.9 | 367 | 2 | D72469 | probable Sna5 prote | 807 | 38 | 33.9 | 571 | 2 | A81653 | RNA polymerase sig |
| 735 | 38 | 33.9 | 369 | 2 | T25321 | hypothetical prote | 808 | 38 | 33.9 | 572 | 2 | UCS317 | dihydropyrimidinas |
| 736 | 38 | 33.9 | 371 | 2 | A10301 | probable exported | 809 | 38 | 33.9 | 572 | 2 | S49985 | dihydropyrimidinas |
| 737 | 38 | 33.9 | 372 | 2 | AF1220 | NADPH-dependent bu | 810 | 38 | 33.9 | 575 | 2 | C85059 | probable calcium d |
| 738 | 38 | 33.9 | 372 | 2 | A11573 | NADPH-dependent bu | 811 | 38 | 33.9 | 586 | 2 | C83262 | hypothetical prote |
| 739 | 38 | 33.9 | 376 | 2 | D97175 | nifs family enzyme | 812 | 38 | 33.9 | 587 | 2 | E82431 | methyl--accepting c |
| 740 | 38 | 33.9 | 376 | 2 | B96698 | unknown protein p1 | 813 | 38 | 33.9 | 589 | 2 | AB0613 | conserved hypoteth |
| 741 | 38 | 33.9 | 377 | 2 | S44844 | KO6H7.4 protein - | 814 | 38 | 33.9 | 591 | 2 | P95152 | v-type sodium ATP |
| 742 | 38 | 33.9 | 379 | 2 | F71533 | hypothetical prote | 815 | 38 | 33.9 | 592 | 2 | F81417 | MCP-domain signal |
| 743 | 38 | 33.9 | 381 | 2 | S61229 | cych protein - Rhl | 816 | 38 | 33.9 | 596 | 2 | T23685 | hypothetical prote |
| 744 | 38 | 33.9 | 382 | 2 | S51962 | FUN49 protein - Ye | 817 | 38 | 33.9 | 600 | 2 | C69371 | conserved hypoteth |
| 745 | 38 | 33.9 | 382 | 2 | F82428 | iron-containing al | 818 | 38 | 33.9 | 602 | 2 | T13219 | major capsid prote |
| 746 | 38 | 33.9 | 388 | 1 | S22387 | cuticle-degrading | 819 | 38 | 33.9 | 602 | 2 | C75120 | hypothetical prote |
| 747 | 38 | 33.9 | 394 | 2 | F82507 | proteinase VCA0045 | 820 | 38 | 33.9 | 614 | 1 | QRECBT | vitamin b12 recept |
| 748 | 38 | 33.9 | 396 | 2 | AE2151 | glycerol dehydroge | 821 | 38 | 33.9 | 614 | 2 | A98241 | hypothetical prote |
| 749 | 38 | 33.9 | 397 | 2 | S30023 | antiviral protein | 822 | 38 | 33.9 | 614 | 2 | F86088 | hypothetical prote |
| 750 | 38 | 33.9 | 399 | 1 | D64327 | H+-transporting tw | 823 | 38 | 33.9 | 622 | 2 | A32742 | murine ecotropic r |
| 751 | 38 | 33.9 | 400 | 2 | B81087 | Ftpp-C-related pro | 824 | 38 | 33.9 | 624 | 2 | AS3035 | ecotropic retrovir |
| 752 | 38 | 33.9 | 407 | 2 | G90875 | hypothetical prote | 825 | 38 | 33.9 | 627 | 2 | B70122 | glucose-inhibited |
| 753 | 38 | 33.9 | 414 | 2 | D86764 | hypothetical prote | 826 | 38 | 33.9 | 627 | 2 | T02415 | probable homeodoma |
| 754 | 38 | 33.9 | 420 | 2 | S73475 | serine-tRNA ligase | 827 | 38 | 33.9 | 627 | 2 | D96956 | ntrc family transc |
| 755 | 38 | 33.9 | 420 | 2 | S21052 | interleukin-5 rece | 828 | 38 | 33.9 | 629 | 2 | S29685 | retroviral recepto |
| 756 | 38 | 33.9 | 421 | 2 | C70038 | maltose/maltodextr | 829 | 38 | 33.9 | 629 | 2 | T07426 | probable polygalac |
| 757 | 38 | 33.9 | 426 | 1 | A48829 | transcription fact | 830 | 38 | 33.9 | 630 | 1 | A37097 | fimbrin - chicken |
| 758 | 38 | 33.9 | 429 | 1 | B82181 | GGDPF family prote | 831 | 38 | 33.9 | 630 | 1 | AC1681 | probable ABC trans |
| 759 | 38 | 33.9 | 431 | 2 | A72549 | probable pyruvate | 832 | 38 | 33.9 | 634 | 2 | E96840 | hypothetical prote |

| | | | | | | | | | | | | | |
|-----|------|------|------|---|--------|---------------------|-----|------|------|------|---|--------|--------------------|
| 833 | 38 | 33.9 | 640 | 2 | T32885 | hypothetical prote | 906 | 37.5 | 33.5 | 113 | 1 | R6D0P1 | acidic ribosomal p |
| 834 | 38 | 33.9 | 650 | 2 | T00094 | endostyle-specific | 907 | 37.5 | 33.5 | 114 | 2 | E86353 | protein P282.12 (l |
| 835 | 38 | 33.9 | 650 | 2 | AB1738 | probable Na+/H+ an | 908 | 37.5 | 33.5 | 150 | 2 | T05295 | hypothetical prote |
| 836 | 38 | 33.9 | 650 | 2 | AI1168 | probable Na+/H+ an | 909 | 37.5 | 33.5 | 157 | 2 | P83464 | flagellar motor sw |
| 837 | 38 | 33.9 | 654 | 2 | I56134 | tumor necrosis fac | 910 | 37.5 | 33.5 | 162 | 2 | T52639 | hypothetical prote |
| 838 | 38 | 33.9 | 657 | 2 | A46128 | histidine ammonia- | 911 | 37.5 | 33.5 | 171 | 2 | S08245 | hypothetical prote |
| 839 | 38 | 33.9 | 657 | 2 | A54011 | cationic amino aci | 912 | 37.5 | 33.5 | 189 | 2 | S39864 | late competence op |
| 840 | 38 | 33.9 | 663 | 2 | AF1799 | hypothetical prote | 913 | 37.5 | 33.5 | 231 | 2 | G70000 | two-component resp |
| 841 | 38 | 33.9 | 666 | 1 | D63103 | DNA helicase (EC 3 | 914 | 37.5 | 33.5 | 238 | 2 | B69373 | phosphoribosylform |
| 842 | 38 | 33.9 | 666 | 2 | D63166 | conserved hypothe | 915 | 37.5 | 33.5 | 240 | 2 | D75203 | hypothetical prote |
| 843 | 38 | 33.9 | 682 | 1 | HHBYK2 | dnak-type molecula | 916 | 37.5 | 33.5 | 271 | 2 | G64959 | hypothetical prote |
| 844 | 38 | 33.9 | 687 | 2 | T16352 | hypothetical prote | 917 | 37.5 | 33.5 | 271 | 2 | E85813 | hypothetical prote |
| 845 | 38 | 33.9 | 687 | 2 | D84126 | penicillin-binding | 918 | 37.5 | 33.5 | 271 | 2 | E90965 | hypothetical prote |
| 846 | 38 | 33.9 | 719 | 1 | JC4580 | replication licens | 919 | 37.5 | 33.5 | 276 | 2 | AD1765 | hypothetical cell |
| 847 | 38 | 33.9 | 719 | 1 | S70583 | replication licens | 920 | 37.5 | 33.5 | 279 | 2 | A86312 | Flv6.5 protein - |
| 848 | 38 | 33.9 | 750 | 2 | C87159 | cation-transportin | 921 | 37.5 | 33.5 | 282 | 2 | S75960 | nitrate transport |
| 849 | 38 | 33.9 | 750 | 2 | S77653 | cation-transportin | 922 | 37.5 | 33.5 | 291 | 2 | AI3092 | hypothetical prote |
| 850 | 38 | 33.9 | 796 | 2 | D97065 | transketolase (imp | 923 | 37.5 | 33.5 | 293 | 2 | T46812 | isopentenyl-diphos |
| 851 | 38 | 33.9 | 802 | 1 | A44223 | DNA excision repai | 924 | 37.5 | 33.5 | 293 | 2 | T51248 | isopentenyl-diphos |
| 852 | 38 | 33.9 | 809 | 2 | E71265 | hypothetical prote | 925 | 37.5 | 33.5 | 298 | 2 | C86871 | conserved hypothe |
| 853 | 38 | 33.9 | 812 | 2 | S74856 | hypothetical prote | 926 | 37.5 | 33.5 | 305 | 2 | T52027 | isopentenyl-diphos |
| 854 | 38 | 33.9 | 819 | 1 | B72128 | endopeptidase Ia (| 927 | 37.5 | 33.5 | 323 | 2 | U70755 | ethylene-forming e |
| 855 | 38 | 33.9 | 819 | 1 | E86494 | Lon ATP-dependent | 928 | 37.5 | 33.5 | 323 | 2 | AB6184 | hypothetical prote |
| 856 | 38 | 33.9 | 821 | 2 | E87503 | 1,4-beta-D-glucan | 929 | 37.5 | 33.5 | 339 | 2 | P85098 | hypothetical prote |
| 857 | 38 | 33.9 | 826 | 1 | A31822 | villin - chicken | 930 | 37.5 | 33.5 | 357 | 2 | A96194 | hypothetical prote |
| 858 | 38 | 33.9 | 833 | 2 | H90821 | probable portal pr | 931 | 37.5 | 33.5 | 393 | 2 | T00647 | glycosyl transfera |
| 859 | 38 | 33.9 | 859 | 2 | S51546 | probable portal pr | 932 | 37.5 | 33.5 | 398 | 2 | C86749 | hypothetical prote |
| 860 | 38 | 33.9 | 861 | 2 | B85844 | probable portal pr | 933 | 37.5 | 33.5 | 407 | 2 | H85091 | hypothetical prote |
| 861 | 38 | 33.9 | 871 | 2 | S62415 | major facilitator | 934 | 37.5 | 33.5 | 424 | 2 | S12785 | protein ch-42 prec |
| 862 | 38 | 33.9 | 881 | 2 | E82097 | protein-P-II uridy | 935 | 37.5 | 33.5 | 440 | 2 | AF1953 | two-component hybr |
| 863 | 38 | 33.9 | 886 | 2 | T47455 | centromere protein | 936 | 37.5 | 33.5 | 482 | 2 | T33651 | hypothetical prote |
| 864 | 38 | 33.9 | 915 | 2 | C71455 | alanine-tRNA ligase | 937 | 37.5 | 33.5 | 503 | 2 | T52172 | probable cytochrom |
| 865 | 38 | 33.9 | 918 | 2 | E90542 | lipoprotein (impor | 938 | 37.5 | 33.5 | 529 | 2 | E97025 | spovB related memb |
| 866 | 38 | 33.9 | 943 | 2 | S59317 | DIP2 protein - yea | 939 | 37.5 | 33.5 | 532 | 2 | T33511 | hypothetical prote |
| 867 | 38 | 33.9 | 954 | 2 | G71496 | conserved hypothe | 940 | 37.5 | 33.5 | 567 | 2 | T33650 | hypothetical prote |
| 868 | 38 | 33.9 | 956 | 2 | H81654 | hypothetical prote | 941 | 37.5 | 33.5 | 605 | 2 | JC5239 | insulin-like growt |
| 869 | 38 | 33.9 | 979 | 2 | D96574 | hypothetical prote | 942 | 37.5 | 33.5 | 605 | 2 | A41915 | insulin-like growt |
| 870 | 38 | 33.9 | 985 | 2 | D82776 | pyruvate dehydrog | 943 | 37.5 | 33.5 | 642 | 2 | G69786 | ABC transporter (A |
| 871 | 38 | 33.9 | 1003 | 1 | GNMWLV | HIV-1 retropepsin | 944 | 37.5 | 33.5 | 702 | 2 | G83386 | elongation factor |
| 872 | 38 | 33.9 | 1005 | 2 | P90099 | hypothetical prote | 945 | 37.5 | 33.5 | 837 | 2 | B82932 | preprotein translo |
| 873 | 38 | 33.9 | 1012 | 1 | GNMWVL | HIV-1 retropepsin | 946 | 37.5 | 33.5 | 912 | 2 | T31223 | crag protein homol |
| 874 | 38 | 33.9 | 1015 | 1 | GNWMH3 | HIV-1 retropepsin | 947 | 37.5 | 33.5 | 957 | 2 | AH2227 | cation-transportin |
| 875 | 38 | 33.9 | 1037 | 2 | S51900 | hypothetical prote | 948 | 37.5 | 33.5 | 1005 | 2 | T18537 | Ig heavy chain - c |
| 876 | 38 | 33.9 | 1072 | 2 | AD1280 | SNF2-type helicase | 949 | 37.5 | 33.5 | 1076 | 2 | T39580 | ncca protein - Alc |
| 877 | 38 | 33.9 | 1181 | 2 | B64516 | hypothetical prote | 950 | 37.5 | 33.5 | 1113 | 2 | H84105 | hypothetical prote |
| 878 | 38 | 33.9 | 1187 | 2 | T46637 | transcription fact | 951 | 37.5 | 33.5 | 1114 | 2 | S51470 | hypothetical prote |
| 879 | 38 | 33.9 | 1188 | 2 | T46608 | zinc finger protei | 952 | 37.5 | 33.5 | 1224 | 1 | S58884 | Ran-binding protei |
| 880 | 38 | 33.9 | 1190 | 2 | A82615 | cobalamine-depende | 953 | 37.5 | 33.0 | 72 | 2 | A35731 | retrovirus-related |
| 881 | 38 | 33.9 | 1212 | 2 | A96971 | P-glycoprotein-11k | 954 | 37.5 | 33.0 | 75 | 2 | S36422 | hypothetical prote |
| 882 | 38 | 33.9 | 1229 | 2 | D85023 | P-glycoprotein-11k | 955 | 37.5 | 33.0 | 75 | 2 | AC1755 | hypothetical prote |
| 883 | 38 | 33.9 | 1229 | 2 | TS2319 | probable P-glycop | 956 | 37.5 | 33.0 | 87 | 2 | H64540 | hypothetical prote |
| 884 | 38 | 33.9 | 1230 | 2 | E85023 | probable P-glycop | 957 | 37.5 | 33.0 | 87 | 2 | C71966 | hypothetical prote |
| 885 | 38 | 33.9 | 1278 | 2 | E86155 | period protein hom | 958 | 37.5 | 33.0 | 88 | 2 | E75144 | conserved hypothe |
| 886 | 38 | 33.9 | 1290 | 2 | T00018 | period protein hom | 959 | 37.5 | 33.0 | 93 | 2 | H69289 | partial transposas |
| 887 | 38 | 33.9 | 1291 | 2 | T00019 | period protein hom | 960 | 37.5 | 33.0 | 104 | 2 | H90489 | arsenate reductase |
| 888 | 38 | 33.9 | 1305 | 2 | T00670 | probable inositol | 961 | 37.5 | 33.0 | 116 | 2 | F82110 | hypothetical 13.0 |
| 889 | 38 | 33.9 | 1350 | 2 | T31353 | polyprotein - Arab | 962 | 37.5 | 33.0 | 116 | 2 | C65214 | hypothetical prote |
| 890 | 38 | 33.9 | 1471 | 2 | T19506 | hypothetical prote | 963 | 37.5 | 33.0 | 116 | 2 | F86099 | hypothetical prote |
| 891 | 38 | 33.9 | 1489 | 2 | G83771 | glucosyltransferas | 964 | 37.5 | 33.0 | 116 | 2 | B91259 | hypothetical prote |
| 892 | 38 | 33.9 | 1599 | 2 | S22737 | glucosyltransferas | 965 | 37.5 | 33.0 | 124 | 2 | G84294 | hypothetical prote |
| 893 | 38 | 33.9 | 1614 | 2 | T29861 | hypothetical prote | 966 | 37.5 | 33.0 | 127 | 2 | D75264 | transcription regu |
| 894 | 38 | 33.9 | 1635 | 2 | AI0452 | hemolysin (impor | 967 | 37.5 | 33.0 | 130 | 2 | S55385 | PEA-15 protein - m |
| 895 | 38 | 33.9 | 1778 | 2 | T50074 | probable nucleopor | 968 | 37.5 | 33.0 | 135 | 2 | D71659 | hypothetical prote |
| 896 | 38 | 33.9 | 1849 | 2 | T00415 | hypothetical prote | 969 | 37.5 | 33.0 | 139 | 2 | S22510 | H+-transporting tw |
| 897 | 38 | 33.9 | 1935 | 1 | S06006 | myosin beta heavy | 970 | 37.5 | 33.0 | 142 | 2 | T24862 | hypothetical prote |
| 898 | 38 | 33.9 | 1935 | 1 | A59286 | myosin heavy chain | 971 | 37.5 | 33.0 | 142 | 2 | S75218 | hypothetical prote |
| 899 | 38 | 33.9 | 2020 | 2 | C48399 | ABC-type transport | 972 | 37.5 | 33.0 | 142 | 2 | D86348 | F2498.15 protein (|
| 900 | 38 | 33.9 | 2025 | 2 | T03884 | hypothetical prote | 973 | 37.5 | 33.0 | 143 | 2 | JC5246 | allograft inflama |
| 901 | 38 | 33.9 | 2241 | 2 | S09811 | hypothetical prote | 974 | 37.5 | 33.0 | 146 | 2 | JC4902 | ionized calcium bl |
| 902 | 38 | 33.9 | 2829 | 2 | A42771 | reticulocyte-bind | 975 | 37.5 | 33.0 | 147 | 2 | C95869 | probable transcrip |
| 903 | 38 | 33.9 | 2839 | 2 | A59404 | plectin (imported) | 976 | 37.5 | 33.0 | 147 | 2 | I55617 | hypothetical prote |
| 904 | 38 | 33.9 | 4687 | 1 | A39638 | plectin - rat | 977 | 37.5 | 33.0 | 151 | 2 | D86891 | hypothetical prote |
| 905 | 37.5 | 33.5 | 92 | 2 | H82371 | conserved hypothe | 978 | 37.5 | 33.0 | 154 | 2 | AB1270 | hypothetical prote |


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979 37 33.0 154 2 AD1632 hypothetical prote
980 37 33.0 156 2 E90510 conserved hypothet
981 37 33.0 157 2 AD2320 hypothetical prote
982 37 33.0 159 2 F84091 hypothetical prote
983 37 33.0 163 2 H64320 molybdenum cofacto
984 37 33.0 168 2 S62881 calcium binding pr
985 37 33.0 169 2 S77820 hypothetical excinucle
986 37 33.0 171 2 C64122 hypothetical prote
987 37 33.0 184 2 S56441 18.2K protein prec
988 37 33.0 184 2 B91278 hypothetical prote
989 37 33.0 184 2 B86119 hypothetical prote
990 37 33.0 185 2 AE1320 hypothetical prote
991 37 33.0 185 2 S50537 hypothetical prote
992 37 33.0 186 2 AB0062 conserved hypothet
993 37 33.0 187 2 H81033 oligoribonuclease
994 37 33.0 187 2 F81978 probable oligoribo
995 37 33.0 187 2 AG2721 conserved hypothet
996 37 33.0 189 2 T46076 conserved hypothet
997 37 33.0 190 2 T08258 conserved hypothet
998 37 33.0 192 2 D97503 hypothetical prote
999 37 33.0 195 2 F81255 amidotransferase H
1000 37 33.0 195 2 A96731 unknown protein F5
```

ALIGNMENTS

RESULT 1

homocitrate synthase (EC 4.1.3.21) [validated] - Thermus aquaticus

C/Species: Thermus aquaticus

C/Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 09-Jul-2004

C/Accession: T51170

R/Kosuge, T.; Hoshino, T.

submitted to the EMBL Data Library, October 1998

A/Description: lysine is synthesized through the alpha-aminoadipate pathway in Thermus

A/Reference number: Z25321

A/Status: preliminary

A/Accession: T51170 translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-376 <ROS>

A/Cross-references: UNIPROT:O87198; EMBL:AB018379; PIDD:BAA33785.1

A/Experimental source: strain HB27

C/Genetics:

A/Function:

A/Description: EC 4.1.3.21 [validated, PMID:99085673]

A/Superfamily: hydroxymethylglutaryl-CoA lyase

C/Keywords: carbon-carbon lyase; coenzyme A; oxo-acid-lyase

Query Match 51.8%; Score 58; DB 2; Length 376;

Best Local Similarity 47.4%; Pred. No. 2.9;

Matches 9; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 MADNGTITVEBKQLLEQW 19

DB 355 LADRGQTLEELDRILREW 373

RESULT 2

TVHUA

transforming protein ralA - human

N/Alternate names: GTP-binding protein ral

C/Species: Homo sapiens (man)

C/Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004

C/Accession: S04596; A34387

R/Chardin, P.; Tavlitian, A.

Nucleic Acids Res. 17, 4380, 1989

A/Title: Coding sequences of human ralA and ralB cDNAs.

A/Reference number: S04596, PMID:89296492; PMID:2662142

A/Accession: S04596

A/Molecule type: mRNA

A/Residues: 1-206 <CHA>

A/Cross-references: UNIPROT:P11233; GB:X15014; NID:g35845; PIDD:CAA33118.1; PID:g35846

J/Polak, P.G.; Weber, R.F.; Nevins, B.; Didsbury, J.R.; Evans, T.; Snyderman, R.

J. Biol. Chem. 264, 16383-16389, 1989

A/Title: Identification of the ral and rac1 gene products, low molecular mass GTP-binding

A/Reference number: A34387, PMID:89380251; PMID:2550440

A/Accession: A34387

A/Molecule type: mRNA

A/Residues: 1,'VDYL',3-206 <POL>

A/Cross-references: GB:M29893; NID:g190849; PIDD:AAA6542.1; PID:g190850

A/Note: parts of this sequence were confirmed by peptide sequencing

C/Genetics:

A/Gene: GDB:RALA

A/Cross-references: GDB:120723; OMIM:179550

A/Map position: 7pter-7cen

C/Superfamily: ras transforming protein; translation elongation factor Tu homology

C/Keywords: GTP binding; lipoprotein; membrane protein; methylated carboxyl end; nucleoti

F:15-130/Domain: translation elongation factor Tu homology <ETU>

F:21-28/Region: nucleotide-binding motif A (P-loop)

F:127-130/Region: GTP-binding NKXD motif

F:157-159/Region: GTP-binding SAK/L motif

F:27-28,46,127,128,130,157/Binding site: Mg-GTP (Lys, Ser, Thr, Asn, Lys, Asp, Ser) #strat

F:203/Binding site: geranyl-geranyl (Cys) (covalent) #status predicted

F:203/Modified site: methyl ester carboxyl end (Cys) (in mature form) #status predicted

Query Match 45.5%; Score 51; DB 1; Length 206;

Best Local Similarity 42.9%; Pred. No. 13;

Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 MADNGTITVEBKQLLEQWNL 21

DB 131 LBDKROVSVEAKNRABQNNV 151

RESULT 3

hypothetical protein BH1956 [imported] - Bacillus halodurans (strain C-125)

C/Species: Bacillus halodurans

C/Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004

C/Accession: D83894

R/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Maui, N.; Fuji, F.; Hiran

Nucleic Acids Res. 28, 4317-4331, 2000

A/Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A/Reference number: A83650; PMID:20512582; PMID:11058132

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-344 <STO>

A/Cross-references: UNIPROT:Q9KH1; GB:AP001513; GB:BA000004; NID:g10174345; PIDD:BA056;

A/Experimental source: strain C-125

C/Genetics:

Query Match 45.5%; Score 51; DB 2; Length 344;

Best Local Similarity 41.4%; Pred. No. 23;

Matches 12; Conservative 3; Mismatches 6; Indels 8; Gaps 1;

QY 1 MADNGTITVE-----LKQLLEQWNL 21

DB 273 MGDNGQATVGENKQALVDLRRLPEWKI 301

RESULT 4

E97225

carbamoylphosphate synthase small chain [imported] - Clostridium acetobutylicum

C/Species: Clostridium acetobutylicum

C/Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004

C/Accession: E97225

R/Molling, J.; Breton, G.; Onelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,

J. Daily, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo

A/Reference number: A96900; PMID:21359325; PMID:21359325

A/Accession: E97225

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-351 <RUR>
A:Cross-references: UNIPROT:Q97FT2; GB:AE001437; PIDN:AAK80592.1; PID:IG15025673; GSPDB:G
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC2445
C:Superfamily: carbamoyl-phosphate synthase (glutamine-hydrolyzing) small chain; carbam

Query Match 45.5%; Score 51; DB 2; Length 351;
Best Local Similarity 42.1%; Pred. No. 24;
Matches 8; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 4 NGTITVEELKOLLEQNLV 22
DB 132 NGELSTIELKMMADSNIV 150

RESULT 5
C64087
exopolyphosphatase ppx homolog - Haemophilus influenzae (strain Rd KM20)
C:Species: Haemophilus influenzae
C>Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C:Accession: C64087
R:Feilschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Keriavage, A
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraeier, C.M.; Smith, H.O.; Venter,
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630; PMID:7542800
A:Accession: C64087
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-323 <TIGR>
A:Cross-references: UNIPROT:P44828; GB:U32752; GB:I42023; NID:G1573692; PIDN:AAK22355.1;

Query Match 44.6%; Score 50; DB 2; Length 323;
Best Local Similarity 66.7%; Pred. No. 29;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 NGTITVEELKOLLEQ 18
DB 238 NGTITAEKRLALIEQ 252

RESULT 6
F82930
DNA ligase UUI21 (imported) - Ureaplasma urealyticum
C:Species: Ureaplasma urealyticum
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 12-Jul-2004
C:Accession: F82930
R:Glaser, J.I.; Lefkowitz, E.J.; Glaser, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to Genbank, February 2000
A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mir
A:Reference number: A82870
A:Accession: F82930
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-673 <GIA>
A:Cross-references: GB:AE002113; GB:AF222894; NID:G6899078; PIDN:AAF30527.1; GSPDB:GN001
A:Experimental source: serovar 3; biovar 1
C:Genetics:
A:Gene: lig; UUI21
A:Gene code: SGC3
C:Superfamily: NAD+-dependent DNA ligase, ligA type

Query Match 44.6%; Score 50; DB 2; Length 673;
Best Local Similarity 66.7%; Pred. No. 63;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 9 VEELKOLLEQNL 20
:::|||||:::|||||

DB 8 IDELKOKLDQNL 19

RESULT 7
S41034
hypothetical protein R10E12.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S41034
R:Smith, A.
submitted to the EMBL Data Library, January 1994
A:Reference number: S41034
A:Accession: S41034
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-882 <SMT>
A:Cross-references: UNIPROT:Q81115; EMBL:Z29561; NID:G450897; PID:G450898
C:Genetics:
A:Introns: 72/2; 324/3; 359/1; 400/2; 722/1; 743/1; 782/1; 818/1

Query Match 44.6%; Score 50; DB 2; Length 882;
Best Local Similarity 47.6%; Pred. No. 84;
Matches 10; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 2 ADNGTITVEELKOLLEQNLV 22
DB 548 ATGCTDTVQLRQFMSQNLV 568

RESULT 8
S50566
hypothetical protein YER063w - Yeast (Saccharomyces cerevisiae)
C:Species: Saccharomyces cerevisiae
C>Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 09-Jul-2004
C:Accession: S50566
R:Dietrich, F.S.
submitted to the EMBL Data Library, December 1994
A:Description: The sequence of S. cerevisiae lambda clones 6592, 4678, 4742, and 3612.
A:Reference number: S50427
A:Accession: S50566
A:Molecule type: DNA
A:Residues: 1-218 <DIE>
A:Cross-references: UNIPROT:P40040; EMBL:U1813; NID:G1381127; PID:G603299; GSPDB:GN00001;
C:Genetics:
A:Gene: SGD:THO1; MIPS:YER063w
A:Cross-references: SGD:S0000865
A:Map position: 5R

Query Match 43.8%; Score 49; DB 2; Length 218;
Best Local Similarity 52.4%; Pred. No. 27;
Matches 11; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKOLLEQNL 21
DB 1 MADYSLTVQLKDLITKRL 21

RESULT 9
B32840
anthranilate synthase (EC 4.1.3.27) component I - Leptospira biflexa
C:Species: Leptospira biflexa
C>Date: 08-Dec-1989 #sequence_revision 08-Dec-1989 #text_change 09-Jul-2004
C:Accession: B32840
R:Yelton, D.B.; Peng, S.L.
J. Bacteriol. 171, 2083-2089, 1989
A:Title: Identification and nucleotide sequence of the Leptospira biflexa serovar patoc
A:Reference number: A32840; MUID:89197778; PMID:2703466
A:Accession: B32840
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-462 <YEL>
A:Cross-references: UNIPROT:P20463; GB:M22468; NID:G149627; PIDN:AAA89216.1; PID:G149628
C:Superfamily: anthranilate synthase component I

S60545
envelope polyprotein gp41 - human immunodeficiency virus type 1 (isolate CI-45-1) (fragm
C/Species: human immunodeficiency virus type 1, HIV-1
A/Variety: isolate CI-45-1
C/Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C/Accession: S60545
R/Janssens, W.; Heyndrickx, L.; Van de Peer, Y.; Bouckaert, A.; Franssen, K.; Motte, J.;
AIDS 8, 21-26, 1994
A/Title: Molecular phylogeny of part of the env gene of HIV-1 strains isolated in Cote d
A/Reference number: S60521; MUID:94280700; PMID:8011235
A/Accession: S60545
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-294 <UN>
A/Cross-references: UNIPROT:Q76190; EMBL:X72047; NID:9468669; PIDN:CAA50930.1; PID:94686
A/Experimental source: isolate CI-45-1
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1993
C/Genetics:
A/Gene: env
C/Superfamily: type E retrovirus env polyprotein
C/Keywords: AIDS; glycoprotein; immunodeficiency; polyprotein

Query Match 42.4%; Score 47.5; DB 2; Length 294;
Best Local Similarity 45.0%; Pred. No. 58;
Matches 9; Conservative 6; Mismatches 4; Indels 1; Gaps 1;

OY 4 NGTTTVE-ELKQLEQNNLV 22
DB 136 NGTTTLOCKIKQIVNMQKV 155

RESULT 15
S60524
envelope polyprotein gp41 - human immunodeficiency virus type 1 (isolate CI-45-3) (fragm
C/Species: human immunodeficiency virus type 1, HIV-1
A/Variety: isolate CI-45-3
C/Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C/Accession: S60524
R/Janssens, W.; Heyndrickx, L.; Van de Peer, Y.; Bouckaert, A.; Franssen, K.; Motte, J.;
AIDS 8, 21-26, 1994
A/Title: Molecular phylogeny of part of the env gene of HIV-1 strains isolated in Cote d
A/Reference number: S60521; MUID:94280700; PMID:8011235
A/Accession: S60524
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-294 <UN>
A/Cross-references: UNIPROT:Q76169; EMBL:X72027; NID:9468780; PIDN:CAA50910.1; PID:94687
A/Experimental source: isolate CI-45-3
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1993
C/Genetics:
A/Gene: env
C/Superfamily: type E retrovirus env polyprotein
C/Keywords: AIDS; glycoprotein; immunodeficiency; polyprotein

Query Match 42.4%; Score 47.5; DB 2; Length 294;
Best Local Similarity 45.0%; Pred. No. 58;
Matches 9; Conservative 6; Mismatches 4; Indels 1; Gaps 1;

OY 4 NGTTTVE-ELKQLEQNNLV 22
DB 136 NGTTTLOCKIKQIVNMQKV 155

RESULT 16
S56237
glucosamine-phosphate N-acetyltransferase (EC 2.3.1.4) [validated] - yeast (Saccharomyce
N/Alternate names: phosphoglucosamine acetylase; phosphoglucosamine transacetylase; pro
C/Species: Saccharomyces cerevisiae
C/Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 09-Jul-2004
C/Accession: S56237; S46321; S62236
R/Murakami, Y.; Naitou, M.; Hagihara, H.; Shibata, T.; Oawa, M.; Sasamura, S.I.; Sasa
submitted to the EMBL Data Library, May 1995
A/Description: Analysis of the nucleotide sequence of chromosome VI from Saccharomyces ce

A/Reference number: S56186
A/Accession: S56237
A/Molecule type: DNA
A/Residues: 1-159 <MUR>
A/Cross-references: UNIPROT:P43577; EMBL:D50617; NID:9836685; PIDN:BAA09221.1; PID:98367;
R/Churcher, C.
submitted to the EMBL Data Library, September 1994
A/Reference number: S48310
A/Accession: S48321
A/Molecule type: DNA
A/Residues: 1-111, 'AS', <CU>
A/Cross-references: EMBL:D46255; NID:9559925; PIDN:CAA86352.1; PID:9559937; GSPDB:GN00004
R/Murakami, Y.
submitted to the EMBL Data Library, December 1994
A/Reference number: S62230
A/Accession: S62296
A/Molecule type: DNA
A/Residues: 1-159 <MUM>
A/Cross-references: EMBL:D44596; NID:91100783; PIDN:BAA08000.1; PID:91100787
C/Genetics:
A/Gene: SGD:GNA1; GNA1; MIPS:YFL017C
A/Cross-references: MIPS:YFL017C; SGD:S0001877
A/Map position: 6L
C/Function:
A/Description: EC 2.3.1.4 [validated, MUID:99085039]; glucosamine-phosphate N-acetyltran
A/Note: phosphoglucosamine acetyltransferase activity has been shown in vitro. By incubat
-acetylglucosamine is produced from glucosamine 6-phosphate, indicating that 142-Phe and
C/Superfamily: Saccharomyces glucosamine-phosphate N-acetyltransferase
C/Keywords: acyltransferase; coenzyme A

Query Match 42.0%; Score 47; DB 1; Length 159;
Best Local Similarity 50.0%; Pred. No. 36;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 5 GTTVEELKQLEQNNLV 20
DB 31 GTTTPESFKLIKRYNN 46

RESULT 17
AC0897
TDC operon transcription activator STY3428 [imported] - Salmonella enterica subsp. enteri
C/Species: Salmonella enterica subsp. enterica serovar Typh
A/Note: this species has also been called Salmonella typhi
C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C/Accession: AC0897
R/Parikh, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Garra, P.
Nature 413, 848-852, 2001
A/Author: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A/Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A/Reference number: AB0502; MUID:2153947; PMID:1167608
A/Accession: AC0897
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1312 <PAR>
A/Cross-references: GB:AL513382; PIDN:CAD07769.1; PID:916504318; GSPDB:GN00176
C/Genetics:
A/Gene: STY3428
C/Superfamily: regulatory protein 11VY

Query Match 42.0%; Score 47; DB 2; Length 312;
Best Local Similarity 64.7%; Pred. No. 72;
Matches 11; Conservative 1; Mismatches 3; Indels 2; Gaps 1;

OY 5 GTTVEELKQLEQNNLV 21
DB 185 GTTTLSSKND--EQNAL 199

RESULT 18
AG2311

Db 49 DRGTTTEBACRCEKRDPHNAKYIREVMETWN 81

RESULT 23

G82238

adenosylmethionine-8-amino-7-oxononanoate aminotransferase VC1111 [imported] - *Vibrio cholerae*

C/Species: *Vibrio cholerae*

C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C/Accession: G82238

R/Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardon, D.; Ermolaeva, M.D.; Vamathevan, J.; Bae, S.; Qin, H.; Dragol, I.; Sellers, F.1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A/Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.

A/Reference number: A82035; PMID:20406833; PMID:10952301

A/Accession: G82238

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-428 <HEI>

A/Cross-references: UNIPROT:Q9K525; GB:AE004192; GB:AE003852; NID:99655581; PIDN:AAF9427

A/Experimental source: serogroup O1; strain N16961; biotype El Tor

C/Genetics:

A/Gene: VC1111

A/Map position: 1

C/Superfamily: ornithine-oxo-acid aminotransferase

Query Match 41.1%; Score 46.5; DB 2; Length 428;

Best Local Similarity 42.9%; Pred. No. 1.2e+02;

Matches 9; Conservative 6; Mismatches 5; Indels 1; Gaps 1;

Qy 1 MADNGTITVE-ELKQLEQWN 20

Db 107 LADSGSVAVEVSLKMLQGMH 127

RESULT 24

E80178

hypothetical protein pdcfs [imported] - *Sulfolobus solfataricus*

C/Species: *Sulfolobus solfataricus*

C/Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004

C/Accession: E80178

R/She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aways, M.J.; Chan-Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F. et al., R.A.; Ragan, M.A.; Sengen, C.W.; Van der Oost, J.

submitted to GenBank, April 2001

A/Description: *Sulfolobus solfataricus* complete genome.

A/Reference number: A99139

A/Accession: E90178

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-118 <KUR>

A/Cross-references: UNIPROT:Q980F8; GB:AE006641; NID:913813498; PIDN:AAK40684.1; GSPDB:C

C/Genetics:

A/Gene: pdcfs

C/Superfamily: DNA-binding protein, TPA19 type

Query Match 41.1%; Score 46; DB 2; Length 118;

Best Local Similarity 83.3%; Pred. No. 36;

Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 ITVEELKQLEQ 18

Db 88 ITDEELKQLEQ 99

RESULT 25

E69527

hypothetical protein AF2221 - *Archaeoglobus fulgidus*

C/Species: *Archaeoglobus fulgidus*

C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

C/Accession: E69527

R/Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, R.; Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, R.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.

Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997

A/Authors: Uitterlinden, T.; Cotton, M.D.; Spriggs, T.; Artach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Moese, C.R.; Venter, J.C.

A/Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo

A/Reference number: A69250; PMID:98049343; PMID:9989475

A/Accession: E69527

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-340 <LE>

A/Cross-references: UNIPROT:Q28062; GB:AE000952; GB:AE000782; NID:92689275; PIDN:AA89043

C/Superfamily: Archaeoglobus fulgidus hypothetical protein AF2221

Query Match 41.1%; Score 46; DB 2; Length 340;

Best Local Similarity 53.3%; Pred. No. 1.1e+02;

Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 7 ITVEELKQLEQWN 21

Db 208 LDVQELKLEKXNI 222

RESULT 26

C71407

hypothetical protein - *Arabidopsis thaliana*

C/Species: *Arabidopsis thaliana* (mouse-ear cress)

A/Variety: Columbia

C/Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 09-Jul-2004

C/Accession: C71407

R/Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Ditzel, P.; Medler, H.; Medler, E.; Wambutt, R.; Welzenegger, T.; Pohl, T.M.; Terry, N.; Glebe, A.; Weller, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.

Nature 391, 485-488, 1998

A/Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech, ernof, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ans C.; Chalwatzis, N.

A/Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of *Arabidopsis thal*

A/Reference number: A71400; PMID:98121113; PMID:9461215

A/Accession: C71407

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-420 <BEV>

A/Cross-references: UNIPROT:Q23306; GB:Z97336; NID:92244788; PID:92244806

C/Genetics:

A/Map position: 4COP9-4G3845

C/Superfamily: Arabidopsis thaliana hypothetical protein P107554.0

Query Match 41.1%; Score 46; DB 2; Length 420;

Best Local Similarity 44.4%; Pred. No. 1.3e+02;

Matches 12; Conservative 3; Mismatches 4; Indels 8; Gaps 1;

Qy 2 ADNGTITVE-ELKQLEQWN 20

Db 127 SDNGTITVE-ELKQLEQWN 153

RESULT 27

H90563

hypothetical protein MYU 4160 [imported] - *Mycoplasma pulmonis* (strain UAB CTIP)

C/Species: *Mycoplasma pulmonis*

C/Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004

C/Accession: H90563

R/Chandaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.; Nucleic Acids Res. 29, 2145-2153, 2001

A/Title: The complete genome sequence of the murine respiratory pathogen *Mycoplasma pulm*

A/Reference number: A99512; PMID:21267165; PMID:11353084

A/Accession: H90563

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-472 <KUR>

A/Cross-references: UNIPROT:Q980F0; GB:AL445566; PID:G14089830; PIDN:CAC13589.1; GSPDB:G

A/Experimental source: strain UAB CTIP

C/Genetics:

A:Gene: MYPU_4160
A:Genetic code: SGC3

Query Match 41.1%; Score 46; DB 2; Length 472;
Best Local Similarity 47.1%; Pred. No. 1.5e+02;
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 4 NGTIVTEELKOLLEQNN 20
|||::|::|::|::|
DB 105 NGSISISEIKKQIEQNN 121

RESULT 28

H72403 glycine dehydrogenase (decarboxylating) subunit 2 - Thermotoga maritima (strain MSB8)

C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: H72403
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.

Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A:Reference number: A72200; WUID:99287316; PMID:10360571

A:Accession: H72403
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-474 <ARN>
A:Cross-references: UNIPROT:Q9WY57; GB:AE001706; GB:AE000512; NID:g4980707; PIDN:AAD3530
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TW0214

C:Superfamily: glycine dehydrogenase (decarboxylating)

Query Match 41.1%; Score 46; DB 2; Length 474;
Best Local Similarity 53.3%; Pred. No. 1.5e+02;
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 4 NGTIVTEELKOLLEQ 18
|||::|::|::|::|
DB 184 NGKWDVEDLKKLDE 198

RESULT 29

AC0845 probable sigma-54-dependent transcriptional regulator STY2961 [imported] - Salmonella ent

C:Species: Salmonella enterica subsp. enterica serovar typh
A:Note: this species has also been called Salmonella typh
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 28-Apr-2003
C:Accession: AC0845

R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; WUID:21534947; PMID:11677608

A:Accession: AC0845
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-506 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD05946.1; PID:g16503917; GSPDB:GN00176
C:Genetics:
A:Gene: STY2961

C:Superfamily: Response regulator (sigma54-dependent transcriptional activator), FlhA ty

Query Match 41.1%; Score 46; DB 2; Length 506;
Best Local Similarity 53.3%; Pred. No. 1.6e+02;
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKOL 15
|||||::|::|::|
DB 277 MADNGTITVEELKOL 291

RESULT 30

A65051 ygaA protein - Escherichia coli (strain K-12)

C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C:Accession: A65051
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col
A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; WUID:97426617; PMID:9278503

A:Accession: A65051
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA

A:Residues: 1-529 <BLAT>
A:Cross-references: UNIPROT:P37013; GB:AE000354; GB:U00096; NID:g2367149; PIDN:AACT5751.1
A:Experimental source: strain K-12, substrain MG1655

C:Genetics:
A:Superfamily: Response regulator (sigma54-dependent transcriptional activator), FlhA ty

C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: E91074
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
gasaara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.

DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom
A:Reference number: A99629; WUID:21156231; PMID:11258796

A:Accession: E91074
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-529 <HAY>
A:Cross-references: UNIPROT:Q8X954; GB:BA000007; PIDN:BA836988.1; PID:g13363036; GSPDB:G
A:Experimental source: strain O157:H7, substrain RIMD 0509952

C:Genetics:
A:Gene: EC63565

C:Superfamily: Response regulator (sigma54-dependent transcriptional activator), FlhA ty

Query Match 41.1%; Score 46; DB 2; Length 529;
Best Local Similarity 53.3%; Pred. No. 1.7e+02;
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKOL 15
|||||::|::|::|
DB 302 MADNGTITVEELKOL 316

RESULT 32

DB5919 probable 2-component transcription regulator ygaA [imported] - Escherichia coli (strain C

C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: DB5919

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glaeser, J.D.; Rose, D.G.; Mayhew,
Hiller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousts, K.; Apodaca,
Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: A99629; WUID:21156231; PMID:11258796

A:Reference number: AB5480; MWID:21074935; PMID:11206551
A:Accession: D85919
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-529 <STO>
A:Cross-references: UNIPROT:Q8X854; GB:AB005174; NID:g12517154; PIDN:AAG57816.1; GSPDB:G
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: ypaA
C:Superfamily: Response regulator (sigma54-dependent transcriptional activator), FHA ty

Query Match 41.1%; Score 46; DB 2; Length 529;
Best Local Similarity 53.3%; Pred. No. 1.7e+02;
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 MADNGTIVEELKQL 15
DB 302 MADNGTFLFDEIGEL 316

RESULT 33
JC6129
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 1B, calmodulin-dependent, 63k s
N:Alternate names: 63k calmodulin-stimulated phosphodiesterase, brain; CAM-PDE1B1
C:Species: Homo sapiens (man)
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: JC6129; G02260
R:Jiang, X.; Li, J.; Parkind, M.; Epstein, P.M.
Proc. Natl. Acad. Sci. U.S.A. 93, 11236-11241, 1996
A:Title: Inhibition of calmodulin-dependent phosphodiesterase induces apoptosis in human
A:Reference number: JC6129; MWID:97008163; PMID:8855339
A:Accession: JC6129
A:Molecule type: mRNA
A:Residues: 1-536 <JIA>
A:Cross-references: UNIPROT:Q01064; GB:U56976; NID:g1621591; PIDN:AAC50769.1; PID:g16215
A:Experimental source: lymphoblastoid B-cell
R:Houliay, M.D.; Erdogan, S.; Rena, G.; Sullivan, M.
submitted to the EMBL Data Library, November 1995
A:Reference number: H00937
A:Accession: G02260
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 201-203, 'W', 205-358, 'S', 360-384 <HOU>
A:Cross-references: EMBL:U40584; NID:g1110534; PID:g1110535
C:Comment: This enzyme is a useful target for inducing the death of leukemic cells, and
C:Genetics:
A:Gene: GDB:PDE1B; PDE51B
A:Cross-references: GDB:120264; OMIM:171891
A:Map position: 16p13.11
C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin binding, cAMP binding, phosphoric diester h
C:Keyword: alternative splicing; calmodulin binding; cAMP binding; phosphoric diester h
F:222-439/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNPD>

Query Match 41.1%; Score 46; DB 1; Length 536;
Best Local Similarity 60.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 DNGTIVEELKQLE 17
DB 47 ENGEINIEELKQLE 61

RESULT 34
GB1328
60 kD chaperonin (cpn60) G11221 [imported] - Campylobacter jejuni (strain NCTC 11168)
C:Species: Campylobacter jejuni
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: GB1328
R:Parhill, J.; Wren, B.W.; Mungall, K.; Kelley, J.M.; Churcher, C.; Basham, D.; Chilling
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrer
Nature 403, 665-668, 2000
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals h
A:Reference number: AB1250; MWID:20150912; PMID:10688204

A:Accession: GB1328
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-545 <PAR>
A:Cross-references: UNIPROT:O69289; GB:AL139077; GB:AL111168; NID:s6968444; PIDN:CA87347;
A:Experimental source: serotype O2, strain NCTC 11168
C:Genetics:
A:Gene: groEL; G11221
C:Superfamily: chaperonin groEL

Query Match 41.1%; Score 46; DB 2; Length 545;
Best Local Similarity 47.4%; Pred. No. 1.8e+02;
Matches 9; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 4 NGTIVEELKQLEONLV 22
DB 171 DGVTIVEAKSINDELNV 189

RESULT 35
AB2913
hypothetical protein UH263 [imported] - Ureaplasma urealyticum
C:Species: Ureaplasma urealyticum
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: AB2913
R:Glas, J.I.; Lefkowitz, B.U.; Glas, J.S.; Heiner, C.R.; Chen, E.Y.; Caswell, G.H.
submitted to Genbank, February 2000
A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min
A:Reference number: AB2870
A:Accession: AB2913
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-594 <GLA>
A:Cross-references: GB:AE002123; GB:AF222894; NID:g6899229; PIDN:AAF30672.1; GSPDB:GN001;
A:Experimental source: serovar 3; biovar 1
C:Genetics:
A:Gene: UH263
A:Genetic code: SGC3

Query Match 41.1%; Score 46; DB 2; Length 594;
Best Local Similarity 72.7%; Pred. No. 1.9e+02;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 11 ELKQLEONML 21
DB 347 ELKQLEKMKL 357

RESULT 36
AB2591
conserved hypothetical protein Atu0119 [imported] - Agrobacterium tumefaciens (strain C58
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AB2591
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
erge, G.; Giller, W.; Grant, C.; Gunthner, D.; Kutyavln, T.; Levy, R.; Li, M.; McClellan
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E
ster, B.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MWID:21608550; PMID:11743193
A:Accession: AB2591
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-88 <KUR>
A:Cross-references: UNIPROT:Q8UJ19; GB:AB008688; PIDN:PAL41144.1; PID:g17738440; GSPDB:G
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu0119
A:Map position: circular chromosome

Query Match 40.6%; Score 45.5; DB 2; Length 88;

Qy 4 NGTITVEELKQLLEQWN 20
 ||:||||:|
 Db 3 NGSIPVDEVIEHLRNWN 19

RESULT 42

D49591
 Membrane protein M - porcine epidemic diarrhoea virus
 C/Species: porcine epidemic diarrhoea virus
 C/Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
 C/Accession: D49591
 R/Duarte, M.; Tobler, K.; Bridgen, A.; Kassehaert, D.; Ackermann, M.; Laude, H.
 Virology 198, 466-476, 1994
 A>Title: Sequence analysis of the porcine epidemic diarrhoea virus genome between the nuc
 A/Reference number: A49591; MUID:94120721; PMID:8291220
 A/Accession: D49591
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-226 <DUA>
 A/Cross-references: UNIPROT:Q91A19; GB:Z24733
 C/Superfamily: coronavirus E1 membrane glycoprotein

Query Match 40.2%; Score 45; DB 2; Length 226;
 Best Local Similarity 47.1%; Pred. No. 96;
 Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 4 NGTITVEELKQLLEQWN 20
 ||:||||:|
 Db 3 NGSIPVDEVIEHLRNWN 19

RESULT 43

T38795
 conserved uncharacterized protein domain-containing protein - fission yeast (Schizosacch
 C/Species: Schizosaccharomyces pombe
 C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C/Accession: T38795
 R/Gentles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
 Submitted to the EMBL Data Library, August 1996
 A/Reference number: Z21812
 A/Accession: T38795
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-264 <GEN>
 A/Cross-references: UNIPROT:O14171; EMBL:Z98602; PDB:1CAB1276.1; GSPDB:GN00066; SPDB:SF
 A/Experimental source: strain 972h-; cosmid cAD7
 C/Genetics:
 A/Map position: 1
 A/Intons: 69/3; 156/2; 228/3
 C/Superfamily: conserved hypothetical protein YBR002c

Query Match 40.2%; Score 45; DB 2; Length 264;
 Best Local Similarity 40.9%; Pred. No. 1.1e+02;
 Matches 9; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MADNGTITVEELKQLLEQWNLV 22
 ||:||||:|
 Db 181 MADGTITPEDIDEDIFEKRL 202

RESULT 44

T43492
 hypothetical protein DKFZp434A219.1 - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 23-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
 C/Accession: T43492
 R/Pousetka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, December 1999
 A/Reference number: Z22516
 A/Accession: T43492
 A/Status: preliminary

A/Molecule type: mRNA
 A/Residues: 1-318 <AAA>
 A/Cross-references: UNIPROT:O14703; EMBL:AL133583
 A/Experimental source: adult testis; clone DKFZp434A219
 C/Genetics:
 A/Note: DKFZp434A219.1

Query Match 40.2%; Score 45; DB 2; Length 318;
 Best Local Similarity 38.1%; Pred. No. 1.4e+02;
 Matches 8; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

Qy 1 MADNGTITVEELKQLLEQWN 21
 ||:||||:|
 Db 13 MPDTGANIPALNELLSVNM 33

RESULT 45

F72404
 flagellar motor switch protein FlgG - Thermotoga maritima (strain MSB8)
 C/Species: Thermotoga maritima
 C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
 C/Accession: F72404
 R/Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hickey,
 Garrett, M.M.; Stewart, A.M.; Cocton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
 C.M.
 Nature 399, 323-329, 1999
 A>Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
 A/Reference number: A72200; MUID:99287316; PMID:10360571
 A/Accession: F72404
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-335 <ARN>
 A/Cross-references: UNIPROT:Q9WY63; GB:AE001706; GB:AE000512; NID:94980707; PDB:1ADJ351;
 A/Experimental source: strain MSB8
 C/Genetics:
 A/Gene: TW0220
 C/Superfamily: flagellar switch protein FlgG

Query Match 40.2%; Score 45; DB 2; Length 335;
 Best Local Similarity 47.4%; Pred. No. 1.5e+02;
 Matches 9; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MADNGTITVEELKQLLEQWN 19
 ||:||||:|
 Db 43 IANIGRVTEPKQVLEBF 61

RESULT 46

F82012
 hypothetical protein NMA0184 [imported] - Neisseria meningitidis (strain Z2491 serogroup
 C/Species: Neisseria meningitidis
 C/Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
 C/Accession: F82012
 R/Parikh, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
 J.; Holroyd, S.; Jørgensen, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
 Nature 404, 502-506, 2000
 A>Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
 A/Reference number: AB1775; MUID:20222556; PMID:10761919
 A/Accession: F82012
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-468 <PAR>
 A/Cross-references: UNIPROT:Q9JWX2; GB:AL162752; GB:AL157959; NID:97378778; PDB:1CAB8349;
 A/Experimental source: serogroup A, strain Z2491
 C/Genetics:
 A/Gene: NMA0184

Query Match 40.2%; Score 45; DB 2; Length 468;
 Best Local Similarity 56.2%; Pred. No. 2.1e+02;
 Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 4 NGTITVEELKQLLEQWN 19
 ||:||||:|

Db 440 NGHTSABSLSLAEQW 455

RESULT 47
T10938
Calcium-dependent protein kinase (EC 2.7.1.-) - sweet potato
C/Species: Ipomoea batatas (sweet potato)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C/Accession: T10938
R/Kojima, H.; Sasaki, M.; Mano, S.; Nakamura, K.
Submitted to the EMBL Data Library, September 1996
A/Description: cDNA for a homologue of calcium-dependent protein kinase from petioles of
A/Reference number: Z17218
A/Accession: T10938
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-514 <KOJ>
A/Cross-references: UNIPROT:Q96469; EMBL:DB87707
A/Experimental source: cv. Kokei No.14; petiole
C/Genetics:
A/Note: CDPK
A/Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase; calmodulin repeat homology; protein kin
C/Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-specific
F:403-435/Domain: calmodulin repeat homology <EFH>

Query Match 40.2%; Score 45; DB 1; Length 514;
Best Local Similarity 62.5%; Pred. No. 2.3e+02;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 DNGTIVEELKQLE 18
:|||||:|
Db 383 NSGTIVEELKQIAQ 398

RESULT 48
A44162
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 1B, calmodulin-dependent, 63K sp
N/Alternate names: 63K calmodulin-stimulated phosphodiesterase, brain; CAM-PDE1B1
C/Species: Bos primigenius taurus (cattle)
C/Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C/Accession: A44162; B40283
R/Bentley, J.K.; Kadlecck, A.; Sherbert, C.H.; Seger, D.; Sonnenburg, W.K.; Charbonneau,
J. Biol. Chem. 267, 18676-18682, 1992
A/Title: Molecular cloning of cDNA encoding a "63"-kDa calmodulin-stimulated phosphodies
A/Reference number: A44162; MUID:92406781; PMID:1326531
A/Molecule type: mRNA
A/Residues: 1-534 <BEN>
A/Cross-references: UNIPROT:Q01061; GB:M94867; NID:g162782; PIDN:AAA74558.1; PID:g162783
A/Experimental source: brain
A/Note: sequence extracted from NCBI backbone (NCBI:113352)
R/Novack, J.P.; Charbonneau, H.; Bentley, J.K.; Walsh, K.A.; Beavo, J.A.
Biochemistry 30, 7940-7947, 1991
A/Title: Sequence comparison of the 63-, 61-, and 59-kDa calmodulin-dependent cyclic nuc
A/Reference number: A40283; MUID:91329366; PMID:165112
A/Accession: B40283
A/Molecule type: protein
A/Residues: 29-55, '1P', 48, 'R', 50-52, 'IS', 55-85, 196-215, 277, 'D', 279, 'T', 281-287, 'T', 289-2
A/Experimental source: brain
C/Comment: This enzyme is a useful target for inducing the death of leukemic cells, and
C/Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'-
C/Keywords: alternative splicing; calmodulin binding; cGMP binding; phosphoric diester h
F:220-437/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CND>

Query Match 40.2%; Score 45; DB 1; Length 534;
Best Local Similarity 53.3%; Pred. No. 2.4e+02;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 DNGTIVEELKQLE 17
:|||||:|
Db 46 ENGEVITEELKQLE 60

RESULT 49
A44161
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 1B, calmodulin-dependent, 63K sp

N/Alternate names: 63K calmodulin-stimulated phosphodiesterase, brain; CAM-PDE1B1
C/Species: Rattus norvegicus (Norway rat)
C/Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C/Accession: A44161
R/Repaske, D.R.; Swinnen, J.V.; Jin, S.L.; Van Wyk, J.J.; Conti, M.
J. Biol. Chem. 267, 18683-18688, 1992
A/Title: A polymerase chain reaction strategy to identify and clone cyclic nucleotide ph
A/Reference number: A44161; MUID:92406782; PMID:1326532
A/Accession: A44161
A/Molecule type: mRNA
A/Residues: 1-535 <REP>
A/Cross-references: UNIPROT:Q01066; GB:M94537; NID:g203268; PIDN:AAA16530.1; PID:g203269
A/Experimental source: brain
A/Note: sequence extracted from NCBI backbone (NCBI:113357)
C/Comment: This enzyme is a useful target for inducing the death of leukemic cells, and
C/Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'-
C/Keywords: alternative splicing; calmodulin binding; cGMP binding; phosphoric diester h
F:221-438/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CND>

Query Match 40.2%; Score 45; DB 1; Length 535;
Best Local Similarity 53.3%; Pred. No. 2.4e+02;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 DNGTIVEELKQLE 17
:|||||:|
Db 46 ENGEVITEELKQLE 60

RESULT 50
A46378
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 1B, calmodulin-dependent, 63K sp
N/Alternate names: 63K calmodulin-stimulated phosphodiesterase, brain; CAM-PDE1B1
C/Species: Mus musculus (house mouse)
C/Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C/Accession: A46378; B44161
R/Poll, J.W.; Kincaid, R.L.
Proc. Natl. Acad. Sci. U.S.A. 89, 11079-11083, 1992
A/Title: Molecular cloning of DNA encoding a calmodulin-dependent phosphodiesterase enric
A/Reference number: A46378; MUID:9306388; PMID:1332068
A/Accession: A46378
A/Molecule type: mRNA; protein
A/Residues: 1-535 <POL>
A/Cross-references: UNIPROT:Q01065; GB:L01695; NID:g200269; PIDN:AAA39902.1; PID:g200270
A/Experimental source: brain
A/Note: sequence extracted from NCBI backbone (NCBI:118901, NCBI:118903)
R/Repaske, D.R.; Swinnen, J.V.; Jin, S.L.; Van Wyk, J.J.; Conti, M.
J. Biol. Chem. 267, 18683-18688, 1992
A/Title: A polymerase chain reaction strategy to identify and clone cyclic nucleotide ph
A/Reference number: A44161; MUID:92406782; PMID:1326532
A/Accession: B44161
A/Molecule type: mRNA
A/Residues: 221-223, 'R', 225-336 <REP>
A/Cross-references: GB:M94538; NID:g192368; PIDN:AAA37367.1; PID:g192369
A/Note: sequence extracted from NCBI backbone (NCBI:113365)
C/Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'-
C/Keywords: alternative splicing; calmodulin binding; cGMP binding; phosphoric diester h
F:221-438/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 40.2%; Score 45; DB 1; Length 535;
Best Local Similarity 53.3%; Pred. No. 2.4e+02;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 DNGTIVEELKQLE 17
:|||||:|
Db 46 ENGEVITEELKQLE 60

Thu May 12 09:59:46 2005

us-10-712-812-5.rpr

Page 19

Search completed: May 11, 2005, 21:23:10
Job time : 48 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 11, 2005, 21:15:49 ; Search time 106.255 Seconds
(without alignments)
106.025 Million cell updates/sec

Title: US-10-712-812-5
Perfect score: 112
Sequence: 1 MADNGTIVEELKQLEQNNLV 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1613378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Uniprot_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 112 | 100.0 | 143 | 2 | Q6SR10 |
| 2 | 112 | 100.0 | 143 | 2 | Q6SR14 |
| 3 | 112 | 100.0 | 143 | 2 | Q6SR18 |
| 4 | 112 | 100.0 | 143 | 2 | Q6SRJ2 |
| 5 | 112 | 100.0 | 143 | 2 | Q6SRJ6 |
| 6 | 112 | 100.0 | 143 | 2 | Q6SRK4 |
| 7 | 112 | 100.0 | 143 | 2 | Q6SRK8 |
| 8 | 112 | 100.0 | 143 | 2 | Q6SRL2 |
| 9 | 112 | 100.0 | 143 | 2 | Q6SRL6 |
| 10 | 112 | 100.0 | 143 | 2 | Q6SRM0 |
| 11 | 112 | 100.0 | 143 | 2 | Q6SRM4 |
| 12 | 112 | 100.0 | 143 | 2 | Q6SRM8 |
| 13 | 112 | 100.0 | 143 | 2 | Q6SRN2 |
| 14 | 112 | 100.0 | 143 | 2 | Q6SRN6 |
| 15 | 112 | 100.0 | 143 | 2 | Q6SRP0 |
| 16 | 112 | 100.0 | 143 | 2 | Q6SRP4 |
| 17 | 112 | 100.0 | 143 | 2 | Q6SRP8 |
| 18 | 112 | 100.0 | 221 | 1 | Q6SRP8 |
| 19 | 112 | 100.0 | 221 | 1 | Q6SRP8 |
| 20 | 112 | 100.0 | 221 | 1 | Q6SRP8 |
| 21 | 112 | 100.0 | 221 | 1 | Q6SRP8 |
| 22 | 112 | 100.0 | 221 | 1 | Q6SRP8 |
| 23 | 112 | 100.0 | 221 | 1 | Q6SRP8 |
| 24 | 112 | 100.0 | 221 | 1 | Q6SRP8 |
| 25 | 112 | 100.0 | 221 | 1 | Q6SRP8 |
| 26 | 112 | 100.0 | 221 | 1 | Q6SRP8 |
| 27 | 112 | 100.0 | 221 | 1 | Q6SRP8 |
| 28 | 112 | 100.0 | 221 | 1 | Q6SRP8 |
| 29 | 112 | 100.0 | 221 | 1 | Q6SRP8 |
| 30 | 112 | 100.0 | 221 | 1 | Q6SRP8 |
| 31 | 112 | 100.0 | 221 | 1 | Q6SRP8 |

| | | | | | | | |
|-----|-----|-------|-----|---|--------|--------|-------------|
| 32 | 112 | 100.0 | 221 | 2 | Q6RD49 | Q6RD49 | sars corona |
| 33 | 112 | 100.0 | 221 | 2 | Q6RD60 | Q6RD60 | sars corona |
| 34 | 112 | 100.0 | 221 | 2 | Q6RD63 | Q6RD63 | sars corona |
| 35 | 112 | 100.0 | 221 | 2 | Q6RD68 | Q6RD68 | sars corona |
| 36 | 112 | 100.0 | 221 | 2 | Q6RD69 | Q6RD69 | sars corona |
| 37 | 112 | 100.0 | 221 | 2 | Q6RD73 | Q6RD73 | sars corona |
| 38 | 112 | 100.0 | 221 | 2 | Q6RD74 | Q6RD74 | sars corona |
| 39 | 112 | 100.0 | 221 | 2 | Q6RD75 | Q6RD75 | sars corona |
| 40 | 112 | 100.0 | 221 | 2 | Q6RD76 | Q6RD76 | sars corona |
| 41 | 112 | 100.0 | 221 | 2 | Q6RD77 | Q6RD77 | sars corona |
| 42 | 112 | 100.0 | 221 | 2 | Q6RD78 | Q6RD78 | sars corona |
| 43 | 112 | 100.0 | 221 | 2 | Q6RD79 | Q6RD79 | sars corona |
| 44 | 112 | 100.0 | 221 | 2 | Q6RD80 | Q6RD80 | sars corona |
| 45 | 112 | 100.0 | 221 | 2 | Q6RD81 | Q6RD81 | sars corona |
| 46 | 112 | 100.0 | 221 | 2 | Q6RD82 | Q6RD82 | sars corona |
| 47 | 112 | 100.0 | 221 | 2 | Q6RD83 | Q6RD83 | sars corona |
| 48 | 112 | 100.0 | 221 | 2 | Q6RD84 | Q6RD84 | sars corona |
| 49 | 112 | 100.0 | 221 | 2 | Q6RD85 | Q6RD85 | sars corona |
| 50 | 112 | 100.0 | 221 | 2 | Q6RD86 | Q6RD86 | sars corona |
| 51 | 112 | 100.0 | 221 | 2 | Q6RD87 | Q6RD87 | sars corona |
| 52 | 112 | 100.0 | 221 | 2 | Q6RD88 | Q6RD88 | sars corona |
| 53 | 112 | 100.0 | 221 | 2 | Q6RD89 | Q6RD89 | sars corona |
| 54 | 112 | 100.0 | 221 | 2 | Q6RD90 | Q6RD90 | sars corona |
| 55 | 112 | 100.0 | 221 | 2 | Q6RD91 | Q6RD91 | sars corona |
| 56 | 112 | 100.0 | 221 | 2 | Q6RD92 | Q6RD92 | sars corona |
| 57 | 112 | 100.0 | 221 | 2 | Q6RD93 | Q6RD93 | sars corona |
| 58 | 112 | 100.0 | 221 | 2 | Q6RD94 | Q6RD94 | sars corona |
| 59 | 112 | 100.0 | 221 | 2 | Q6RD95 | Q6RD95 | sars corona |
| 60 | 112 | 100.0 | 221 | 2 | Q6RD96 | Q6RD96 | sars corona |
| 61 | 112 | 100.0 | 221 | 2 | Q6RD97 | Q6RD97 | sars corona |
| 62 | 112 | 100.0 | 221 | 2 | Q6RD98 | Q6RD98 | sars corona |
| 63 | 112 | 100.0 | 221 | 2 | Q6RD99 | Q6RD99 | sars corona |
| 64 | 112 | 100.0 | 221 | 2 | Q6RD00 | Q6RD00 | sars corona |
| 65 | 112 | 100.0 | 221 | 2 | Q6RD01 | Q6RD01 | sars corona |
| 66 | 112 | 100.0 | 221 | 2 | Q6RD02 | Q6RD02 | sars corona |
| 67 | 112 | 100.0 | 221 | 2 | Q6RD03 | Q6RD03 | sars corona |
| 68 | 112 | 100.0 | 221 | 2 | Q6RD04 | Q6RD04 | sars corona |
| 69 | 112 | 100.0 | 221 | 2 | Q6RD05 | Q6RD05 | sars corona |
| 70 | 112 | 100.0 | 221 | 2 | Q6RD06 | Q6RD06 | sars corona |
| 71 | 112 | 100.0 | 221 | 2 | Q6RD07 | Q6RD07 | sars corona |
| 72 | 112 | 100.0 | 221 | 2 | Q6RD08 | Q6RD08 | sars corona |
| 73 | 112 | 100.0 | 221 | 2 | Q6RD09 | Q6RD09 | sars corona |
| 74 | 112 | 100.0 | 221 | 2 | Q6RD10 | Q6RD10 | sars corona |
| 75 | 112 | 100.0 | 221 | 2 | Q6RD11 | Q6RD11 | sars corona |
| 76 | 112 | 100.0 | 221 | 2 | Q6RD12 | Q6RD12 | sars corona |
| 77 | 112 | 100.0 | 221 | 2 | Q6RD13 | Q6RD13 | sars corona |
| 78 | 112 | 100.0 | 221 | 2 | Q6RD14 | Q6RD14 | sars corona |
| 79 | 112 | 100.0 | 221 | 2 | Q6RD15 | Q6RD15 | sars corona |
| 80 | 112 | 100.0 | 221 | 2 | Q6RD16 | Q6RD16 | sars corona |
| 81 | 112 | 100.0 | 221 | 2 | Q6RD17 | Q6RD17 | sars corona |
| 82 | 112 | 100.0 | 221 | 2 | Q6RD18 | Q6RD18 | sars corona |
| 83 | 112 | 100.0 | 221 | 2 | Q6RD19 | Q6RD19 | sars corona |
| 84 | 112 | 100.0 | 221 | 2 | Q6RD20 | Q6RD20 | sars corona |
| 85 | 112 | 100.0 | 221 | 2 | Q6RD21 | Q6RD21 | sars corona |
| 86 | 112 | 100.0 | 221 | 2 | Q6RD22 | Q6RD22 | sars corona |
| 87 | 112 | 100.0 | 221 | 2 | Q6RD23 | Q6RD23 | sars corona |
| 88 | 112 | 100.0 | 221 | 2 | Q6RD24 | Q6RD24 | sars corona |
| 89 | 112 | 100.0 | 221 | 2 | Q6RD25 | Q6RD25 | sars corona |
| 90 | 112 | 100.0 | 221 | 2 | Q6RD26 | Q6RD26 | sars corona |
| 91 | 112 | 100.0 | 221 | 2 | Q6RD27 | Q6RD27 | sars corona |
| 92 | 112 | 100.0 | 221 | 2 | Q6RD28 | Q6RD28 | sars corona |
| 93 | 112 | 100.0 | 221 | 2 | Q6RD29 | Q6RD29 | sars corona |
| 94 | 112 | 100.0 | 221 | 2 | Q6RD30 | Q6RD30 | sars corona |
| 95 | 112 | 100.0 | 221 | 2 | Q6RD31 | Q6RD31 | sars corona |
| 96 | 112 | 100.0 | 221 | 2 | Q6RD32 | Q6RD32 | sars corona |
| 97 | 112 | 100.0 | 221 | 2 | Q6RD33 | Q6RD33 | sars corona |
| 98 | 112 | 100.0 | 221 | 2 | Q6RD34 | Q6RD34 | sars corona |
| 99 | 112 | 100.0 | 221 | 2 | Q6RD35 | Q6RD35 | sars corona |
| 100 | 112 | 100.0 | 221 | 2 | Q6RD36 | Q6RD36 | sars corona |
| 101 | 112 | 100.0 | 221 | 2 | Q6RD37 | Q6RD37 | sars corona |
| 102 | 112 | 100.0 | 221 | 2 | Q6RD38 | Q6RD38 | sars corona |
| 103 | 112 | 100.0 | 221 | 2 | Q6RD39 | Q6RD39 | sars corona |
| 104 | 112 | 100.0 | 221 | 2 | Q6RD40 | Q6RD40 | sars corona |

| | | | | | | | | | | | | | | | |
|-----|------|------|-----|---|------------|-------------------------|-------|-----|----|------|------|---|-------------|--------|--------------|
| 105 | 48.5 | 43.3 | 872 | 2 | Q91U20 | G91uz0 human | immun | 178 | 47 | 42.0 | 159 | 1 | GNA1_YEAST | P43577 | saccharomyc |
| 106 | 48.5 | 43.3 | 872 | 2 | Q91U21 | G91uz1 human | immun | 179 | 47 | 42.0 | 184 | 2 | Q8KV60 | Q8kv60 | uncultured |
| 107 | 48.5 | 42.9 | 125 | 2 | O05614 | P05614 pseudomonas | | 180 | 47 | 42.0 | 184 | 2 | Q8KH75 | Q8kh75 | clostridium |
| 108 | 48 | 42.9 | 143 | 2 | O67T02 | O67t02 symbiobacte | | 181 | 47 | 42.0 | 199 | 2 | Q7WV58 | Q7wv58 | porphyromon |
| 109 | 48 | 42.9 | 206 | 1 | RALA_CALJA | P63320 calyithrix | | 182 | 47 | 42.0 | 312 | 2 | Q8ZK33 | Q8zk33 | salmonella |
| 110 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63321 mus musculus | | 183 | 47 | 42.0 | 335 | 2 | Q81P24 | Q81p24 | anabaena sp |
| 111 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 184 | 47 | 42.0 | 493 | 2 | Q8A2F4 | Q8a2f4 | bacteroides |
| 112 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 185 | 47 | 42.0 | 508 | 2 | Q6HU05 | Q6hu05 | bacillus an |
| 113 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 186 | 47 | 42.0 | 510 | 2 | Q636N5 | Q636n5 | bacillus ce |
| 114 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 187 | 47 | 42.0 | 510 | 2 | Q732T5 | Q732t5 | bacillus ce |
| 115 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 188 | 47 | 42.0 | 510 | 2 | Q81WPS | Q81wps | bacillus an |
| 116 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 189 | 47 | 42.0 | 510 | 2 | Q6HF24 | Q6hf24 | bacillus th |
| 117 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 190 | 47 | 42.0 | 547 | 1 | CH60_WOLRE | Q93gw2 | wolynella r |
| 118 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 191 | 47 | 42.0 | 577 | 2 | Q9SE62 | Q9se62 | solanum tub |
| 119 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 192 | 47 | 42.0 | 627 | 2 | Q9KEY2 | Q9kye2 | bacillus ha |
| 120 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 193 | 47 | 42.0 | 657 | 2 | Q8AF15 | Q8af15 | chimpanzee |
| 121 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 194 | 47 | 42.0 | 659 | 1 | SPA2_SYNY3 | P72587 | synchocyst |
| 122 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 195 | 47 | 42.0 | 759 | 1 | PURL_THREAC | Q91j34 | thermoplasma |
| 123 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 196 | 47 | 42.0 | 863 | 2 | Q76148 | Q76148 | anopheles s |
| 124 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 197 | 47 | 42.0 | 867 | 2 | Q70BJ3 | Q70bj3 | anopheles s |
| 125 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 198 | 47 | 42.0 | 961 | 1 | GCSF_STRAW | Q827d7 | streptomyce |
| 126 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 199 | 47 | 42.0 | 1027 | 2 | Q9WPF5 | Q9wpf5 | chimpanzee |
| 127 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 200 | 47 | 42.0 | 1067 | 2 | Q9S257 | Q9s257 | arabidopsis |
| 128 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 201 | 47 | 42.0 | 1256 | 2 | Q81DB7 | Q81db7 | bacillus ce |
| 129 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 202 | 47 | 42.0 | 2816 | 2 | Q8G983 | Q8g983 | oscellator |
| 130 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 203 | 47 | 42.0 | 4091 | 2 | Q7QA48 | Q7qa48 | anopheles s |
| 131 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 204 | 47 | 42.0 | 4091 | 2 | Q78877 | Q78877 | human |
| 132 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 205 | 47 | 42.0 | 104 | 2 | Q78881 | Q78881 | human |
| 133 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 206 | 47 | 42.0 | 159 | 2 | Q9JES7 | Q9jes7 | human |
| 134 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 207 | 47 | 42.0 | 161 | 2 | Q70R49 | Q70r49 | human |
| 135 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 208 | 47 | 42.0 | 162 | 2 | Q70QK1 | Q70qk1 | human |
| 136 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 209 | 47 | 42.0 | 169 | 2 | Q70QZ6 | Q70qz6 | human |
| 137 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 210 | 47 | 42.0 | 169 | 2 | Q70R29 | Q70r29 | human |
| 138 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 211 | 47 | 42.0 | 176 | 2 | Q70R40 | Q70r40 | human |
| 139 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 212 | 47 | 42.0 | 183 | 2 | Q9DVA1 | Q9dva1 | human |
| 140 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 213 | 47 | 42.0 | 184 | 2 | Q8Q1U2 | Q8q1u2 | human |
| 141 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 214 | 47 | 42.0 | 184 | 2 | Q8Q1U3 | Q8q1u3 | human |
| 142 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 215 | 47 | 42.0 | 184 | 2 | Q8Q1U4 | Q8q1u4 | human |
| 143 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 216 | 47 | 42.0 | 184 | 2 | Q8Q1U5 | Q8q1u5 | human |
| 144 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 217 | 47 | 42.0 | 184 | 2 | Q8Q1U6 | Q8q1u6 | human |
| 145 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 218 | 47 | 42.0 | 184 | 2 | Q8Q1U7 | Q8q1u7 | human |
| 146 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 219 | 47 | 42.0 | 184 | 2 | Q8Q1U8 | Q8q1u8 | human |
| 147 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 220 | 47 | 42.0 | 184 | 2 | Q8Q1U9 | Q8q1u9 | human |
| 148 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 221 | 47 | 42.0 | 184 | 2 | Q8Q1V0 | Q8q1v0 | human |
| 149 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 222 | 47 | 42.0 | 184 | 2 | Q8Q1V1 | Q8q1v1 | human |
| 150 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 223 | 47 | 42.0 | 190 | 2 | Q8Q1V2 | Q8q1v2 | human |
| 151 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 224 | 47 | 42.0 | 191 | 2 | Q70R37 | Q70r37 | human |
| 152 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 225 | 47 | 42.0 | 194 | 2 | Q91VVS | Q91vvs | human |
| 153 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 226 | 47 | 42.0 | 195 | 2 | Q9QNX2 | Q9qnx2 | human |
| 154 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 227 | 47 | 42.0 | 196 | 2 | Q70R78 | Q70r78 | human |
| 155 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 228 | 47 | 42.0 | 197 | 2 | Q6SUU1 | Q6suu1 | human |
| 156 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 229 | 47 | 42.0 | 197 | 2 | Q6SUU2 | Q6suu2 | human |
| 157 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 230 | 47 | 42.0 | 197 | 2 | Q6SUU3 | Q6suu3 | human |
| 158 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 231 | 47 | 42.0 | 197 | 2 | Q6SUU4 | Q6suu4 | human |
| 159 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 232 | 47 | 42.0 | 197 | 2 | Q6SUU5 | Q6suu5 | human |
| 160 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 233 | 47 | 42.0 | 197 | 2 | Q6SUU6 | Q6suu6 | human |
| 161 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 234 | 47 | 42.0 | 197 | 2 | Q6SUU7 | Q6suu7 | human |
| 162 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 235 | 47 | 42.0 | 197 | 2 | Q6SUU8 | Q6suu8 | human |
| 163 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 236 | 47 | 42.0 | 198 | 2 | Q7SKS3 | Q7sks3 | human |
| 164 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 237 | 47 | 42.0 | 199 | 2 | Q7SU41 | Q7su41 | human |
| 165 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 238 | 47 | 42.0 | 201 | 2 | Q7SU42 | Q7su42 | human |
| 166 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 239 | 47 | 42.0 | 201 | 2 | Q7SU43 | Q7su43 | human |
| 167 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 240 | 47 | 42.0 | 201 | 2 | Q7SU44 | Q7su44 | human |
| 168 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 241 | 47 | 42.0 | 201 | 2 | Q7SU45 | Q7su45 | human |
| 169 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 242 | 47 | 42.0 | 201 | 2 | Q7SU46 | Q7su46 | human |
| 170 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 243 | 47 | 42.0 | 202 | 2 | Q7SU47 | Q7su47 | human |
| 171 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 244 | 47 | 42.0 | 202 | 2 | Q7SU48 | Q7su48 | human |
| 172 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 245 | 47 | 42.0 | 202 | 2 | Q7SU49 | Q7su49 | human |
| 173 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 246 | 47 | 42.0 | 203 | 2 | Q7SU50 | Q7su50 | human |
| 174 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 247 | 47 | 42.0 | 203 | 2 | Q7SU51 | Q7su51 | human |
| 175 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 248 | 47 | 42.0 | 203 | 2 | Q7SU52 | Q7su52 | human |
| 176 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 249 | 47 | 42.0 | 205 | 2 | Q7SU53 | Q7su53 | human |
| 177 | 48 | 42.9 | 206 | 1 | RALA_MOUSE | P63322 rat mus musculus | | 250 | 47 | 42.0 | 206 | 2 | Q7SU54 | Q7su54 | human |

| | | | | | | | | | | | | | |
|-----|------|------|------|---|------------|---------------------|-----|------|------|------|---|-------------|---------------------|
| 251 | 46.5 | 41.5 | 206 | 2 | Q7SU37 | Q7bu37 human immun | 324 | 46 | 41.1 | 512 | 2 | Q6DBR9 | Q6db9 erwinia car |
| 252 | 46.5 | 41.5 | 206 | 2 | Q7SU58 | Q7bu58 human immun | 325 | 46 | 41.1 | 513 | 2 | Q6YIH2 | Q6yih2 oryza sativ |
| 253 | 46.5 | 41.5 | 206 | 2 | Q7SUH8 | Q7buH8 human immun | 326 | 46 | 41.1 | 516 | 2 | Q6GKP3 | Q6gkp3 homo sapien |
| 254 | 46.5 | 41.5 | 206 | 2 | Q7SUI2 | Q7bu12 human immun | 327 | 46 | 41.1 | 534 | 2 | Q6KCS3 | Q6kcs3 nicotiana p |
| 255 | 46.5 | 41.5 | 206 | 2 | Q7SUI3 | Q7bu13 human immun | 328 | 46 | 41.1 | 536 | 1 | CN1B_HUMAN | CN1b64 homo sapien |
| 256 | 46.5 | 41.5 | 207 | 2 | Q6SUS8 | Q6su8 human immun | 329 | 46 | 41.1 | 542 | 2 | Q7VC71 | Q7vc71 prochloroco |
| 257 | 46.5 | 41.5 | 209 | 2 | Q7SUI6 | Q7bu6 human immun | 330 | 46 | 41.1 | 545 | 1 | CH60_CAMJBE | Q6z289 campylobact |
| 258 | 46.5 | 41.5 | 214 | 2 | Q7SUI34 | Q7bu34 human immun | 331 | 46 | 41.1 | 558 | 1 | Q8BK21 | Q8bk21 synchococc |
| 259 | 46.5 | 41.5 | 215 | 2 | Q8JSD8 | Q8j948 human immun | 332 | 46 | 41.1 | 572 | 1 | DPY4_HUMAN | Q14511 homo sapien |
| 260 | 46.5 | 41.5 | 218 | 2 | Q7SUM0 | Q7sum0 human immun | 333 | 46 | 41.1 | 594 | 2 | Q9PCW8 | Q9pcw8 ureaplasma |
| 261 | 46.5 | 41.5 | 218 | 2 | Q7SUM1 | Q7sum1 human immun | 334 | 46 | 41.1 | 644 | 2 | Q9FM17 | Q9fm17 arabidopsis |
| 262 | 46.5 | 41.5 | 218 | 2 | Q9WLK7 | Q9wl7 human immun | 335 | 46 | 41.1 | 797 | 2 | Q8A6B8 | Q8a6b8 bacteroides |
| 263 | 46.5 | 41.5 | 220 | 2 | Q7SU44 | Q7bu44 human immun | 336 | 46 | 41.1 | 999 | 2 | Q6GIM3 | Q6gim3 bartonella |
| 264 | 46.5 | 41.5 | 220 | 2 | Q7ZMF5 | Q7zmf5 human immun | 337 | 46 | 41.1 | 1052 | 1 | MS1P_RAT | Q9wt3 rattus norv |
| 265 | 46.5 | 41.5 | 223 | 2 | Q7SUI39 | Q7bu39 human immun | 338 | 46 | 41.1 | 1284 | 2 | Q7WRJ5 | Q7wrj5 anabaena c1 |
| 266 | 46.5 | 41.5 | 265 | 2 | Q9WTT3 | Q9wt3 human immun | 339 | 46 | 41.1 | 2787 | 2 | Q9S1A9 | Q9s1a9 microcyctis |
| 267 | 46.5 | 41.5 | 276 | 2 | Q9WE10 | Q9we10 human immun | 340 | 46 | 41.1 | 2795 | 2 | Q8RTG5 | Q8rtg5 microcyctis |
| 268 | 46.5 | 41.5 | 277 | 2 | Q8DBM8 | Q8dbm8 vibrio vuln | 341 | 46 | 41.1 | 2795 | 2 | Q9RNB1 | Q9rnb1 microcyctis |
| 269 | 46.5 | 41.5 | 278 | 2 | Q76212 | Q76212 human immun | 342 | 46 | 41.1 | 4416 | 2 | Q9J3F3 | Q9j3f3 murine hepa |
| 270 | 46.5 | 41.5 | 288 | 2 | Q73316 | Q73316 human immun | 343 | 46 | 41.1 | 4416 | 2 | Q9J3F8 | Q9j3f8 murine hepa |
| 271 | 46.5 | 41.5 | 301 | 2 | Q70212 | Q70212 human immun | 344 | 46 | 41.1 | 7124 | 1 | RIAB_CVM2 | Q9py23 m repilicase |
| 272 | 46.5 | 41.5 | 328 | 2 | Q9IU84 | Q9iu84 human immun | 345 | 46 | 41.1 | 7389 | 1 | BPA1_MOUSE | Q91z6 mus musculu |
| 273 | 46.5 | 41.5 | 347 | 2 | Q7ZP53 | Q7zp53 human immun | 346 | 45.5 | 40.6 | 70 | 1 | SLYX_AGRIS | Q8uj19 agrobacteri |
| 274 | 46.5 | 41.5 | 359 | 2 | P87967 | P87967 human immun | 347 | 45.5 | 40.6 | 70 | 1 | SLYX_RHIME | Q92kt8 rhizobium m |
| 275 | 46.5 | 41.5 | 386 | 2 | Q8Q843 | Q8q843 human immun | 348 | 45.5 | 40.6 | 177 | 2 | Q8JF19 | Q8jfi9 human immun |
| 276 | 46.5 | 41.5 | 386 | 2 | Q8Q846 | Q8q846 human immun | 349 | 45.5 | 40.6 | 177 | 2 | Q8JF20 | Q8jfi20 human immun |
| 277 | 46.5 | 41.5 | 409 | 2 | Q41635 | Q41635 human immun | 350 | 45.5 | 40.6 | 179 | 2 | Q7ZPM0 | Q7zpm0 human immun |
| 278 | 46.5 | 41.5 | 426 | 2 | Q87ON7 | Q87on7 vibrio para | 351 | 45.5 | 40.6 | 183 | 2 | Q7ZNA1 | Q7zna1 human immun |
| 279 | 46.5 | 41.5 | 428 | 2 | Q6LPR1 | Q6lpr1 photobacter | 352 | 45.5 | 40.6 | 183 | 2 | Q9DV55 | Q9dv55 human immun |
| 280 | 46.5 | 41.5 | 429 | 2 | Q9KS25 | Q9ks25 vibrio chol | 353 | 45.5 | 40.6 | 187 | 2 | Q6UDP2 | Q6udp2 human immun |
| 281 | 46.5 | 41.5 | 429 | 2 | Q7MLV1 | Q7mlv1 vibrio vuln | 354 | 45.5 | 40.6 | 194 | 2 | Q6VGY9 | Q6vgy9 human immun |
| 282 | 46.5 | 41.5 | 462 | 2 | Q82V00 | Q82v00 nitrosozona | 355 | 45.5 | 40.6 | 195 | 2 | Q7ZND6 | Q7znd6 human immun |
| 283 | 46.5 | 41.5 | 801 | 2 | Q9WMU9 | Q9wmu9 human immun | 356 | 45.5 | 40.6 | 195 | 2 | Q7ZNG0 | Q7zng0 human immun |
| 284 | 46.5 | 41.5 | 847 | 2 | Q9WIS1 | Q9wis1 human immun | 357 | 45.5 | 40.6 | 196 | 2 | Q681D5 | Q681d5 human immun |
| 285 | 46.5 | 41.5 | 849 | 2 | Q9YKT4 | Q9ykt4 human immun | 358 | 45.5 | 40.6 | 196 | 2 | Q9JBI0 | Q9jbi0 human immun |
| 286 | 46.5 | 41.5 | 849 | 2 | Q9YKT7 | Q9ykt7 human immun | 359 | 45.5 | 40.6 | 196 | 2 | Q9JBI1 | Q9jbi1 human immun |
| 287 | 46.5 | 41.5 | 850 | 2 | Q9QBY2 | Q9qby2 human immun | 360 | 45.5 | 40.6 | 196 | 2 | Q9JBI2 | Q9jbi2 human immun |
| 288 | 46.5 | 41.5 | 858 | 2 | Q6UFG9 | Q6ufg9 human immun | 361 | 45.5 | 40.6 | 196 | 2 | Q9JBJ0 | Q9jbj0 human immun |
| 289 | 46.5 | 41.5 | 858 | 2 | Q73293 | Q73293 human immun | 362 | 45.5 | 40.6 | 196 | 2 | Q9JBJ5 | Q9jbj5 human immun |
| 290 | 46.5 | 41.5 | 1373 | 1 | RPC2_CHAGL | Q8ma10 chaetocphae | 363 | 45.5 | 40.6 | 196 | 2 | Q9JBK0 | Q9jbk0 human immun |
| 291 | 46 | 41.1 | 114 | 2 | Q8S3L3 | Q8s3l3 populus tre | 364 | 45.5 | 40.6 | 197 | 2 | Q6SUT5 | Q6sut5 human immun |
| 292 | 46 | 41.1 | 118 | 1 | Y352_SULSO | Q980t8 sulfolobus | 365 | 45.5 | 40.6 | 197 | 2 | Q6SUT4 | Q6sut4 human immun |
| 293 | 46 | 41.1 | 119 | 2 | Q6PRV2 | Q6prv2 coturnix co | 366 | 45.5 | 40.6 | 197 | 2 | Q6SUT6 | Q6sut6 human immun |
| 294 | 46 | 41.1 | 124 | 2 | Q6RJZ7 | Q6rjz7 capsicum an | 367 | 45.5 | 40.6 | 197 | 2 | Q6SUT5 | Q6sut5 human immun |
| 295 | 46 | 41.1 | 124 | 2 | Q6RJZ7 | Q6rjz7 capsicum an | 368 | 45.5 | 40.6 | 197 | 2 | Q6SUT5 | Q6sut5 human immun |
| 296 | 46 | 41.1 | 126 | 2 | P84137 | P84137 bacillus sc | 369 | 45.5 | 40.6 | 198 | 2 | Q9JBT1 | Q9jbt1 human immun |
| 297 | 46 | 41.1 | 149 | 2 | Q9VD13 | Q9vd13 drosophila | 370 | 45.5 | 40.6 | 199 | 2 | Q9JBC6 | Q9jbc6 human immun |
| 298 | 46 | 41.1 | 185 | 2 | Q938Z8 | Q938z8 campylobact | 371 | 45.5 | 40.6 | 199 | 2 | Q72NI1 | Q7zni1 human immun |
| 299 | 46 | 41.1 | 185 | 2 | Q938Z9 | Q938z9 campylobact | 372 | 45.5 | 40.6 | 199 | 2 | Q9JBD1 | Q9jbd1 human immun |
| 300 | 46 | 41.1 | 185 | 2 | Q939A0 | Q939a0 campylobact | 373 | 45.5 | 40.6 | 200 | 2 | Q72062 | Q72062 human immun |
| 301 | 46 | 41.1 | 216 | 2 | Q8CTQ3 | Q8ctq3 staphylococ | 374 | 45.5 | 40.6 | 201 | 2 | Q6J9C1 | Q6j9c1 human immun |
| 302 | 46 | 41.1 | 217 | 2 | Q7P7B3 | Q7p7b3 fusobacteri | 375 | 45.5 | 40.6 | 201 | 2 | Q9JBD8 | Q9jbd8 human immun |
| 303 | 46 | 41.1 | 229 | 2 | Q8ECT2 | Q8ect2 shewanella | 376 | 45.5 | 40.6 | 202 | 2 | Q9JBI8 | Q9jbi8 human immun |
| 304 | 46 | 41.1 | 300 | 2 | Q7WVC9 | Q7wvc9 acinetobact | 377 | 45.5 | 40.6 | 202 | 2 | Q9JBI9 | Q9jbi9 human immun |
| 305 | 46 | 41.1 | 300 | 2 | Q9F7D7 | Q9f7d7 acinetobact | 378 | 45.5 | 40.6 | 202 | 2 | Q9JBJ1 | Q9jbj1 human immun |
| 306 | 46 | 41.1 | 306 | 2 | Q8XLD5 | Q8xld5 clostridium | 379 | 45.5 | 40.6 | 202 | 2 | Q9JBJ2 | Q9jbj2 human immun |
| 307 | 46 | 41.1 | 312 | 2 | Q8ZLM0 | Q8zlm0 salmonella | 380 | 45.5 | 40.6 | 203 | 2 | Q6SUN1 | Q6sun1 human immun |
| 308 | 46 | 41.1 | 340 | 1 | YM21_ARCFU | Q82062 archaeoglob | 381 | 45.5 | 40.6 | 203 | 2 | Q70521 | Q70521 human immun |
| 309 | 46 | 41.1 | 401 | 2 | Q8VQ27 | Q8vq27 campylobact | 382 | 45.5 | 40.6 | 203 | 2 | Q70528 | Q70528 human immun |
| 310 | 46 | 41.1 | 401 | 2 | Q90HM7 | Q90hm7 human immun | 383 | 45.5 | 40.6 | 203 | 2 | Q9JBB6 | Q9jbb6 human immun |
| 311 | 46 | 41.1 | 410 | 2 | Q8VQ28 | Q8vq28 campylobact | 384 | 45.5 | 40.6 | 203 | 2 | Q9JBB8 | Q9jbb8 human immun |
| 312 | 46 | 41.1 | 420 | 2 | Q24306 | Q24306 arabidopsis | 385 | 45.5 | 40.6 | 203 | 2 | Q9JBB9 | Q9jbb9 human immun |
| 313 | 46 | 41.1 | 433 | 2 | Q944M2 | Q944m2 arabidopsis | 386 | 45.5 | 40.6 | 203 | 2 | Q9JBC5 | Q9jbc5 human immun |
| 314 | 46 | 41.1 | 457 | 2 | Q741W2 | Q741w2 lactobacill | 387 | 45.5 | 40.6 | 203 | 2 | Q9JBC9 | Q9jbc9 human immun |
| 315 | 46 | 41.1 | 458 | 2 | Q7ROF8 | Q7roef8 giardia lam | 388 | 45.5 | 40.6 | 203 | 2 | Q9JBD2 | Q9jbd2 human immun |
| 316 | 46 | 41.1 | 472 | 2 | Q9ROF0 | Q9rof0 mycoplasma | 389 | 45.5 | 40.6 | 203 | 2 | Q9JBF3 | Q9jbf3 human immun |
| 317 | 46 | 41.1 | 474 | 1 | GC5B_THBMA | Q9w57 thermocoga | 390 | 45.5 | 40.6 | 204 | 2 | Q6RHM5 | Q6rhm5 human immun |
| 318 | 46 | 41.1 | 504 | 1 | NORR_ECO57 | Q8x64 escherichia | 391 | 45.5 | 40.6 | 204 | 2 | Q9JBD7 | Q9jbd7 human immun |
| 319 | 46 | 41.1 | 504 | 1 | NORR_ECOL6 | Q8x66 escherichia | 392 | 45.5 | 40.6 | 204 | 2 | Q9JBP5 | Q9jbp5 human immun |
| 320 | 46 | 41.1 | 504 | 1 | NORR_ECOL7 | Q8x66 escherichia | 393 | 45.5 | 40.6 | 205 | 2 | Q6RHM3 | Q6rhm3 human immun |
| 321 | 46 | 41.1 | 504 | 1 | NORR_SHIFL | P59402 shigella fl | 394 | 45.5 | 40.6 | 205 | 2 | Q6RHM4 | Q6rhm4 human immun |
| 322 | 46 | 41.1 | 506 | 1 | NORR_SALTI | Q8z466 salmonella | 395 | 45.5 | 40.6 | 205 | 2 | Q8AL66 | Q8al66 human immun |
| 323 | 46 | 41.1 | 506 | 1 | NORR_SALTY | Q8zmj8 salmonella | 396 | 45.5 | 40.6 | 207 | 2 | Q6SUP2 | Q6sup2 human immun |

| | | | | | | | | | | | | | |
|-----|------|------|-----|---|-------------|----------------------|-----|------|------|------|---|------------|---------------------|
| 397 | 45.5 | 40.6 | 207 | 2 | Q6SUR4 | Q6sur4 human immun | 470 | 45 | 40.2 | 382 | 2 | Q69BD1 | Q69bd1 campylobact |
| 398 | 45.5 | 40.6 | 215 | 2 | Q9YXG5 | Q9yxg5 human immun | 471 | 45 | 40.2 | 382 | 2 | Q69B11 | Q69b11 campylobact |
| 399 | 45.5 | 40.6 | 216 | 2 | Q90R12 | Q90r12 human immun | 472 | 45 | 40.2 | 399 | 2 | Q8LG40 | Q8lg40 arabadiposis |
| 400 | 45.5 | 40.6 | 218 | 2 | Q7SUI9 | Q7sui9 human immun | 473 | 45 | 40.2 | 399 | 2 | Q67XY1 | Q67xy1 arabadiposis |
| 401 | 45.5 | 40.6 | 219 | 2 | Q7ZMC1 | Q7zmc1 human immun | 474 | 45 | 40.2 | 402 | 2 | Q90IM7 | Q90im7 human immun |
| 402 | 45.5 | 40.6 | 219 | 2 | Q9WLS0 | Q9wls0 human immun | 475 | 45 | 40.2 | 423 | 2 | Q6XS08 | Q6xs08 human immun |
| 403 | 45.5 | 40.6 | 221 | 2 | Q90QY4 | Q90qy4 human immun | 476 | 45 | 40.2 | 444 | 2 | Q73FT9 | Q73ft9 wolbachia p |
| 404 | 45.5 | 40.6 | 221 | 2 | Q7ZMB5 | Q7zmb5 human immun | 477 | 45 | 40.2 | 458 | 2 | Q6PDS5 | Q6pds5 mus musculu |
| 405 | 45.5 | 40.6 | 244 | 2 | Q6IXG6 | Q6ixg6 human immun | 478 | 45 | 40.2 | 460 | 2 | Q76HZ2 | Q76hz2 bartonella |
| 406 | 45.5 | 40.6 | 244 | 2 | Q6IXH1 | Q6ixh1 human immun | 479 | 45 | 40.2 | 468 | 2 | Q9JWX2 | Q9jwx2 neisseria m |
| 407 | 45.5 | 40.6 | 248 | 2 | Q9WTF6 | Q9wtf6 human immun | 480 | 45 | 40.2 | 481 | 2 | Q94KU1 | Q94ku1 spinacia ol |
| 408 | 45.5 | 40.6 | 258 | 2 | Q8ACR6 | Q8acr6 human immun | 481 | 45 | 40.2 | 495 | 2 | Q9DBS6 | Q9db6 mus musculu |
| 409 | 45.5 | 40.6 | 258 | 2 | Q9WDN2 | Q9wdn2 human immun | 482 | 45 | 40.2 | 514 | 2 | Q96469 | Q96469 ipomoea bat |
| 410 | 45.5 | 40.6 | 289 | 2 | Q83CA6 | Q83ca6 coxiella bu | 483 | 45 | 40.2 | 516 | 2 | Q81DB5 | Q81db5 bacillus ce |
| 411 | 45.5 | 40.6 | 293 | 2 | Q9J4P0 | Q9j4p0 human immun | 484 | 45 | 40.2 | 516 | 2 | Q9CKZ8 | Q9ckz8 pasteurella |
| 412 | 45.5 | 40.6 | 303 | 2 | Q9J4N0 | Q9j4n0 human immun | 485 | 45 | 40.2 | 528 | 2 | Q6F3J9 | Q6f3j9 oryza sativ |
| 413 | 45.5 | 40.6 | 343 | 2 | Q91U97 | Q91u97 human immun | 486 | 45 | 40.2 | 531 | 2 | Q989T4 | Q989t4 rhizobium l |
| 414 | 45.5 | 40.6 | 347 | 2 | Q6CKS6 | Q6cks6 kluyveromyc | 487 | 45 | 40.2 | 534 | 1 | CN1B_BOVIN | CN1b_bovin |
| 415 | 45.5 | 40.6 | 347 | 2 | Q91UB8 | Q91ub8 human immun | 488 | 45 | 40.2 | 535 | 1 | CN1B_MOUSE | CN1b_mouse |
| 416 | 45.5 | 40.6 | 359 | 2 | P87965 | P87965 human immun | 489 | 45 | 40.2 | 535 | 1 | CN1B_RAT | CN1b_rat |
| 417 | 45.5 | 40.6 | 392 | 2 | Q9APR4 | Q9apr4 uncultured | 490 | 45 | 40.2 | 536 | 2 | Q9BE16 | Q9be16 macaca faec |
| 418 | 45.5 | 40.6 | 397 | 2 | O11547 | O11547 human immun | 491 | 45 | 40.2 | 548 | 2 | Q9YJD1 | Q9yjd1 drosofila |
| 419 | 45.5 | 40.6 | 402 | 2 | Q66IA3 | Q66ia3 human immun | 492 | 45 | 40.2 | 582 | 2 | Q8BU59 | Q8bu59 mus musculu |
| 420 | 45.5 | 40.6 | 405 | 2 | Q66IA5 | Q66ia5 human immun | 493 | 45 | 40.2 | 595 | 2 | Q89BH2 | Q89bh2 braehyrizob |
| 421 | 45.5 | 40.6 | 410 | 2 | Q8QZF9 | Q8qzf9 human immun | 494 | 45 | 40.2 | 626 | 1 | PR1M_LISMO | PR1m_listeria in |
| 422 | 45.5 | 40.6 | 422 | 2 | Q8ZGX3 | Q8zgx3 yerislinia pe | 495 | 45 | 40.2 | 626 | 2 | Q71ZL5 | Q71z5 listeria mo |
| 423 | 45.5 | 40.6 | 425 | 1 | B10A_SERMA | B36568 serralia ma | 496 | 45 | 40.2 | 630 | 2 | Q97J38 | Q97j38 haemophilus |
| 424 | 45.5 | 40.6 | 426 | 2 | Q6D6F8 | Q6d6f8 yerislinia pe | 497 | 45 | 40.2 | 643 | 1 | SYT_HAEIN | SYT_haein |
| 425 | 45.5 | 40.6 | 426 | 2 | Q8D003 | Q8d003 human immun | 498 | 45 | 40.2 | 644 | 2 | Q80814 | Q80814 arabadiposis |
| 426 | 45.5 | 40.6 | 430 | 2 | Q6R3J2 | Q6r3j2 human immun | 499 | 45 | 40.2 | 644 | 2 | Q80814 | Q80814 arabadiposis |
| 427 | 45.5 | 40.6 | 438 | 2 | Q90C05 | Q90cus human immun | 500 | 45 | 40.2 | 649 | 2 | Q7RT54 | Q7rt54 plasmodium |
| 428 | 45.5 | 40.6 | 454 | 2 | Q7ZBH6 | Q7zbh6 simian-huma | 501 | 45 | 40.2 | 673 | 2 | Q8BVD6 | Q8bvd6 mus musculu |
| 429 | 45.5 | 40.6 | 455 | 2 | Q7ZB10 | Q7zb10 simian-huma | 502 | 45 | 40.2 | 674 | 2 | Q91Y31 | Q91y31 mus musculu |
| 430 | 45.5 | 40.6 | 456 | 2 | Q7ZB12 | Q7zb12 simian-huma | 503 | 45 | 40.2 | 755 | 2 | Q9M1Z2 | Q9m1z2 arabadiposis |
| 431 | 45.5 | 40.6 | 501 | 2 | Q6U9B2 | Q6ub2 bacterioph | 504 | 45 | 40.2 | 808 | 2 | Q8N270 | Q8n270 homo sapien |
| 432 | 45.5 | 40.6 | 582 | 1 | MSBA_VIBPA | Q8716 vibrio para | 505 | 45 | 40.2 | 877 | 1 | SYA_WOLPM | SYA_wolbachia p |
| 433 | 45.5 | 40.6 | 795 | 2 | Q99BX6 | Q99bx6 human immun | 506 | 45 | 40.2 | 895 | 2 | Q8CL17 | Q8cl17 mus musculu |
| 434 | 45.5 | 40.6 | 799 | 2 | Q7ZGR4 | Q7zgr4 human immun | 507 | 45 | 40.2 | 897 | 2 | Q8YMP3 | Q8ymp3 anabaena sp |
| 435 | 45.5 | 40.6 | 833 | 2 | Q9QKH9 | Q9qkh9 human immun | 508 | 45 | 40.2 | 902 | 2 | Q7PX97 | Q7px97 anopheles g |
| 436 | 45.5 | 40.6 | 833 | 2 | Q9OKI3 | Q9ok13 human immun | 509 | 45 | 40.2 | 974 | 2 | Q6PG27 | Q6pg27 homo sapien |
| 437 | 45.5 | 40.6 | 841 | 2 | Q8DYI7 | Q8dy17 human immun | 510 | 45 | 40.2 | 1052 | 1 | MS1P_CRIGR | MS1p_cricetulus |
| 438 | 45.5 | 40.6 | 849 | 2 | Q6H1S7 | Q6h1s7 human immun | 511 | 45 | 40.2 | 1052 | 1 | MS1P_HUMAN | MS1p_homo sapien |
| 439 | 45.5 | 40.6 | 854 | 2 | Q9WSE4 | Q9wse4 human immun | 512 | 45 | 40.2 | 1052 | 1 | MS1P_MOUSE | MS1p_mouse |
| 440 | 45.5 | 40.6 | 855 | 2 | Q8UL67 | Q8ul67 human immun | 513 | 45 | 40.2 | 1052 | 1 | Q6PG67 | Q6pg67 mus musculu |
| 441 | 45.5 | 40.6 | 858 | 2 | Q90ZS4 | Q90z84 human immun | 514 | 45 | 40.2 | 1055 | 2 | Q80U80 | Q80u80 mus musculu |
| 442 | 45.5 | 40.6 | 859 | 2 | Q6JNM4 | Q6jnm4 human immun | 515 | 45 | 40.2 | 1366 | 2 | Q8K7N9 | Q8k7n9 streptococc |
| 443 | 45.5 | 40.6 | 861 | 2 | Q6JNP2 | Q6jnp2 human immun | 516 | 45 | 40.2 | 1366 | 2 | Q8B2P2 | Q8b2f2 streptococc |
| 444 | 45.5 | 40.6 | 861 | 2 | Q80367 | Q80367 human immun | 517 | 45 | 40.2 | 1372 | 2 | Q878N3 | Q878n3 streptococc |
| 445 | 45.5 | 40.6 | 863 | 2 | Q6BC68 | Q6bc68 human immun | 518 | 45 | 40.2 | 1504 | 2 | Q6BD66 | Q6bd66 homo sapien |
| 446 | 45.5 | 40.6 | 867 | 2 | Q8UB10 | Q8jb10 human immun | 519 | 45 | 40.2 | 1723 | 2 | Q9Y4F4 | Q9y4f4 homo sapien |
| 447 | 45 | 40.2 | 66 | 2 | Q8BR91 | Q8br91 oceanobacil | 520 | 45 | 40.2 | 2443 | 2 | Q96CJ7 | Q96cj7 mus musculu |
| 448 | 45 | 40.2 | 82 | 2 | Q6MC16 | Q6mc16 parachlamyd | 521 | 45 | 40.2 | 2471 | 2 | Q6C0J8 | Q6c0j8 klyveromyc |
| 449 | 45 | 40.2 | 104 | 2 | Q980B8 | Q980b8 sulfolobus | 522 | 45 | 40.2 | 2811 | 2 | Q7Q9V2 | Q7q9v2 anopheles g |
| 450 | 45 | 40.2 | 118 | 2 | Q99MN5 | Q99mns rattus norv | 523 | 45 | 40.2 | 7756 | 2 | Q70LMS | Q70lms bacillus br |
| 451 | 45 | 40.2 | 128 | 2 | O26723 | O26723 methanobact | 524 | 44.5 | 39.7 | 84 | 2 | O40374 | O40374 human immun |
| 452 | 45 | 40.2 | 154 | 2 | Q8GXV2 | Q8gxv2 arabadiposis | 525 | 44.5 | 39.7 | 84 | 2 | O40376 | O40376 human immun |
| 453 | 45 | 40.2 | 184 | 2 | Q8KP48 | Q8kp48 peptostrept | 526 | 44.5 | 39.7 | 84 | 2 | O40380 | O40380 human immun |
| 454 | 45 | 40.2 | 204 | 1 | HAM1_CLOPE | HAM168 clostridium | 527 | 44.5 | 39.7 | 84 | 2 | O40382 | O40382 human immun |
| 455 | 45 | 40.2 | 226 | 1 | VME1_PEDV7 | P59771 porcine epi | 528 | 44.5 | 39.7 | 84 | 2 | O40384 | O40384 human immun |
| 456 | 45 | 40.2 | 226 | 1 | VME1_PEDV8 | P59770 porcine epi | 529 | 44.5 | 39.7 | 84 | 2 | O40386 | O40386 human immun |
| 457 | 45 | 40.2 | 226 | 2 | Q91AU9 | Q91au9 porcine epi | 530 | 44.5 | 39.7 | 84 | 2 | O40389 | O40389 human immun |
| 458 | 45 | 40.2 | 230 | 2 | Q692M0 | Q692m0 porcine epi | 531 | 44.5 | 39.7 | 84 | 2 | O40391 | O40391 human immun |
| 459 | 45 | 40.2 | 232 | 2 | Q98FUS | Q98fus rhicobium l | 532 | 44.5 | 39.7 | 84 | 2 | O40393 | O40393 human immun |
| 460 | 45 | 40.2 | 262 | 2 | Q8BMM1 | Q8bmm1 mus musculu | 533 | 44.5 | 39.7 | 84 | 2 | O40395 | O40395 human immun |
| 461 | 45 | 40.2 | 264 | 1 | YES4_SCHPO | O1471 echizosacch | 534 | 44.5 | 39.7 | 84 | 2 | O40401 | O40401 human immun |
| 462 | 45 | 40.2 | 274 | 2 | Q8RI36 | O8ri36 fusobacteri | 535 | 44.5 | 39.7 | 84 | 2 | O40402 | O40402 human immun |
| 463 | 45 | 40.2 | 296 | 2 | Q73JA0 | Q73ja0 treponema d | 536 | 44.5 | 39.7 | 84 | 2 | O40414 | O40414 human immun |
| 464 | 45 | 40.2 | 321 | 2 | Q8JB39 | Q8jb39 human immun | 537 | 44.5 | 39.7 | 84 | 2 | O40423 | O40423 human immun |
| 465 | 45 | 40.2 | 327 | 1 | Q87LIA9 | Q87lia9 vibrio para | 538 | 44.5 | 39.7 | 84 | 2 | O40424 | O40424 human immun |
| 466 | 45 | 40.2 | 335 | 1 | FLIG_THEMEA | Q9w63 thermocoga | 539 | 44.5 | 39.7 | 84 | 2 | O40425 | O40425 human immun |
| 467 | 45 | 40.2 | 338 | 2 | Q7WZ12 | Q7wz12 haemophilus | 540 | 44.5 | 39.7 | 84 | 2 | O40428 | O40428 human immun |
| 468 | 45 | 40.2 | 368 | 2 | Q754L5 | Q754l5 ashuya gose | 541 | 44.5 | 39.7 | 84 | 2 | O40430 | O40430 human immun |
| 469 | 45 | 40.2 | 377 | 2 | Q9FNC6 | Q9fnc6 arabadiposis | 542 | 44.5 | 39.7 | 84 | 2 | O40433 | O40433 human immun |

| | | | | | | | | | | | | | |
|-----|------|------|-----|---|--------|--------------------|-----|------|------|-----|---|--------|--------------------|
| 543 | 44.5 | 39.7 | 84 | 2 | 040435 | 040435 human immut | 616 | 44.5 | 39.7 | 202 | 2 | 09JBC1 | 09jbc1 human immut |
| 544 | 44.5 | 39.7 | 84 | 2 | 040441 | 040441 human immut | 617 | 44.5 | 39.7 | 202 | 2 | 09JBC7 | 09jbc7 human immut |
| 545 | 44.5 | 39.7 | 84 | 2 | 040442 | 040442 human immut | 618 | 44.5 | 39.7 | 202 | 2 | 09JBC8 | 09jbc8 human immut |
| 546 | 44.5 | 39.7 | 93 | 2 | 091293 | 091293 human immut | 619 | 44.5 | 39.7 | 203 | 2 | 06SY32 | 06sy32 human immut |
| 547 | 44.5 | 39.7 | 146 | 2 | 09UWV7 | 09UWV7 bullIolopus | 620 | 44.5 | 39.7 | 203 | 2 | 06SY33 | 06sy33 human immut |
| 548 | 44.5 | 39.7 | 156 | 2 | 091W58 | 091W58 human immut | 621 | 44.5 | 39.7 | 203 | 2 | 06SY34 | 06sy34 human immut |
| 549 | 44.5 | 39.7 | 157 | 2 | 070RS3 | 070RS3 human immut | 622 | 44.5 | 39.7 | 203 | 2 | 06SY35 | 06sy35 human immut |
| 550 | 44.5 | 39.7 | 158 | 2 | 09MWV3 | 09MWV3 human immut | 623 | 44.5 | 39.7 | 203 | 2 | 06SY36 | 06sy36 human immut |
| 551 | 44.5 | 39.7 | 159 | 2 | 09JER4 | 09JER4 human immut | 624 | 44.5 | 39.7 | 203 | 2 | 06SY37 | 06sy37 human immut |
| 552 | 44.5 | 39.7 | 159 | 2 | 09JER4 | 09JER4 human immut | 625 | 44.5 | 39.7 | 203 | 2 | 07ZNH4 | 07znh4 human immut |
| 553 | 44.5 | 39.7 | 168 | 2 | 06J4B0 | 06J4B0 human immut | 626 | 44.5 | 39.7 | 203 | 2 | 09JB95 | 09jb95 human immut |
| 554 | 44.5 | 39.7 | 168 | 2 | 070R09 | 070R09 human immut | 627 | 44.5 | 39.7 | 203 | 2 | 09JB96 | 09jb96 human immut |
| 555 | 44.5 | 39.7 | 169 | 2 | 091WT3 | 091WT3 human immut | 628 | 44.5 | 39.7 | 203 | 2 | 09JB97 | 09jb97 human immut |
| 556 | 44.5 | 39.7 | 171 | 2 | 070R20 | 070R20 human immut | 629 | 44.5 | 39.7 | 203 | 2 | 09JBC3 | 09jbc3 human immut |
| 557 | 44.5 | 39.7 | 177 | 2 | 0698V0 | 0698V0 human immut | 630 | 44.5 | 39.7 | 204 | 2 | 06V7Y0 | 06v7y0 human immut |
| 558 | 44.5 | 39.7 | 178 | 2 | 08UPR4 | 08UPR4 human immut | 631 | 44.5 | 39.7 | 204 | 2 | 06V7Y9 | 06v7y9 human immut |
| 559 | 44.5 | 39.7 | 178 | 2 | 08UPR6 | 08UPR6 human immut | 632 | 44.5 | 39.7 | 204 | 2 | 06V7Z0 | 06v7z0 human immut |
| 560 | 44.5 | 39.7 | 178 | 2 | 08UPR8 | 08UPR8 human immut | 633 | 44.5 | 39.7 | 204 | 2 | 06V7Z4 | 06v7z4 human immut |
| 561 | 44.5 | 39.7 | 178 | 2 | 08UPR1 | 08UPR1 human immut | 634 | 44.5 | 39.7 | 204 | 2 | 07ZNH0 | 07znh0 human immut |
| 562 | 44.5 | 39.7 | 179 | 2 | 090CM9 | 090CM9 human immut | 635 | 44.5 | 39.7 | 204 | 2 | 090Q01 | 09q001 human immut |
| 563 | 44.5 | 39.7 | 186 | 2 | 090RS9 | 090RS9 human immut | 636 | 44.5 | 39.7 | 204 | 2 | 09YKX0 | 09yxx0 human immut |
| 564 | 44.5 | 39.7 | 188 | 2 | 092963 | 092963 human immut | 637 | 44.5 | 39.7 | 204 | 2 | 09YKX8 | 09yxx8 human immut |
| 565 | 44.5 | 39.7 | 188 | 2 | 09DVH3 | 09DVH3 human immut | 638 | 44.5 | 39.7 | 206 | 2 | 071852 | 071852 human immut |
| 566 | 44.5 | 39.7 | 194 | 2 | 092254 | 092254 human immut | 639 | 44.5 | 39.7 | 206 | 2 | 08AL78 | 08al78 human immut |
| 567 | 44.5 | 39.7 | 194 | 2 | 070QM0 | 070QM0 human immut | 640 | 44.5 | 39.7 | 206 | 2 | 09JBE1 | 09jbe1 human immut |
| 568 | 44.5 | 39.7 | 195 | 2 | 0681E4 | 0681E4 human immut | 641 | 44.5 | 39.7 | 206 | 2 | 09YRM7 | 09yrm7 human immut |
| 569 | 44.5 | 39.7 | 195 | 2 | 0681E4 | 0681E4 human immut | 642 | 44.5 | 39.7 | 207 | 2 | 0681E3 | 0681e3 human immut |
| 570 | 44.5 | 39.7 | 196 | 2 | 07SKV3 | 07SKV3 human immut | 643 | 44.5 | 39.7 | 207 | 2 | 09JBA2 | 09jba2 human immut |
| 571 | 44.5 | 39.7 | 196 | 2 | 09JBI9 | 09JBI9 human immut | 644 | 44.5 | 39.7 | 207 | 2 | 09JBB0 | 09jbb0 human immut |
| 572 | 44.5 | 39.7 | 196 | 2 | 09JBI3 | 09JBI3 human immut | 645 | 44.5 | 39.7 | 207 | 2 | 09JBB3 | 09jbb3 human immut |
| 573 | 44.5 | 39.7 | 196 | 2 | 09JBI4 | 09JBI4 human immut | 646 | 44.5 | 39.7 | 209 | 2 | 09JBB9 | 09jbb9 human immut |
| 574 | 44.5 | 39.7 | 196 | 2 | 09JBI6 | 09JBI6 human immut | 647 | 44.5 | 39.7 | 210 | 2 | 076528 | 076528 human immut |
| 575 | 44.5 | 39.7 | 196 | 2 | 09JBE2 | 09JBE2 human immut | 648 | 44.5 | 39.7 | 211 | 2 | 070QJ4 | 070qj4 human immut |
| 576 | 44.5 | 39.7 | 196 | 2 | 09JBE5 | 09JBE5 human immut | 649 | 44.5 | 39.7 | 212 | 2 | 070QJ4 | 070qj4 human immut |
| 577 | 44.5 | 39.7 | 197 | 2 | 06SUT4 | 06SUT4 human immut | 650 | 44.5 | 39.7 | 213 | 2 | 075119 | 075119 human immut |
| 578 | 44.5 | 39.7 | 198 | 2 | 08QAA4 | 08QAA4 human immut | 651 | 44.5 | 39.7 | 214 | 2 | 090AP2 | 090a22 human immut |
| 579 | 44.5 | 39.7 | 198 | 2 | 06SY26 | 06SY26 human immut | 652 | 44.5 | 39.7 | 214 | 2 | 090AP3 | 090aF3 human immut |
| 580 | 44.5 | 39.7 | 198 | 2 | 06SY27 | 06SY27 human immut | 653 | 44.5 | 39.7 | 214 | 2 | 090AP4 | 090aF4 human immut |
| 581 | 44.5 | 39.7 | 198 | 2 | 06SY28 | 06SY28 human immut | 654 | 44.5 | 39.7 | 214 | 2 | 090AP5 | 090aF5 human immut |
| 582 | 44.5 | 39.7 | 198 | 2 | 06SY29 | 06SY29 human immut | 655 | 44.5 | 39.7 | 214 | 2 | 070CK9 | 070ck9 human immut |
| 583 | 44.5 | 39.7 | 198 | 2 | 07ZNH2 | 07ZNH2 human immut | 656 | 44.5 | 39.7 | 216 | 2 | 09YKX9 | 09yxx9 human immut |
| 584 | 44.5 | 39.7 | 198 | 2 | 09JBU1 | 09JBU1 human immut | 657 | 44.5 | 39.7 | 217 | 2 | 073094 | 073094 human immut |
| 585 | 44.5 | 39.7 | 198 | 2 | 09JBU2 | 09JBU2 human immut | 658 | 44.5 | 39.7 | 217 | 2 | 073095 | 073095 human immut |
| 586 | 44.5 | 39.7 | 198 | 2 | 09OP28 | 09OP28 human immut | 659 | 44.5 | 39.7 | 217 | 2 | 073097 | 073097 human immut |
| 587 | 44.5 | 39.7 | 199 | 2 | 08ALG7 | 08ALG7 human immut | 660 | 44.5 | 39.7 | 217 | 2 | 073106 | 073106 human immut |
| 588 | 44.5 | 39.7 | 200 | 2 | 06V7Y5 | 06V7Y5 human immut | 661 | 44.5 | 39.7 | 217 | 2 | 073108 | 073108 human immut |
| 589 | 44.5 | 39.7 | 200 | 2 | 06V7Z1 | 06V7Z1 human immut | 662 | 44.5 | 39.7 | 217 | 2 | 073109 | 073109 human immut |
| 590 | 44.5 | 39.7 | 200 | 2 | 06V7Z2 | 06V7Z2 human immut | 663 | 44.5 | 39.7 | 219 | 2 | 06DWCO | 06dwco human immut |
| 591 | 44.5 | 39.7 | 200 | 2 | 06V7Z3 | 06V7Z3 human immut | 664 | 44.5 | 39.7 | 219 | 2 | 0730S8 | 0730s8 human immut |
| 592 | 44.5 | 39.7 | 200 | 2 | 06V7Z5 | 06V7Z5 human immut | 665 | 44.5 | 39.7 | 219 | 2 | 073096 | 073096 human immut |
| 593 | 44.5 | 39.7 | 200 | 2 | 09JBA7 | 09JBA7 human immut | 666 | 44.5 | 39.7 | 219 | 2 | 073098 | 073098 human immut |
| 594 | 44.5 | 39.7 | 200 | 2 | 09JBB2 | 09JBB2 human immut | 667 | 44.5 | 39.7 | 219 | 2 | 073110 | 073110 human immut |
| 595 | 44.5 | 39.7 | 200 | 2 | 09QAD0 | 09QAD0 human immut | 668 | 44.5 | 39.7 | 219 | 2 | 073111 | 073111 human immut |
| 596 | 44.5 | 39.7 | 201 | 2 | 06V7Y3 | 06V7Y3 human immut | 669 | 44.5 | 39.7 | 219 | 2 | 073112 | 073112 human immut |
| 597 | 44.5 | 39.7 | 201 | 2 | 06V7Y6 | 06V7Y6 human immut | 670 | 44.5 | 39.7 | 219 | 2 | 073113 | 073113 human immut |
| 598 | 44.5 | 39.7 | 201 | 2 | 09JBB9 | 09JBB9 human immut | 671 | 44.5 | 39.7 | 219 | 2 | 073114 | 073114 human immut |
| 599 | 44.5 | 39.7 | 201 | 2 | 09JBA0 | 09JBA0 human immut | 672 | 44.5 | 39.7 | 219 | 2 | 073115 | 073115 human immut |
| 600 | 44.5 | 39.7 | 201 | 2 | 09JBA3 | 09JBA3 human immut | 673 | 44.5 | 39.7 | 219 | 2 | 073116 | 073116 human immut |
| 601 | 44.5 | 39.7 | 201 | 2 | 09JBA4 | 09JBA4 human immut | 674 | 44.5 | 39.7 | 219 | 2 | 073117 | 073117 human immut |
| 602 | 44.5 | 39.7 | 201 | 2 | 09JBA5 | 09JBA5 human immut | 675 | 44.5 | 39.7 | 220 | 2 | 089555 | 089555 human immut |
| 603 | 44.5 | 39.7 | 201 | 2 | 09JBA6 | 09JBA6 human immut | 676 | 44.5 | 39.7 | 220 | 2 | 073090 | 073090 human immut |
| 604 | 44.5 | 39.7 | 201 | 2 | 09JBA9 | 09JBA9 human immut | 677 | 44.5 | 39.7 | 220 | 2 | 073087 | 073087 human immut |
| 605 | 44.5 | 39.7 | 201 | 2 | 09JBB1 | 09JBB1 human immut | 678 | 44.5 | 39.7 | 225 | 2 | 06RUX1 | 06rux1 human immut |
| 606 | 44.5 | 39.7 | 201 | 2 | 09JBB4 | 09JBB4 human immut | 679 | 44.5 | 39.7 | 225 | 2 | 073083 | 073083 human immut |
| 607 | 44.5 | 39.7 | 201 | 2 | 09JBB5 | 09JBB5 human immut | 680 | 44.5 | 39.7 | 225 | 2 | 073084 | 073084 human immut |
| 608 | 44.5 | 39.7 | 201 | 2 | 09JBC0 | 09JBC0 human immut | 681 | 44.5 | 39.7 | 225 | 2 | 073085 | 073085 human immut |
| 609 | 44.5 | 39.7 | 201 | 2 | 09JBC2 | 09JBC2 human immut | 682 | 44.5 | 39.7 | 225 | 2 | 073086 | 073086 human immut |
| 610 | 44.5 | 39.7 | 202 | 2 | 06V7Y1 | 06V7Y1 human immut | 683 | 44.5 | 39.7 | 225 | 2 | 073087 | 073087 human immut |
| 611 | 44.5 | 39.7 | 202 | 2 | 06V7Y2 | 06V7Y2 human immut | 684 | 44.5 | 39.7 | 225 | 2 | 073088 | 073088 human immut |
| 612 | 44.5 | 39.7 | 202 | 2 | 06V7Y4 | 06V7Y4 human immut | 685 | 44.5 | 39.7 | 257 | 2 | 081XX3 | 081xx3 homo sapien |
| 613 | 44.5 | 39.7 | 202 | 2 | 06V7Y7 | 06V7Y7 human immut | 686 | 44.5 | 39.7 | 259 | 2 | 056080 | 056080 human immut |
| 614 | 44.5 | 39.7 | 202 | 2 | 06V7Y8 | 06V7Y8 human immut | 687 | 44.5 | 39.7 | 259 | 2 | 056085 | 056085 human immut |
| 615 | 44.5 | 39.7 | 202 | 2 | 09JBB8 | 09JBB8 human immut | 688 | 44.5 | 39.7 | 259 | 2 | 056089 | 056089 human immut |

| | | | | | | | | | | | | | | |
|-----|------|------|-----|--------|--------------|--------|------|------|------|-----|--------|--------|--------------|-------------|
| 689 | 44.5 | 39.7 | 259 | 092758 | human | immun | 752 | 44.5 | 39.7 | 455 | 2 | Q7ZB18 | Q7Zb18 | simian-huma |
| 690 | 44.5 | 39.7 | 259 | 092759 | human | immun | 753 | 44.5 | 39.7 | 455 | 2 | Q7ZBK0 | Q7ZbK0 | simian-huma |
| 691 | 44.5 | 39.7 | 259 | 092760 | human | immun | 764 | 44.5 | 39.7 | 455 | 2 | Q7ZBK1 | Q7ZbK1 | simian-huma |
| 692 | 44.5 | 39.7 | 259 | 09W1Y3 | human | immun | 765 | 44.5 | 39.7 | 455 | 2 | Q7ZBK6 | Q7ZbK6 | simian-huma |
| 693 | 44.5 | 39.7 | 259 | 09W1Y4 | human | immun | 766 | 44.5 | 39.7 | 455 | 2 | Q7ZBK7 | Q7ZbK7 | simian-huma |
| 694 | 44.5 | 39.7 | 259 | 09W1Y5 | human | immun | 767 | 44.5 | 39.7 | 455 | 2 | Q7ZBK9 | Q7ZbK9 | simian-huma |
| 695 | 44.5 | 39.7 | 265 | 09WE23 | human | immun | 768 | 44.5 | 39.7 | 455 | 2 | Q7ZBL0 | Q7ZbL0 | simian-huma |
| 696 | 44.5 | 39.7 | 265 | 09WE27 | human | immun | 769 | 44.5 | 39.7 | 455 | 2 | Q7ZBL1 | Q7ZbL1 | simian-huma |
| 697 | 44.5 | 39.7 | 295 | 09J4F8 | human | immun | 770 | 44.5 | 39.7 | 455 | 2 | Q7ZBL2 | Q7ZbL2 | simian-huma |
| 698 | 44.5 | 39.7 | 311 | 09TNU1 | haplomitricu | 771 | 44.5 | 39.7 | 455 | 2 | Q7ZBL5 | Q7ZbL5 | simian-huma | |
| 699 | 44.5 | 39.7 | 311 | 071332 | human | immun | 772 | 44.5 | 39.7 | 455 | 2 | Q7ZBL6 | Q7ZbL6 | simian-huma |
| 700 | 44.5 | 39.7 | 311 | 072513 | human | immun | 773 | 44.5 | 39.7 | 455 | 2 | Q7ZBL7 | Q7ZbL7 | simian-huma |
| 701 | 44.5 | 39.7 | 322 | 07ZOG3 | human | immun | 774 | 44.5 | 39.7 | 456 | 2 | Q7ZBL9 | Q7ZbL9 | simian-huma |
| 702 | 44.5 | 39.7 | 325 | 07ZQF7 | human | immun | 775 | 44.5 | 39.7 | 456 | 2 | Q7ZBL0 | Q7ZbL0 | simian-huma |
| 703 | 44.5 | 39.7 | 326 | 07ZRS6 | human | immun | 776 | 44.5 | 39.7 | 456 | 2 | Q7ZBL1 | Q7ZbL1 | simian-huma |
| 704 | 44.5 | 39.7 | 328 | 07ZRS5 | human | immun | 777 | 44.5 | 39.7 | 456 | 2 | Q7ZBL3 | Q7ZbL3 | simian-huma |
| 705 | 44.5 | 39.7 | 329 | 07ZRA0 | human | immun | 778 | 44.5 | 39.7 | 456 | 2 | Q7ZBL4 | Q7ZbL4 | simian-huma |
| 706 | 44.5 | 39.7 | 329 | 07ZRA1 | human | immun | 779 | 44.5 | 39.7 | 456 | 2 | Q7ZBL5 | Q7ZbL5 | simian-huma |
| 707 | 44.5 | 39.7 | 329 | 07ZRA2 | human | immun | 780 | 44.5 | 39.7 | 456 | 2 | Q7ZBL6 | Q7ZbL6 | simian-huma |
| 708 | 44.5 | 39.7 | 329 | 07ZRA3 | human | immun | 781 | 44.5 | 39.7 | 456 | 2 | Q7ZBL7 | Q7ZbL7 | simian-huma |
| 709 | 44.5 | 39.7 | 329 | 07ZRA4 | human | immun | 782 | 44.5 | 39.7 | 456 | 2 | Q7ZBL8 | Q7ZbL8 | simian-huma |
| 710 | 44.5 | 39.7 | 329 | 07ZRA5 | human | immun | 783 | 44.5 | 39.7 | 456 | 2 | Q7ZBL9 | Q7ZbL9 | simian-huma |
| 711 | 44.5 | 39.7 | 329 | 07ZRA6 | human | immun | 784 | 44.5 | 39.7 | 456 | 2 | Q7ZBK2 | Q7ZbK2 | simian-huma |
| 712 | 44.5 | 39.7 | 329 | 07ZRA7 | human | immun | 785 | 44.5 | 39.7 | 456 | 2 | Q7ZBK3 | Q7ZbK3 | simian-huma |
| 713 | 44.5 | 39.7 | 329 | 07ZRA8 | human | immun | 786 | 44.5 | 39.7 | 456 | 2 | Q7ZBK4 | Q7ZbK4 | simian-huma |
| 714 | 44.5 | 39.7 | 329 | 07ZRA9 | human | immun | 787 | 44.5 | 39.7 | 456 | 2 | Q7ZBL3 | Q7ZbL3 | simian-huma |
| 715 | 44.5 | 39.7 | 329 | 07ZRS0 | human | immun | 788 | 44.5 | 39.7 | 456 | 2 | Q7ZBL8 | Q7ZbL8 | simian-huma |
| 716 | 44.5 | 39.7 | 329 | 07ZRS2 | human | immun | 789 | 44.5 | 39.7 | 456 | 2 | Q7ZBL9 | Q7ZbL9 | simian-huma |
| 717 | 44.5 | 39.7 | 329 | 07ZRS3 | human | immun | 790 | 44.5 | 39.7 | 456 | 2 | Q7ZBL0 | Q7ZbL0 | simian-huma |
| 718 | 44.5 | 39.7 | 329 | 07ZRS4 | human | immun | 791 | 44.5 | 39.7 | 456 | 2 | Q7ZBL1 | Q7ZbL1 | simian-huma |
| 719 | 44.5 | 39.7 | 329 | 07ZRS6 | human | immun | 792 | 44.5 | 39.7 | 456 | 2 | Q7ZBL2 | Q7ZbL2 | simian-huma |
| 720 | 44.5 | 39.7 | 348 | 07ZRP5 | human | immun | 793 | 44.5 | 39.7 | 456 | 2 | Q7ZBL9 | Q7ZbL9 | simian-huma |
| 721 | 44.5 | 39.7 | 348 | 09IU99 | human | immun | 794 | 44.5 | 39.7 | 457 | 2 | Q7ZBN2 | Q7ZbN2 | simian-huma |
| 722 | 44.5 | 39.7 | 352 | 09W7W0 | human | immun | 795 | 44.5 | 39.7 | 457 | 2 | Q7ZBN3 | Q7ZbN3 | simian-huma |
| 723 | 44.5 | 39.7 | 359 | P87975 | human | immun | 796 | 44.5 | 39.7 | 457 | 2 | Q7ZBN4 | Q7ZbN4 | simian-huma |
| 724 | 44.5 | 39.7 | 360 | 08QAX4 | human | immun | 797 | 44.5 | 39.7 | 457 | 2 | Q7ZBN5 | Q7ZbN5 | simian-huma |
| 725 | 44.5 | 39.7 | 379 | 07ZBN5 | simian-huma | Q7ZbN5 | 798 | 44.5 | 39.7 | 457 | 2 | Q7ZBN6 | Q7ZbN6 | simian-huma |
| 726 | 44.5 | 39.7 | 380 | 07ZBN3 | simian-huma | Q7ZbN3 | 799 | 44.5 | 39.7 | 457 | 2 | Q7ZBN7 | Q7ZbN7 | simian-huma |
| 727 | 44.5 | 39.7 | 380 | 07ZBN4 | simian-huma | Q7ZbN4 | 800 | 44.5 | 39.7 | 457 | 2 | Q7ZBN8 | Q7ZbN8 | simian-huma |
| 728 | 44.5 | 39.7 | 380 | 07ZBN6 | simian-huma | Q7ZbN6 | 801 | 44.5 | 39.7 | 457 | 2 | Q7ZBN9 | Q7ZbN9 | simian-huma |
| 729 | 44.5 | 39.7 | 380 | 07ZBN8 | simian-huma | Q7ZbN8 | 802 | 44.5 | 39.7 | 457 | 2 | Q7ZBP0 | Q7ZbP0 | simian-huma |
| 730 | 44.5 | 39.7 | 380 | 07ZBN9 | simian-huma | Q7ZbN9 | 803 | 44.5 | 39.7 | 457 | 2 | Q7ZBP1 | Q7ZbP1 | simian-huma |
| 731 | 44.5 | 39.7 | 380 | 07ZBN0 | simian-huma | Q7ZbN0 | 804 | 44.5 | 39.7 | 457 | 2 | Q7ZBP2 | Q7ZbP2 | simian-huma |
| 732 | 44.5 | 39.7 | 380 | 07ZBN1 | simian-huma | Q7ZbN1 | 805 | 44.5 | 39.7 | 457 | 2 | Q7ZBP3 | Q7ZbP3 | simian-huma |
| 733 | 44.5 | 39.7 | 386 | 040372 | human | immun | 806 | 44.5 | 39.7 | 457 | 2 | Q7ZBP4 | Q7ZbP4 | simian-huma |
| 734 | 44.5 | 39.7 | 386 | 040426 | human | immun | 807 | 44.5 | 39.7 | 457 | 2 | Q7ZBP5 | Q7ZbP5 | simian-huma |
| 735 | 44.5 | 39.7 | 386 | 040437 | human | immun | 808 | 44.5 | 39.7 | 457 | 2 | Q7ZBP6 | Q7ZbP6 | simian-huma |
| 736 | 44.5 | 39.7 | 386 | 06A922 | human | immun | 809 | 44.5 | 39.7 | 457 | 2 | Q7ZBP7 | Q7ZbP7 | simian-huma |
| 737 | 44.5 | 39.7 | 388 | 066LE0 | human | immun | 810 | 44.5 | 39.7 | 457 | 2 | Q7ZBP8 | Q7ZbP8 | simian-huma |
| 738 | 44.5 | 39.7 | 405 | 06W2X1 | human | immun | 811 | 44.5 | 39.7 | 457 | 2 | Q7ZBP9 | Q7ZbP9 | simian-huma |
| 739 | 44.5 | 39.7 | 405 | 06W2X3 | human | immun | 812 | 44.5 | 39.7 | 457 | 2 | Q7ZBP0 | Q7ZbP0 | simian-huma |
| 740 | 44.5 | 39.7 | 416 | 072602 | human | immun | 813 | 44.5 | 39.7 | 457 | 2 | Q7ZBP1 | Q7ZbP1 | simian-huma |
| 741 | 44.5 | 39.7 | 416 | 08J513 | human | immun | 814 | 44.5 | 39.7 | 457 | 2 | Q7ZBP2 | Q7ZbP2 | simian-huma |
| 742 | 44.5 | 39.7 | 422 | 09RMP4 | xenorthobius | Q7ZbP4 | 815 | 44.5 | 39.7 | 457 | 2 | Q7ZBP3 | Q7ZbP3 | simian-huma |
| 743 | 44.5 | 39.7 | 423 | 07N6Q8 | photorhabdu | Q7ZbQ8 | 816 | 44.5 | 39.7 | 457 | 2 | Q7ZBP4 | Q7ZbP4 | simian-huma |
| 744 | 44.5 | 39.7 | 441 | 07ZBK8 | simian-huma | Q7ZbK8 | 817 | 44.5 | 39.7 | 457 | 2 | Q7ZBP5 | Q7ZbP5 | simian-huma |
| 745 | 44.5 | 39.7 | 449 | 07ZBH3 | simian-huma | Q7ZbH3 | 818 | 44.5 | 39.7 | 457 | 2 | Q7ZBP6 | Q7ZbP6 | simian-huma |
| 746 | 44.5 | 39.7 | 449 | 07ZBH8 | simian-huma | Q7ZbH8 | 819 | 44.5 | 39.7 | 457 | 2 | Q7ZBP7 | Q7ZbP7 | simian-huma |
| 747 | 44.5 | 39.7 | 451 | 07ZBK5 | simian-huma | Q7ZbK5 | 820 | 44.5 | 39.7 | 457 | 2 | Q7ZBP8 | Q7ZbP8 | simian-huma |
| 748 | 44.5 | 39.7 | 453 | 07ZBL4 | simian-huma | Q7ZbL4 | 821 | 44.5 | 39.7 | 457 | 2 | Q7ZBP0 | Q7ZbP0 | simian-huma |
| 749 | 44.5 | 39.7 | 454 | 07ZBH1 | simian-huma | Q7ZbH1 | 822 | 44.5 | 39.7 | 457 | 2 | Q7ZBP1 | Q7ZbP1 | simian-huma |
| 750 | 44.5 | 39.7 | 454 | 07ZBH2 | simian-huma | Q7ZbH2 | 823 | 44.5 | 39.7 | 457 | 2 | Q7ZBP2 | Q7ZbP2 | simian-huma |
| 751 | 44.5 | 39.7 | 454 | 07ZBH1 | simian-huma | Q7ZbH1 | 824 | 44.5 | 39.7 | 457 | 2 | Q7ZBP3 | Q7ZbP3 | simian-huma |
| 752 | 44.5 | 39.7 | 455 | 07ZBG9 | simian-huma | Q7ZbG9 | 825 | 44.5 | 39.7 | 464 | 2 | Q9Q6W5 | Q9Q6W5 | human |
| 753 | 44.5 | 39.7 | 455 | 07ZBH0 | simian-huma | Q7ZbH0 | 826 | 44.5 | 39.7 | 470 | 2 | Q7QB71 | Q7Qb71 | anopheles g |
| 754 | 44.5 | 39.7 | 455 | 07ZBH4 | simian-huma | Q7ZbH4 | 827 | 44.5 | 39.7 | 517 | 2 | Q7Z643 | human | |
| 755 | 44.5 | 39.7 | 455 | 07ZBH5 | simian-huma | Q7ZbH5 | 828 | 44.5 | 39.7 | 536 | 2 | 065644 | arabidopsi.s | |
| 756 | 44.5 | 39.7 | 455 | 07ZBH9 | simian-huma | Q7ZbH9 | 829 | 44.5 | 39.7 | 561 | 2 | 08OC17 | human | |
| 757 | 44.5 | 39.7 | 455 | 07ZBH9 | simian-huma | Q7ZbH9 | 830 | 44.5 | 39.7 | 565 | 2 | 08OC16 | human | |
| 758 | 44.5 | 39.7 | 455 | 07ZBI4 | simian-huma | Q7ZbI4 | 831 | 44.5 | 39.7 | 792 | 2 | 06FYB5 | candida gla | |
| 759 | 44.5 | 39.7 | 455 | 07ZBI5 | simian-huma | Q7ZbI5 | 832 | 44.5 | 39.7 | 833 | 2 | 09QK14 | human | |
| 760 | 44.5 | 39.7 | 455 | 07ZBI6 | simian-huma | Q7ZbI6 | 833 | 44.5 | 39.7 | 837 | 2 | 08JD06 | human | |
| | 44.5 | 39.7 | 455 | 07ZBI7 | simian-huma | Q7ZbI7 | 834 | 44.5 | 39.7 | 837 | 2 | 08JD06 | human | |

| | | | | | | | | | | | | | |
|-----|------|------|-----|---|-------------|----------------------|-----|----|------|------|---|------------|---------------------|
| 835 | 44.5 | 39.7 | 843 | 2 | Q7SPU1 | Q7SPU1 human immun | 908 | 44 | 39.3 | 533 | 2 | Q7XSQ5 | Q7XSQ5 oryza sativ |
| 836 | 44.5 | 39.7 | 846 | 2 | Q6H1M3 | Q6H1M3 human immun | 909 | 44 | 39.3 | 537 | 2 | Q94KU2 | Q94KU2 spinacia o |
| 837 | 44.5 | 39.7 | 847 | 1 | ENV_HV1.S1 | P195S0 human immun | 910 | 44 | 39.3 | 546 | 1 | CH60_WOLSU | Q7mea3 wolnellsa s |
| 838 | 44.5 | 39.7 | 847 | 2 | Q6RC04 | Q6RC04 human immun | 911 | 44 | 39.3 | 553 | 2 | Q6YUK1 | Q6YUK1 oryza sativ |
| 839 | 44.5 | 39.7 | 847 | 2 | Q6ARC21 | Q6ARC21 human immun | 912 | 44 | 39.3 | 553 | 2 | Q9X664 | Q9X664 bacillus ha |
| 840 | 44.5 | 39.7 | 852 | 2 | Q41883 | Q41883 human immun | 913 | 44 | 39.3 | 557 | 2 | Q9X6Y7 | Q9X6Y7 glycine max |
| 841 | 44.5 | 39.7 | 853 | 2 | Q6X6N4 | Q6X6N4 human immun | 914 | 44 | 39.3 | 559 | 2 | Q7N2L1 | Q7N2L1 photorhabdu |
| 842 | 44.5 | 39.7 | 854 | 2 | Q6JUNK1 | Q6JUNK1 human immun | 915 | 44 | 39.3 | 571 | 2 | Q66855 | Q66855 aquilex aeo |
| 843 | 44.5 | 39.7 | 855 | 2 | Q9DL76 | Q9DL76 human immun | 916 | 44 | 39.3 | 586 | 2 | Q95TL6 | Q95TL6 drosophila |
| 844 | 44.5 | 39.7 | 857 | 2 | P90249 | P90249 human immun | 917 | 44 | 39.3 | 586 | 2 | Q9V4M8 | Q9V4M8 drosophila |
| 845 | 44.5 | 39.7 | 857 | 2 | Q900J6 | Q900J6 human immun | 918 | 44 | 39.3 | 589 | 2 | Q9W4U9 | Q9W4U9 cucumis mel |
| 846 | 44.5 | 39.7 | 858 | 2 | Q8Q0Z4 | Q8Q0Z4 human immun | 919 | 44 | 39.3 | 603 | 2 | Q87EM5 | Q87EM5 xyilella fae |
| 847 | 44.5 | 39.7 | 858 | 2 | Q75114 | Q75114 human immun | 920 | 44 | 39.3 | 603 | 2 | Q9PEP4 | Q9PEP4 xyilella fae |
| 848 | 44.5 | 39.7 | 861 | 2 | Q90599 | Q90599 human immun | 921 | 44 | 39.3 | 739 | 1 | CH6B_DROME | Q9VPS5 drosophila |
| 849 | 44.5 | 39.7 | 861 | 2 | Q6BC66 | Q6BC66 human immun | 922 | 44 | 39.3 | 748 | 2 | Q88XEO | Q88XEO laccobacill |
| 850 | 44.5 | 39.7 | 861 | 2 | Q6RRP1 | Q6RRP1 human immun | 923 | 44 | 39.3 | 744 | 2 | Q91B12 | Q91B12 vibrio para |
| 851 | 44.5 | 39.7 | 868 | 2 | Q6UC35 | Q6UC35 human immun | 924 | 44 | 39.3 | 744 | 2 | Q87MK4 | Q87MK4 vibrio para |
| 852 | 44.5 | 39.7 | 875 | 2 | Q6UF78 | Q6UF78 human immun | 925 | 44 | 39.3 | 750 | 1 | YKS7_YEAST | P34331 saccharomyc |
| 853 | 44.5 | 39.7 | 897 | 2 | Q91ZG4 | Q91ZG4 cache valle | 926 | 44 | 39.3 | 919 | 2 | Q6HYE4 | Q6HYE4 pseudomonas |
| 854 | 44.5 | 39.7 | 897 | 2 | Q91ZG4 | Q91ZG4 cache valle | 927 | 44 | 39.3 | 1019 | 2 | Q66770 | Q66770 aquifex aeo |
| 855 | 44.5 | 39.7 | 100 | 2 | Q91XZ8 | Q91XZ8 plasmodium | 928 | 44 | 39.3 | 1023 | 2 | Q90094 | Q90094 chimpanzee |
| 856 | 44.5 | 39.3 | 100 | 2 | Q91XZ8 | Q91XZ8 arabidopsis | 929 | 44 | 39.3 | 1031 | 2 | Q90273 | Q90273 chimpanzee |
| 857 | 44.5 | 39.3 | 143 | 2 | Q961X6 | Q961X6 homo sapien | 930 | 44 | 39.3 | 1045 | 2 | Q6D7E2 | Q6D7E2 erwinia car |
| 858 | 44.5 | 39.3 | 148 | 2 | Q632M6 | Q632M6 bacillus ce | 931 | 44 | 39.3 | 1209 | 2 | Q6ZES0 | Q6ZES0 synchocyst |
| 859 | 44.5 | 39.3 | 148 | 2 | Q81KD0 | Q81KD0 bacillus an | 932 | 44 | 39.3 | 1210 | 2 | Q8EOJ8 | Q8EOJ8 oceanobacill |
| 860 | 44.5 | 39.3 | 148 | 2 | Q6HC66 | Q6HC66 bacillus th | 933 | 44 | 39.3 | 1223 | 2 | Q6RFU1 | Q6RFU1 candida gla |
| 861 | 44.5 | 39.3 | 149 | 2 | Q83HU3 | Q83HU3 tropheryma | 934 | 44 | 39.3 | 1307 | 2 | Q9C093 | Q9C093 homo sapien |
| 862 | 44.5 | 39.3 | 162 | 2 | Q83GD8 | Q83GD8 tropheryma | 935 | 44 | 39.3 | 1577 | 2 | Q55265 | Q55265 streptococ |
| 863 | 44.5 | 39.3 | 181 | 2 | Q9F119 | Q9F119 arabidopsis | 936 | 44 | 39.3 | 1505 | 2 | Q91823 | Q91823 xenopus lae |
| 864 | 44.5 | 39.3 | 184 | 2 | Q8RKU25 | Q8RKU25 uncultured | 937 | 44 | 39.3 | 2788 | 2 | Q7WRX9 | Q7WRX9 anaobena gi |
| 865 | 44.5 | 39.3 | 184 | 2 | Q68H71 | Q68H71 clostridium | 938 | 44 | 39.3 | 3424 | 2 | Q81BD4 | Q81BD4 bacillus ce |
| 866 | 44.5 | 39.3 | 184 | 2 | Q68H72 | Q68H72 clostridium | 939 | 44 | 39.3 | 4467 | 2 | Q9J3E9 | Q9J3E9 murine hepa |
| 867 | 44.5 | 39.3 | 186 | 2 | Q6G148 | Q6G148 staphylococ | 940 | 44 | 39.3 | 4470 | 2 | Q66MN5 | Q66MN5 murine hepa |
| 868 | 44.5 | 39.3 | 190 | 2 | Q67Q31 | Q67Q31 human immun | 941 | 44 | 39.3 | 5369 | 2 | Q9R9J0 | Q9R9J0 bacillus bu |
| 869 | 44.5 | 39.3 | 196 | 2 | Q84U15 | Q84U15 oryza sativ | 942 | 44 | 39.3 | 7176 | 1 | R1XB_CYMAS | P16342 m replicase |
| 870 | 44.5 | 39.3 | 200 | 1 | COAE_BACAN | Q6heg2 bacillus an | 943 | 44 | 39.3 | 7178 | 2 | Q7Q6N6 | Q7Q6N6 murine hepa |
| 871 | 44.5 | 39.3 | 200 | 2 | Q633L3 | Q633L3 bacillus ce | 944 | 44 | 39.3 | 7667 | 2 | Q7Q6N8 | Q7Q6N8 anopheles g |
| 872 | 44.5 | 39.3 | 200 | 2 | Q6HCU7 | Q6HCU7 bacillus th | 945 | 44 | 39.3 | 79 | 2 | Q7Q493 | Q7Q493 human immun |
| 873 | 44.5 | 39.3 | 223 | 2 | Q91NKA | Q91NKA avian infec | 946 | 44 | 39.3 | 79 | 2 | Q7Q494 | Q7Q494 human immun |
| 874 | 44.5 | 39.3 | 236 | 2 | Q999E5 | Q999E5 human immun | 947 | 44 | 39.3 | 84 | 2 | Q7Q496 | Q7Q496 human immun |
| 875 | 44.5 | 39.3 | 258 | 2 | Q97134 | Q97134 trypanosoma | 948 | 44 | 39.3 | 84 | 2 | Q7Q497 | Q7Q497 human immun |
| 876 | 44.5 | 39.3 | 268 | 2 | Q65U07 | Q65U07 manihemia | 949 | 44 | 39.3 | 84 | 2 | Q7Q499 | Q7Q499 human immun |
| 877 | 44.5 | 39.3 | 282 | 2 | Q8DRY3 | Q8DRY3 streptococ | 950 | 44 | 39.3 | 85 | 2 | Q7P612 | Q7P612 fusobacteri |
| 878 | 44.5 | 39.3 | 282 | 2 | Q8B4C0 | Q8B4C0 streptococ | 951 | 44 | 39.3 | 85 | 2 | Q8BRL5 | Q8BRL5 fusobacteri |
| 879 | 44.5 | 39.3 | 292 | 1 | NIFH_HERSE | P787873 herbaspirill | 952 | 44 | 39.3 | 100 | 2 | Q97767 | Q97767 human immun |
| 880 | 44.5 | 39.3 | 308 | 1 | KDCD_BACSU | P42235 bacillus bu | 953 | 44 | 39.3 | 146 | 2 | Q90BES | Q90BES human immun |
| 881 | 44.5 | 39.3 | 341 | 2 | Q7ZG60 | Q7ZG60 thermus the | 954 | 44 | 39.3 | 157 | 2 | Q91WS3 | Q91WS3 human immun |
| 882 | 44.5 | 39.3 | 350 | 2 | Q6BRAT7 | Q6BRAT7 debaryomyce | 955 | 44 | 39.3 | 158 | 2 | Q41878 | Q41878 human immun |
| 883 | 44.5 | 39.3 | 352 | 2 | Q6COK3 | Q6COK3 yarrowia li | 956 | 44 | 39.3 | 160 | 2 | Q91190 | Q91190 human immun |
| 884 | 44.5 | 39.3 | 357 | 2 | Q89Z29 | Q89Z29 bacteroides | 957 | 44 | 39.3 | 162 | 1 | G160_BACSU | P80872 bacillus bu |
| 885 | 44.5 | 39.3 | 358 | 2 | Q8DKN6 | Q8DKN6 synchococ | 958 | 44 | 39.3 | 162 | 2 | Q91WS9 | Q91WS9 human immun |
| 886 | 44.5 | 39.3 | 401 | 1 | APGM_THEMEA | Q9XZ95 thermotoga | 959 | 44 | 39.3 | 163 | 2 | Q10607 | Q10607 human immun |
| 887 | 44.5 | 39.3 | 410 | 2 | Q6CBL6 | Q6CBL6 yarrowia li | 960 | 44 | 39.3 | 163 | 2 | Q66N50 | Q66N50 human immun |
| 888 | 44.5 | 39.3 | 413 | 2 | Q93Y13 | Q93Y13 cucumis sat | 961 | 44 | 39.3 | 163 | 2 | Q66N51 | Q66N51 human immun |
| 889 | 44.5 | 39.3 | 428 | 2 | Q7XT74 | Q7XT74 oryza sativ | 962 | 44 | 39.3 | 163 | 2 | Q66N54 | Q66N54 human immun |
| 890 | 44.5 | 39.3 | 429 | 2 | Q8DX40 | Q8DX40 streptococ | 963 | 44 | 39.3 | 163 | 2 | Q66N56 | Q66N56 human immun |
| 891 | 44.5 | 39.3 | 447 | 1 | SRS4_SUTLSO | Q9767 sulfolobus | 964 | 44 | 39.3 | 163 | 2 | Q66N57 | Q66N57 human immun |
| 892 | 44.5 | 39.3 | 468 | 2 | Q8P596 | Q8P596 xanthomonas | 965 | 44 | 39.3 | 164 | 2 | Q10599 | Q10599 human immun |
| 893 | 44.5 | 39.3 | 473 | 1 | LCB1_HUMAN | Q15269 homo sapien | 966 | 44 | 39.3 | 166 | 2 | Q9E2U2 | Q9E2U2 human immun |
| 894 | 44.5 | 39.3 | 480 | 2 | Q7FRX8 | Q7FRX8 oryza sativ | 967 | 44 | 39.3 | 168 | 2 | Q9E2U4 | Q9E2U4 human immun |
| 895 | 44.5 | 39.3 | 480 | 2 | Q9L100 | Q9L100 oryza sativ | 968 | 44 | 39.3 | 173 | 2 | Q99F32 | Q99F32 human immun |
| 896 | 44.5 | 39.3 | 483 | 2 | Q6CMZ0 | Q6CMZ0 kluyveromyc | 969 | 44 | 39.3 | 173 | 2 | Q9E2V5 | Q9E2V5 human immun |
| 897 | 44.5 | 39.3 | 490 | 2 | Q75CT5 | Q75CT5 ashyia goss | 970 | 44 | 39.3 | 176 | 2 | Q8JEM3 | Q8JEM3 human immun |
| 898 | 44.5 | 39.3 | 495 | 1 | IAIC_AEARTH | Q89Y0 arabidopsis | 971 | 44 | 39.3 | 177 | 2 | Q8UEW0 | Q8UEW0 human immun |
| 899 | 44.5 | 39.3 | 499 | 2 | Q67C11 | Q67C11 human immun | 972 | 44 | 39.3 | 178 | 2 | Q99F26 | Q99F26 human immun |
| 900 | 44.5 | 39.3 | 504 | 1 | HUTH_STRAA | P64415 staphylococ | 973 | 44 | 39.3 | 178 | 2 | Q9QRM1 | Q9QRM1 human immun |
| 901 | 44.5 | 39.3 | 504 | 1 | HUTH_STRAA | P64416 staphylococ | 974 | 44 | 39.3 | 179 | 2 | Q8JEV9 | Q8JEV9 human immun |
| 902 | 44.5 | 39.3 | 504 | 1 | HUTH_STRAA | Q8HY3 staphylococ | 975 | 44 | 39.3 | 179 | 2 | Q9E1R2 | Q9E1R2 human immun |
| 903 | 44.5 | 39.3 | 504 | 2 | Q6GDB2 | Q6GDB2 staphylococ | 976 | 44 | 39.3 | 181 | 2 | Q8Q3K5 | Q8Q3K5 human immun |
| 904 | 44.5 | 39.3 | 513 | 2 | Q6NU17 | Q6NU17 homo sapien | 977 | 44 | 39.3 | 182 | 2 | Q8Q3K1 | Q8Q3K1 human immun |
| 905 | 44.5 | 39.3 | 514 | 2 | Q9AR15 | Q9AR15 cucumis sat | 978 | 44 | 39.3 | 183 | 2 | Q8UEU1 | Q8UEU1 human immun |
| 906 | 44.5 | 39.3 | 528 | 2 | Q8YVE7 | Q8YVE7 arabidopsis | 979 | 44 | 39.3 | 183 | 2 | Q90CRO | Q90CRO human immun |
| 907 | 44.5 | 39.3 | 528 | 2 | Q9FWP5 | Q9FWP5 arabidopsis | 980 | 44 | 39.3 | 184 | 2 | Q90CQ5 | Q90CQ5 human immun |

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981 43.5 38.8 185 2 Q7ZNM9 07zn19 human immun
982 43.5 38.8 186 2 Q90CP2 090CP2 human immun
983 43.5 38.8 186 2 Q90CR3 090CR3 human immun
984 43.5 38.8 187 2 Q99J34 099J34 human immun
985 43.5 38.8 188 2 Q9DYG3 09dYg3 human immun
986 43.5 38.8 190 2 Q8Q3K2 08q3k2 human immun
987 43.5 38.8 190 2 Q8Q3K6 08q3k6 human immun
988 43.5 38.8 191 2 Q8Q3K9 08q3k9 human immun
989 43.5 38.8 192 2 Q8Q3J9 08q3j9 human immun
990 43.5 38.8 192 2 Q8Q3K8 08q3k8 human immun
991 43.5 38.8 192 2 Q6IXS7 06ixs7 human immun
992 43.5 38.8 192 2 Q7SIR1 07sir1 human immun
993 43.5 38.8 192 2 Q9DV17 09dv17 human immun
994 43.5 38.8 194 2 Q9DV51 09dv51 human immun
995 43.5 38.8 195 2 Q8QA98 08qa98 human immun
996 43.5 38.8 195 2 Q8QAA3 08qa3 human immun
997 43.5 38.8 195 2 Q7O525 07o525 human immun
998 43.5 38.8 195 2 Q7ZP18 07zp18 human immun
999 43.5 38.8 195 2 Q9DVC2 09dvc2 human immun
1000 43.5 38.8 196 2 Q6S2J0 06s2j0 human immun

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ALIGNMENTS

RESULT 1

Q6SR10 PRELIMINARY; PRT; 143 AA.

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AC 06SR10; 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Membrane glycoprotein M (Fragment).
OS SARS coronavirus TW-PH2.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; SARS coronavirus TW.
OX NCBI_TaxId=264387;
RN [1]
RP SEQUENCE FROM N.A.
RA Lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,
RA Yang J.-Y., Chen H.-Y., Chen Y.-M.Arthur.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY451891; AAS44755.1; -
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
FT NON TER 143
SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AE971ED CRC64;

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Query Match 100.0%; Score 112; DB 2; Length 143;
 Best Local Similarity 100.0%; Pred. No. 2.5e-07;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLEQNNLV 22

DB 1 MADNGTITVEELKQLEQNNLV 22

RESULT 2

Q6SR14 PRELIMINARY; PRT; 143 AA.

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AC 06SR14; 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Membrane glycoprotein M (Fragment).
OS SARS coronavirus TW-PH1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; SARS coronavirus TW.
OX NCBI_TaxId=264387;
RN [1]
RP SEQUENCE FROM N.A.
RA Lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,

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RA Yang J.-Y., Chen H.-Y., Chen Y.-M.Arthur.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY451890; AAS44755.1; -
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
FT NON TER 143
SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AE971ED CRC64;

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Query Match 100.0%; Score 112; DB 2; Length 143;
 Best Local Similarity 100.0%; Pred. No. 2.5e-07;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLEQNNLV 22

DB 1 MADNGTITVEELKQLEQNNLV 22

RESULT 3

Q6SR18 PRELIMINARY; PRT; 143 AA.

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AC 06SR18; 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Membrane glycoprotein M (Fragment).
OS SARS coronavirus TW-YM4.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; SARS coronavirus TW.
OX NCBI_TaxId=264386;
RN [1]
RP SEQUENCE FROM N.A.
RA Lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,
RA Yang J.-Y., Chen H.-Y., Chen Y.-M.Arthur.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY451889; AAS44751.1; -
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
FT NON TER 143
SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AE971ED CRC64;

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Query Match 100.0%; Score 112; DB 2; Length 143;
 Best Local Similarity 100.0%; Pred. No. 2.5e-07;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLEQNNLV 22

DB 1 MADNGTITVEELKQLEQNNLV 22

RESULT 4

Q6SRJ2 PRELIMINARY; PRT; 143 AA.

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AC 06SRJ2; 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Membrane glycoprotein M (Fragment).
OS SARS coronavirus TW-YM3.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; SARS coronavirus TW.
OX NCBI_TaxId=264385;
RN [1]
RP SEQUENCE FROM N.A.
RA Lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,
RA Yang J.-Y., Chen H.-Y., Chen Y.-M.Arthur.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY451888; AAS44747.1; -
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
FT NON TER 143

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SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AE971ED CRC64;
Query Match 100.0%; Score 112; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 2.5e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLEQNNLV 22
DB 1 MADNGTITVEELKQLEQNNLV 22

RESULT 5
ID 06SRJ6 PRELIMINARY; PRT; 143 AA.
AC 06SRJ6;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DE Membrane glycoprotein M (Fragment).
OS SARS coronavirus TW-YM2.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; SARS coronavirus TW.
NCBI_TaxId=264384;
RN [1]
RP SEQUENCE FROM N.A.
RA Lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY451887; AAS44743.1; -
DR GO; GO:0019058; Piviral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
FT NON TER 143
SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AE971ED CRC64;

Query Match 100.0%; Score 112; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 2.5e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLEQNNLV 22
DB 1 MADNGTITVEELKQLEQNNLV 22

RESULT 6
ID 06SRK4 PRELIMINARY; PRT; 143 AA.
AC 06SRK4;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
DE Membrane glycoprotein M (Fragment).
OS SARS coronavirus TW-GD5.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; SARS coronavirus TW.
NCBI_TaxId=264382;
RN [1]
RP SEQUENCE FROM N.A.
RA Lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,
RA Yang J.-Y., Chen H.-Y., Chen Y.-M.Arthur.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY451885; AAS44735.1; -
DR GO; GO:0019058; Piviral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
FT NON TER 143
SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AE971ED CRC64;

Query Match 100.0%; Score 112; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 2.5e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLEQNNLV 22

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DB 1 MADNGTITVEELKQLEQNNLV 22

RESULT 7
ID 06SRK8 PRELIMINARY; PRT; 143 AA.
AC 06SRK8;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
DE Membrane glycoprotein M (Fragment).
OS SARS coronavirus TW-GD4.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; SARS coronavirus TW.
NCBI_TaxId=264381;
RN [1]
RP SEQUENCE FROM N.A.
RA Lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,
RA Yang J.-Y., Chen H.-Y., Chen Y.-M.Arthur.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY451884; AAS44731.1; -
DR GO; GO:0019058; Piviral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
FT NON TER 143
SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AE971ED CRC64;

Query Match 100.0%; Score 112; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 2.5e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLEQNNLV 22
DB 1 MADNGTITVEELKQLEQNNLV 22

RESULT 8
ID 06SRL2 PRELIMINARY; PRT; 143 AA.
AC 06SRL2;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
DE Membrane glycoprotein M (Fragment).
OS SARS coronavirus TW-GD3.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; SARS coronavirus TW.
NCBI_TaxId=264380;
RN [1]
RP SEQUENCE FROM N.A.
RA Lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,
RA Yang J.-Y., Chen H.-Y., Chen Y.-M.Arthur.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY451883; AAS44727.1; -
DR GO; GO:0019058; Piviral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
FT NON TER 143
SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AE971ED CRC64;

Query Match 100.0%; Score 112; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 2.5e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLEQNNLV 22
DB 1 MADNGTITVEELKQLEQNNLV 22

RESULT 9
ID 06SRL6 PRELIMINARY; PRT; 143 AA.

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AC Q6SR16;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Membrane glycoprotein M (Fragment).
OS SARS coronavirus TW-GD2.
OC Coronavirus; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; SARS coronavirus TW.
NCBI_TaxID=264379;
RN [1]
RP SEQUENCE FROM N.A.
RA lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,
RA Yang Y.-Y., Chen H.-Y., Chen Y.-M.Arthur.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY451882; AAS44723.1; -.
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
FT NON_TER 143 143
SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AE971ED CRC64;

Query Match 100.0%; Score 112; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 2.5e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLLEQWNLV 22
DB 1 MADNGTITVEELKQLLEQWNLV 22

RESULT 10
Q6SRMO
ID Q6SRMO; PRELIMINARY; PRT; 143 AA.
AC Q6SRMO;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Membrane glycoprotein M (Fragment).
OS SARS coronavirus TW-GD1.
OC Coronavirus; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; SARS coronavirus TW.
NCBI_TaxID=264378;
RN [1]
RP SEQUENCE FROM N.A.
RA lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,
RA Yang Y.-Y., Chen H.-Y., Chen Y.-M.Arthur.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY451881; AAS44719.1; -.
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
FT NON_TER 143 143
SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AE971ED CRC64;

Query Match 100.0%; Score 112; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 2.5e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLLEQWNLV 22
DB 1 MADNGTITVEELKQLLEQWNLV 22

RESULT 11
Q6SRM4
ID Q6SRM4; PRELIMINARY; PRT; 143 AA.
AC Q6SRM4;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Membrane glycoprotein M (Fragment).
OS SARS coronavirus TW-KC3.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
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OC Coronaviridae; Coronavirus; SARS coronavirus TW.
NCBI_TaxID=264377;
RN [1]
RP SEQUENCE FROM N.A.
RA lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,
RA Yang Y.-Y., Chen H.-Y., Chen Y.-M.Arthur.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY451880; AAS44715.1; -.
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
FT NON_TER 143 143
SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AE971ED CRC64;

Query Match 100.0%; Score 112; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 2.5e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLLEQWNLV 22
DB 1 MADNGTITVEELKQLLEQWNLV 22

RESULT 12
Q6SRM8
ID Q6SRM8; PRELIMINARY; PRT; 143 AA.
AC Q6SRM8;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Membrane glycoprotein M (Fragment).
OS SARS coronavirus TW-KC1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; SARS coronavirus TW.
NCBI_TaxID=264376;
RN [1]
RP SEQUENCE FROM N.A.
RA lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,
RA Yang Y.-Y., Chen H.-Y., Chen Y.-M.Arthur.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY451879; AAS44711.1; -.
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
FT NON_TER 143 143
SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AE971ED CRC64;

Query Match 100.0%; Score 112; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 2.5e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLLEQWNLV 22
DB 1 MADNGTITVEELKQLLEQWNLV 22

RESULT 13
Q6SRN2
ID Q6SRN2; PRELIMINARY; PRT; 143 AA.
AC Q6SRN2;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Membrane glycoprotein M (Fragment).
OS SARS coronavirus TW-JC2.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; SARS coronavirus TW.
NCBI_TaxID=264375;
RN [1]
RP SEQUENCE FROM N.A.
RA lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,
RA Yang Y.-Y., Chen H.-Y., Chen Y.-M.Arthur.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
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DR EMBL; AY451878; AAS44707.1; -;
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
DR NON TER 143 143

SEQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AE971ED CRC64;

Query Match 100.0%; Score 112; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 2.5e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MADNGTITVEELKQLEQNNLV 22
Db 1 MADNGTITVEELKQLEQNNLV 22

RESULT 14

Q6SRN6 PRELIMINARY; PRT; 143 AA.

AC Q6SRN6
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Membrane glycoprotein M (Fragment).
OS SARS coronavirus TW-HP4.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; SARS coronavirus TW.
OX NCBI_TaxId=264374;
RN [1]
RP SEQUENCE FROM N.A.
RA Lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,
RA Yang J.-Y., Chen H.-Y., Chen Y.-M, Arthur.;

RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY451877; AAS44703.1; -;
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
DR NON TER 143 143

SEQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AE971ED CRC64;

Query Match 100.0%; Score 112; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 2.5e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MADNGTITVEELKQLEQNNLV 22
Db 1 MADNGTITVEELKQLEQNNLV 22

RESULT 15

Q6SRP0 PRELIMINARY; PRT; 143 AA.

AC Q6SRP0
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Membrane glycoprotein M (Fragment).
OS SARS coronavirus TW-HP3.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; SARS coronavirus TW.
OX NCBI_TaxId=264373;
RN [1]
RP SEQUENCE FROM N.A.
RA Lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,
RA Yang J.-Y., Chen H.-Y., Chen Y.-M, Arthur.;

RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY451876; AAS44699.1; -;
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
DR NON TER 143 143

SEQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AE971ED CRC64;

Query Match 100.0%; Score 112; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 2.5e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MADNGTITVEELKQLEQNNLV 22
Db 1 MADNGTITVEELKQLEQNNLV 22

RESULT 16

Q6SRP4 PRELIMINARY; PRT; 143 AA.

AC Q6SRP4
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Membrane glycoprotein M (Fragment).
OS SARS coronavirus TW-HP2.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; SARS coronavirus TW.
OX NCBI_TaxId=264372;
RN [1]
RP SEQUENCE FROM N.A.
RA Lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,
RA Yang J.-Y., Chen H.-Y., Chen Y.-M, Arthur.;

RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY451875; AAS44695.1; -;
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
DR NON TER 143 143

SEQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AE971ED CRC64;

Query Match 100.0%; Score 112; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 2.5e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MADNGTITVEELKQLEQNNLV 22
Db 1 MADNGTITVEELKQLEQNNLV 22

RESULT 17

Q6SRP8 PRELIMINARY; PRT; 143 AA.

AC Q6SRP8
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Membrane glycoprotein M (Fragment).
OS SARS coronavirus TW-HP1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; SARS coronavirus TW.
OX NCBI_TaxId=264371;
RN [1]
RP SEQUENCE FROM N.A.
RA Lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,
RA Yang J.-Y., Chen H.-Y., Chen Y.-M, Arthur.;

RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY451874; AAS44691.1; -;
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
DR NON TER 143 143

SEQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AE971ED CRC64;

Query Match 100.0%; Score 112; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 2.5e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MADNGTITVEELKQLEQNNLV 22
Db 1 MADNGTITVEELKQLEQNNLV 22

RESULT 18
VME1_CVHSA STANDARD; PRT: 221 AA.
ID VME1_CVHSA STANDARD; PRT: 221 AA.
AC P59596; O68865; Q71608; Q716R1; Q716R3; Q716S0; Q716S3; Q71726;
AD Q717B6; Q717S6; Q71A12;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE E1 glycoprotein (Matrix glycoprotein) (Membrane glycoprotein).
GN Name=M;
OS Human coronavirus (strain SARS) (HCoV-SARS) (SARS-CoV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=227859;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate Urbani;
RX MEDLINE=22660724; PubMed=12730500; DOI=10.1126/science.1085952;
RA Rota P.A., Oberste M.S., Monroe S.S., Nix W.A., Campagnoli R.,
Icenogle J.P., Penaranda S., Bankamp B., Maher K., Chen M.-H.,
Tong S., Tamin A., Lowe L., Frace M., Derisi J.L., Chen Q., Wang D.,
Erkman D.D., Peret T.C.T., Burns C., Ksiazek T.G., Rollin P.E.,
Sanchez A., Liffick S., Holloway B., Iamori J., McCausland K.,
Olson-Rasmussen M., Fouchier R., Guenther S., Osterhaus A.D.M.E.,
Drosten C., Pallansch M.A., Anderson L.J., Bellini W.J.;
RT "Characterization of a novel coronavirus associated with severe acute
respiratory syndrome."; Science 300:1394-1399(2003).
RL Science 300:1394-1399(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate Tor2;
RX MEDLINE=22660725; PubMed=12730501; DOI=10.1126/science.1085953;
RA Maria M.A., Jones S.J.M., Aetell C.R., Holt R.A., Brooks-Wilson A.,
Butterfield Y.S.N., Khattar J., Asano J.K., Barber S.A., Chan S.Y.,
Cloutier A., Coughlin S.M., Freeman D., Gilm N., Griffith O.L.,
Leach S.R., Mayo M., McDonald H., Montgomery S.B., Pandolf P.K.,
Petrescu A.S., Robertson A.G., Schein J.E., Siddiqui A., Smalins D.E.,
Stott J.M., Yang G.S., Plummer F., Andonov A., Atsagh H., Bastien N.,
Bernard K., Booth T.F., Bowness D., Czab M., Drebot M., Fernandez L.,
Flick R., Garbutt M., Gray M., Grolla A., Jones S., Feldmann H.,
Meyers A., Kabani A., Li Y., Normand S., Sticher U., Tipples G.A.,
Tyler S., Vogt R., Ward D., Watson B., Brunham R.C., Kraiden M.,
Petric M., Skowronski D.M., Upton C., Roper R.L.;
RT "The genome sequence of the SARS-associated coronavirus."; Science 300:1399-1404(2003).
RL Science 300:1399-1404(2003).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate CUHK-Su10, and Isolate CUHK-W1;
RX MEDLINE=22737955; PubMed=12853594; DOI=10.1056/NEJM200307103490216;
RA Tsui S.K.W., Chim S.S.C., Lo Y.M.D.;
RT "Coronavirus genomic-sequence variations and the epidemiology of the
severe acute respiratory syndrome."; N. Engl. J. Med. 349:187-188(2003).
RL N. Engl. J. Med. 349:187-188(2003).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate GZ50, and Isolate HKU-36871;
RX MEDLINE=22913660; PubMed=12958366; DOI=10.1126/science.1087139;
RA Guan Y., Zheng B.D., He Y.Q., Liu X.L., Zhuang Z.X., Cheung C.L.,
Luo S.W., Li P.H., Zhang L.D., Guan Y.J., But K.M., Wong K.L.,
Chan K.W., Lim W., Shortridge K.F., Yuen K.Y., Peiris J.S.M.,
Poon L.L.M.;
RT "Isolation and characterization of viruses related to the SARS
coronavirus from animals in southern China."; Science 302:276-278(2003).
RL Science 302:276-278(2003).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate HKU-39849;
RX MEDLINE=22758472; PubMed=12876307;
RA Zeng F.Y., Chan C.W., Chan M.N., Chen J.D., Chow K.Y.C., Hon C.C.C.,
Hui R.K.H., Li J., Li V.Y.Y., Wang C.Y., Wang P.Y., Guan Y., Zheng B.,
Poon L.L.M., Chan K.H., Yuen K.Y., Peiris J.S.M., Leung F.C.;

RT "The complete genome sequence of severe acute respiratory syndrome
coronavirus strain HKU-39849 (HK-39)";
RT exp. Biol. Med. 228:866-873(2003).
RL exp. Biol. Med. 228:866-873(2003).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate Sin2500, Isolate Sin2677, Isolate Sin2679,
Isolate Sin2748, and Isolate Sin2774;
RX MEDLINE=22667074; PubMed=12781537; DOI=10.1016/S0140-6736(03)13414-9;
RA Ruan Y., Wei C.L., Ling A.E., Vega V.B., Thoreau H., Se Thoe S.Y.,
Chia J.-M., Ng P., Chiu K.P., Lim L., Zhang T., Chan K.P., Oon L.E.L.,
Ng M.L., Leo S.Y., Ng L.F.P., Ren E.C., Stanton L.W., Long P.M.,
Lau E.T.;
RT "Comparative full-length genome sequence analysis of 14 SARS
coronavirus isolates and common mutations associated with putative
origins of infection."; Lancet 361:1779-1785(2003).
RL Lancet 361:1779-1785(2003).
RN [7]
RP ERRATUM
RX PubMed=12781581;
RA Ruan Y., Wei C.L., Ling A.E., Vega V.B., Thoreau H., Se Thoe S.Y.,
Chia J.-M., Ng P., Chiu K.P., Lim L., Zhang T., Chan K.P., Oon L.E.L.,
Ng M.L., Leo S.Y., Ng L.F.P., Ren E.C., Stanton L.W., Long P.M.,
Lau E.T.;
RN [8]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate BJ01, Isolate BJ02, Isolate BJ03, Isolate BJ04, and
Isolate GD01;
RX Qin E., Zhu Q., Yu M., Fan B., Chang G., Si B., Yang B., Peng W.,
Jiang T., Liu B., Deng X., Liu H., Zhang Y., Wang C., Li X., Gan Y.,
Li X., Lu F., Tan G., Yang R., Cao W.S., Wang J., Chen W., Cong L.,
Deng Y., Dong W., Han Y., Hu W., Lei M., Li C., Li G., Li H.,
Li S., Li S., Li W., Li W., Lin W., Liu J., Liu Z., Lu H., Ni P.,
Qi Q., Sun Y., Tang L., Tong Z., Wang J., Wang X., Wu Q., Xi Y.,
Xu Z., Yang L., Ye C., Ye J., Zhang B., Zhang F., Zhang J., Zhang X.,
Zhou J., Yang H.;
RT Submitted (Apr-2003) to the EMBL/GenBank/DBJ databases.
RL Submitted (Apr-2003) to the EMBL/GenBank/DBJ databases.
RN [9]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate TW1;
RX Yeh S.-H., Kao C.-L., Tsai C.-Y., Liu C.-J., Chen D.-S., Chen P.-J.;
RT "The complete genome of SARS coronavirus clone TW1";
RL Submitted (May-2003) to the EMBL/GenBank/DBJ databases.
RN [10]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate FRA;
RX Rickmann M., Becker S., Klenk H.-D., Doerr H.W., Stadler K.,
Gensini S., Guidotti S., Maignani V., Scarselli M., Mora M.,
Donati C., Han J., Song H.C., Abriani S., Covacci A., Rappuoli R.;
RT "SARS virus is a close relative of type II coronaviruses";
RL Submitted (May-2003) to the EMBL/GenBank/DBJ databases.
RN [11]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate Frankfurt 1;
RX Thiel V., Herzig T., Putics A., Ivanov K.A., Schelle B., Bayer S.,
Scheiner B., Weiland H., Weisdrich B., Ziebur J.;
RL Submitted (May-2003) to the EMBL/GenBank/DBJ databases.
RN [12]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate Shanghai OXC1;
RX Yuan Z., Zhang X., Hu Y., Ian S., Wang H., Zhou Z., Wen Y.,
Yuan Z., Zhang X., Hu Y., Ian S., Wang H., Zhou Z., Wen Y.;
RT "Analysis of SARS coronavirus genome in Shanghai isolates";
RL Submitted (Jan-2004) to the EMBL/GenBank/DBJ databases.
RN [13]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate ZJ01;
RX Cong L.-M., Ding G.-Q., Lu Y.-Y., Yan J.-Q., Wang J.-Q., Cheng S.-Y.,
Zhang Y.-J., Mei L.-L., Wang Z.-G., Hu N., Wo J., Yao J., Zhu H.-P.,
Lu Q.-Y., Li M.-H., Gong L.-M., Shi W.;
RL Submitted (Jun-2003) to the EMBL/GenBank/DBJ databases.
RN [14]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate TWC;

RA Yang J.-Y., Lin J.-H., Chiu S.-C., Wang S.-F., Lee S.-C., Lin Y.-C.,
 RA Hsu C.-K., Chen H.-Y., Chang J.-G., Chen P.-J., Su I.-J.;
 RT "Genomic sequence of SARS isolate from the first fatal case in
 RT Taiwan.",
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RN (15)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Isolate Taiwan TC1, Isolate Taiwan TC2, and Isolate Taiwan TC3;
 RA Chang J.-G.C., Lin T.-H., Chen C.-M., Lin C.-S., Chan W.-L.,
 RA Shih M.-C.,
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 RN (16)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Isolate TW1, Isolate TWJ, Isolate TWK, Isolate TWS, and
 RC Isolate TWY;
 RA Shu H.-Y., Wu K.-M., Tsai S.-F.,
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 RN (17)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Isolate HSR 1;
 RA Canducci F., Clementi M., Poli G., Vicenzi E.,
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 RN (18)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Isolate TW2, and Isolate TW3;
 RA Yang J.-Y., Lin J.-H., Chiu S.-C., Wang S.-F., Lee H.-C., Lin Y.-C.,
 RA Yao C.-W., Chien T.-S., Lu J.-J., Chen A., Hsu C.-K., Chen H.-Y.,
 RA Chen P.-J., Su I.-J.,
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 RN (19)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Isolate AS;
 RA Balotta C., Corvace S., Violin M., Gallit M., Moroni M.,
 RA Vigeant G.M., Ruan Y.J., Salemi M.,
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Component of the viral envelope that plays a central
 CC role in virus morphogenesis and assembly via its interactions with
 CC other viral proteins (By similarity).
 CC SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- SIMILARITY: Belongs to the coronavirus M protein family.
 CC -----
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AY278741; AAP13444.1; -;
 DR EMBL: AY274119; AAP13444.1; -;
 DR EMBL: AY278554; AAP13571.1; -;
 DR EMBL: AY282752; -; NOT_ANNOTATED_CDS.
 DR EMBL: AY304492; -; NOT_ANNOTATED_CDS.
 DR EMBL: AY304495; -; NOT_ANNOTATED_CDS.
 DR EMBL: AY278491; -; NOT_ANNOTATED_CDS.
 DR EMBL: AY283794; -; NOT_ANNOTATED_CDS.
 DR EMBL: AY283795; -; NOT_ANNOTATED_CDS.
 DR EMBL: AY283795; -; NOT_ANNOTATED_CDS.
 Query Match 100.0%; Score 112; DB 1; Length 221;
 Best Local Similarity 100.0%; Pred. No. 3.9e-07;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DT 25-OCT-2004 (TReMBLrel. 28, last sequence update)
 DT 25-OCT-2004 (TReMBLrel. 28, last annotation update)
 DE M protein.
 OS SARS coronavirus GD322.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
 OC Coronaviridae; Coronavirus.
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Hu Z., Zhao W., Yan H.,
 RT "The analyses of M genes' variation rules of SARS-CoV and their
 RT influence upon the possible B cell epitopes of M genes."
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY702026; AAU07933.1; -;
 DR InterPro: IPR002574; Corona_M.
 DR Pfam: PF01635; Corona_M; 1.
 DR Pfam: PF01635; Corona_M; 1.
 SQ SEQUENCE 221 AA; 25060 MW; 275C37085A0215A8 CRC64;
 Query Match 100.0%; Score 112; DB 2; Length 221;
 Best Local Similarity 100.0%; Pred. No. 3.9e-07;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DT 25-OCT-2004 (TReMBLrel. 28, last sequence update)
 DT 25-OCT-2004 (TReMBLrel. 27, last annotation update)
 DE M protein.
 OS SARS coronavirus GD322.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
 OC Coronaviridae; Coronavirus.
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Hu Z., Zhao W., Yan H.,
 RT "The analyses of M genes' variation rules of SARS-CoV and their
 RT influence upon the possible B cell epitopes of M genes."
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY702026; AAU07933.1; -;
 DR InterPro: IPR002574; Corona_M.
 DR Pfam: PF01635; Corona_M; 1.
 DR Pfam: PF01635; Corona_M; 1.
 SQ SEQUENCE 221 AA; 25060 MW; 275C37085A0215A8 CRC64;
 Query Match 100.0%; Score 112; DB 2; Length 221;
 Best Local Similarity 100.0%; Pred. No. 3.9e-07;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DT 25-OCT-2004 (TReMBLrel. 28, last sequence update)
 DT 25-OCT-2004 (TReMBLrel. 27, last annotation update)
 DE M protein.
 OS SARS coronavirus GD322.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
 OC Coronaviridae; Coronavirus.
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Hu Z., Zhao W., Yan H.,
 RT "The analyses of M genes' variation rules of SARS-CoV and their
 RT influence upon the possible B cell epitopes of M genes."
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY702026; AAU07933.1; -;
 DR InterPro: IPR002574; Corona_M.
 DR Pfam: PF01635; Corona_M; 1.
 DR Pfam: PF01635; Corona_M; 1.
 SQ SEQUENCE 221 AA; 25060 MW; 275C37085A0215A8 CRC64;
 Query Match 100.0%; Score 112; DB 2; Length 221;
 Best Local Similarity 100.0%; Pred. No. 3.9e-07;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sin03-11;
RA Jin W.W., Feng J.D., Du Z.L., Hu L.X., Liu Y.X., Liu Y.F., Zhang X.M.,
RA Gao H., Ning Y., Zhang J.S., Li N., Yin W.D.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY485278; AAR23256.1; -
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
SQ SEQUENCE 221 AA; 25016 MW; 6658652E2927478E CRC64;

Query Match 100.0%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLLEQNNLV 22
DB 1 MADNGTITVEELKQLLEQNNLV 22

RESULT 22
QY 06R7Y2 PRELIMINARY; PRT; 221 AA.
AC 06R7Y2;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Membrane protein M.
OS SARS coronavirus NS-1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxId=260743;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NS-1;
RA Guo H., Chen J., Wei W., Li J., Zhang Y., Wang X., Sun Y., Jiao J.,
RA Wang Y., Zhou C.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.

Query Match 100.0%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLLEQNNLV 22
DB 1 MADNGTITVEELKQLLEQNNLV 22

RESULT 23
QY 06R7Y2 PRELIMINARY; PRT; 221 AA.
AC 06R7Y2;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Membrane protein M.
OS SARS coronavirus NS-1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxId=260743;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NS-1;
RA Guo H., Chen J., Wei W., Li J., Zhang Y., Wang X., Sun Y., Jiao J.,
RA Wang Y., Zhou C.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
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DR EMBL; AY508724; AAR91590.1; -
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
SQ SEQUENCE 221 AA; 25069 MW; 275C37085A0215A8 CRC64;

Query Match 100.0%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLLEQNNLV 22
DB 1 MADNGTITVEELKQLLEQNNLV 22

RESULT 24
QY 06RCW1 PRELIMINARY; PRT; 221 AA.
AC 06RCW1;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Putative envelope protein M.
OS SARS coronavirus TW9.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxId=258972;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14983045; DOI=10.1073/pnas.0307904100;
RG National Taiwan University SARS Research Team;
RA Yeh S.-H., Wang H.-Y., Tsai C.-Y., Kao C.-L., Yang J.-Y., Liu H.-W.,
RA Su I.-J., Tsai S.-F., Chen D.-S., Chen P.-J.;
RT "Characterization of severe acute respiratory syndrome coronavirus
RT genomes in Taiwan: molecular epidemiology and genome evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:2542-2547(2004).
DR EMBL; AY502932; AAR87604.1; -
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
KW Envelope protein.
SQ SEQUENCE 221 AA; 25016 MW; 6658652E2927478E CRC64;

Query Match 100.0%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLLEQNNLV 22
DB 1 MADNGTITVEELKQLLEQNNLV 22

RESULT 25
QY 06RCX2 PRELIMINARY; PRT; 221 AA.
AC 06RCX2;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Putative envelope protein M.
OS SARS coronavirus TW8.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxId=258971;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14963045; DOI=10.1073/pnas.0307904100;
RG National Taiwan University SARS Research Team;
RA Yeh S.-H., Wang H.-Y., Tsai C.-Y., Kao C.-L., Yang J.-Y., Liu H.-W.,
RA Su I.-J., Tsai S.-F., Chen D.-S., Chen P.-J.;
RT "Characterization of severe acute respiratory syndrome coronavirus
RT genomes in Taiwan: molecular epidemiology and genome evolution.";
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RL Proc. Natl. Acad. Sci. U.S.A. 101:2542-2547(2004).
DR EMBL; AY502931; AAR87593.1; -.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
KW Envelope protein.
SQ SEQUENCE 221 AA; 25016 MW; 6658652E2927478E CRC64;

Query Match 100.0%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLLEQNNLV 22
DB 1 MADNGTITVEELKQLLEQNNLV 22

RESULT 26
Q6RCY3 PRELIMINARY; PRT; 221 AA.
AC Q6RCY3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Putative envelope protein M.
OS SARS coronavirus TW7.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OC NCBI_TaxID=258970;
[1]
RP SEQUENCE FROM N.A.
RX PubMed=14983045; DOI=10.1073/pnas.0307904100;
RG National Taiwan University SARS Research Team;
RA Yeh S.-H., Wang H.-Y., Tsai C.-Y., Kao C.-L., Yang J.-Y., Liu H.-W.,
Su I.-J., Tsai S.-F., Chen D.-S., Chen P.-J.;
"Characterization of severe acute respiratory syndrome coronavirus
RT genomes in Taiwan: molecular epidemiology and genome evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:2542-2547(2004).
DR EMBL; AY502930; AAR87582.1; -.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
KW Envelope protein.
SQ SEQUENCE 221 AA; 25016 MW; 6658652E2927478E CRC64;

Query Match 100.0%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLLEQNNLV 22
DB 1 MADNGTITVEELKQLLEQNNLV 22

RESULT 27
Q6RCZ4 PRELIMINARY; PRT; 221 AA.
AC Q6RCZ4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Putative envelope protein M.
OS SARS coronavirus TW6.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OC NCBI_TaxID=258969;
[1]
RP SEQUENCE FROM N.A.
RX PubMed=14983045; DOI=10.1073/pnas.0307904100;
RG National Taiwan University SARS Research Team;
RA Yeh S.-H., Wang H.-Y., Tsai C.-Y., Kao C.-L., Yang J.-Y., Liu H.-W.,

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RA Su I.-J., Tsai S.-F., Chen D.-S., Chen P.-J.;
"Characterization of severe acute respiratory syndrome coronavirus
RT genomes in Taiwan: molecular epidemiology and genome evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:2542-2547(2004).
DR EMBL; AY502929; AAR87571.1; -.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
KW Envelope protein.
SQ SEQUENCE 221 AA; 25016 MW; 6658652E2927478E CRC64;

Query Match 100.0%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLLEQNNLV 22
DB 1 MADNGTITVEELKQLLEQNNLV 22

RESULT 28
Q6RD05 PRELIMINARY; PRT; 221 AA.
AC Q6RD05;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Putative envelope protein M.
OS SARS coronavirus TW5.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OC NCBI_TaxID=258968;
[1]
RP SEQUENCE FROM N.A.
RX PubMed=14983045; DOI=10.1073/pnas.0307904100;
RG National Taiwan University SARS Research Team;
RA Yeh S.-H., Wang H.-Y., Tsai C.-Y., Kao C.-L., Yang J.-Y., Liu H.-W.,
Su I.-J., Tsai S.-F., Chen D.-S., Chen P.-J.;
"Characterization of severe acute respiratory syndrome coronavirus
RT genomes in Taiwan: molecular epidemiology and genome evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:2542-2547(2004).
DR EMBL; AY502928; AAR87560.1; -.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
KW Envelope protein.
SQ SEQUENCE 221 AA; 25016 MW; 6658652E2927478E CRC64;

Query Match 100.0%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLLEQNNLV 22
DB 1 MADNGTITVEELKQLLEQNNLV 22

RESULT 29
Q6RD16 PRELIMINARY; PRT; 221 AA.
AC Q6RD16;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Putative envelope protein M.
OS SARS coronavirus TW4.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OC NCBI_TaxID=258967;
[1]
RP SEQUENCE FROM N.A.

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RX PubMed=14983045; DOI=10.1073/pnas.0307904100;
RG National Taiwan University SARS Research Team;
RA Yeh S.-H., Wang H.-Y., Tsai C.-Y., Kao C.-L., Yang J.-Y., Liu H.-W.,
RA Su I.-J., Tsai S.-F., Chen D.-S., Chen P.-J.;
RT "Characterization of severe acute respiratory syndrome coronavirus
RT genomes in Taiwan: molecular epidemiology and genome evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:2542-2547(2004).
DR EMBL; AY502927; AAR87549.1; -.
RT Genomes in Taiwan: molecular epidemiology and genome evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:2542-2547(2004).
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
KW Envelope protein.
SQ SEQUENCE 221 AA; 25060 MW; 275C37085A0215A8 CRC64;

Query Match 100.0%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLLEQNNLV 22
Db 1 MADNGTITVEELKQLLEQNNLV 22

RESULT 30
QY 1 MADNGTITVEELKQLLEQNNLV 22
Db 1 MADNGTITVEELKQLLEQNNLV 22

PRELIMINARY; PRT; 221 AA.

ID O6RD27 PRELIMINARY; PRT; 221 AA.
AC O6RD27;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Putative envelope protein M.
OS SARS coronavirus TW3.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=258966;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14983045; DOI=10.1073/pnas.0307904100;
RG National Taiwan University SARS Research Team;
RA Yeh S.-H., Wang H.-Y., Tsai C.-Y., Kao C.-L., Yang J.-Y., Liu H.-W.,
RA Su I.-J., Tsai S.-F., Chen D.-S., Chen P.-J.;
RT "Characterization of severe acute respiratory syndrome coronavirus
RT genomes in Taiwan: molecular epidemiology and genome evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:2542-2547(2004).
DR EMBL; AY502926; AAR87538.1; -.
RT Genomes in Taiwan: molecular epidemiology and genome evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:2542-2547(2004).
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
KW Envelope protein.
SQ SEQUENCE 221 AA; 25060 MW; 275C37085A0215A8 CRC64;

Query Match 100.0%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLLEQNNLV 22
Db 1 MADNGTITVEELKQLLEQNNLV 22

RESULT 31
QY 1 MADNGTITVEELKQLLEQNNLV 22
Db 1 MADNGTITVEELKQLLEQNNLV 22

PRELIMINARY; PRT; 221 AA.

ID O6RD38 PRELIMINARY; PRT; 221 AA.
AC O6RD38;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative envelope protein M.
OS SARS coronavirus TW2.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.

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OX NCBI_TaxID=258965;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14983045; DOI=10.1073/pnas.0307904100;
RG National Taiwan University SARS Research Team;
RA Yeh S.-H., Wang H.-Y., Tsai C.-Y., Kao C.-L., Yang J.-Y., Liu H.-W.,
RA Su I.-J., Tsai S.-F., Chen D.-S., Chen P.-J.;
RT "Characterization of severe acute respiratory syndrome coronavirus
RT genomes in Taiwan: molecular epidemiology and genome evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:2542-2547(2004).
DR EMBL; AY502925; AAR87527.1; -.
RT Genomes in Taiwan: molecular epidemiology and genome evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:2542-2547(2004).
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
KW Envelope protein.
SQ SEQUENCE 221 AA; 25060 MW; 275C37085A0215A8 CRC64;

Query Match 100.0%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLLEQNNLV 22
Db 1 MADNGTITVEELKQLLEQNNLV 22

RESULT 32
QY 1 MADNGTITVEELKQLLEQNNLV 22
Db 1 MADNGTITVEELKQLLEQNNLV 22

PRELIMINARY; PRT; 221 AA.

ID O6RD49 PRELIMINARY; PRT; 221 AA.
AC O6RD49;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Putative envelope protein M.
OS SARS coronavirus TW1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=258964;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14983045; DOI=10.1073/pnas.0307904100;
RG National Taiwan University SARS Research Team;
RA Yeh S.-H., Wang H.-Y., Tsai C.-Y., Kao C.-L., Yang J.-Y., Liu H.-W.,
RA Su I.-J., Tsai S.-F., Chen D.-S., Chen P.-J.;
RT "Characterization of severe acute respiratory syndrome coronavirus
RT genomes in Taiwan: molecular epidemiology and genome evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:2542-2547(2004).
DR EMBL; AY502924; AAR87516.1; -.
RT Genomes in Taiwan: molecular epidemiology and genome evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:2542-2547(2004).
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
KW Envelope protein.
SQ SEQUENCE 221 AA; 25006 MW; DBEBBCOABAD77B7D CRC64;

Query Match 100.0%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLLEQNNLV 22
Db 1 MADNGTITVEELKQLLEQNNLV 22

RESULT 33
QY 1 MADNGTITVEELKQLLEQNNLV 22
Db 1 MADNGTITVEELKQLLEQNNLV 22

PRELIMINARY; PRT; 221 AA.

ID O6RD60 PRELIMINARY; PRT; 221 AA.
AC O6RD60;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative envelope protein M.

```

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OS SARS coronavirus TW10.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxId=258963;
RN
  [1]
RP SEQUENCE FROM N.A.
RX PubMed=14983045; DOI=10.1073/pnas.0307904100;
RG National Taiwan University SARS Research Team;
RA Yeh S.-H., Wang H.-Y., Tsai C.-Y., Kao C.-L., Yang J.-Y., Liu H.-W.,
  Su I.-J., Tsai S.-F., Chen D.-S., Chen P.-J.;
RT "Characterization of severe acute respiratory syndrome coronavirus
  genomes in Taiwan: molecular epidemiology and genome evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:2542-2547(2004).
DR EMBL; AY502923; AAR87505.1; -.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0019058; P: viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
DR Envelope protein.
SQ SEQUENCE 221 AA; 25016 MW; 66586529297478E CRC64;

Query Match 100.0%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLEQNNLV 22
DB 1 MADNGTITVEELKQLEQNNLV 22

RESULT 34
06S8D3 PRELIMINARY; PRT; 221 AA.
AC 06S8D3;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE , complete genome.
OS SARS coronavirus ShanghaiQXC2.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxId=2589508;
  [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ShanghaiQXC2;
RA Yuan Z., Zhang X., Hu Y., Ian S., Zhou Z., Wang H., Wen Y.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY463060; AAR86779.1; -.
DR GO; GO:0019058; P: viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
SQ SEQUENCE 221 AA; 25044 MW; 51875ABE9BAE04FC CRC64;

Query Match 100.0%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLEQNNLV 22
DB 1 MADNGTITVEELKQLEQNNLV 22

RESULT 35
06T1D8 PRELIMINARY; PRT; 221 AA.
AC 06T1D8;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Membrane glycoprotein M.
OS SARS coronavirus CUHK-12.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
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OX NCBI_TaxId=260550;
RN
  [1]
RP SEQUENCE FROM N.A.
RX PubMed=14709660;
RA Chim S.S.C., Tong Y.K., Hung E.C.W., Chiu R.W.K., Lo Y.M.D.;
RT "Genomic sequencing of a SARS coronavirus isolate that predated the
  Metropole Hotel case cluster in Hong Kong.";
RL Clin. Chem. 50:231-233(2004).
DR EMBL; AY443095; AAS01068.1; -.
DR GO; GO:0019058; P: viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
SQ SEQUENCE 221 AA; 25060 MW; 275C37085A0215A8 CRC64;

Query Match 100.0%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLEQNNLV 22
DB 1 MADNGTITVEELKQLEQNNLV 22

RESULT 36
06TPE4 PRELIMINARY; PRT; 221 AA.
AC 06TPE4;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Matrix protein.
OS SARS coronavirus GZ02.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxId=256753;
  [1]
RP SEQUENCE FROM N.A.
RA Zhou X., Hou J., He M., Ding Y., Wang Z., Li J., Liu Z., Ma S.,
  Zhang K., Pan W., Zhang J., He J., Wang Y., Xu Y., Wang X.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY390556; AAS00007.1; -.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR GO; GO:0019058; P: viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
SQ SEQUENCE 221 AA; 25060 MW; 275C37085A0215A8 CRC64;

Query Match 100.0%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLEQNNLV 22
DB 1 MADNGTITVEELKQLEQNNLV 22

RESULT 37
06UZE9 PRELIMINARY; PRT; 221 AA.
AC 06UZE9;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Putative M protein.
OS SARS coronavirus PUMC03.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxId=253435;
  [1]
RP SEQUENCE FROM N.A.
RA Zou K., Zhu H., Ding K., Wang Z., Liu Y., Wang T., Yang J., Wei G.,
  Zhou X., Zhang W., Yu Z., Qin C., Liu X., Shen Y., Ni A., Qiang B.;
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RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY357076; ARI4812.1; -;
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
SQ SEQUENCE 221 AA; 25016 MW; 6658652E2927478E CRC64;

Query Match 100.0%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLEQNNLV 22
DB 1 MADNGTITVEELKQLEQNNLV 22

RESULT 38
ID Q6UZF3 PRELIMINARY; PRT; 221 AA.
AC Q6UZF3;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Putative M protein.
OS SARS coronavirus PUMC02.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxId=253434;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhou K., Zhu H., Ding K., Wang Z., Liu Y., Wang T., Yang J., Wei G.,
RA Zhou X., Zhang W., Yu Z., Qin C., Liu X., Shen Y., Ni A., Qiang B.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY357075; ARI4808.1; -;
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
SQ SEQUENCE 221 AA; 25016 MW; 6658652E2927478E CRC64;

Query Match 100.0%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLEQNNLV 22
DB 1 MADNGTITVEELKQLEQNNLV 22

RESULT 39
ID Q6V584 PRELIMINARY; PRT; 221 AA.
AC Q6V584;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Putative M protein.
OS SARS coronavirus PUMC01.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxId=253433;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhou K., Zhu H., Ding K., Wang Z., Liu Y., Wang T., Yang J., Wei G.,
RA Zhou X., Zhang W., Yu Z., Fan Z., Peng X., Qin C., Liu X., Shen Y.,
RA Ni A., Qiang B.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY350750; ARI4804.1; -;
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
SQ SEQUENCE 221 AA; 25016 MW; 6658652E2927478E CRC64;

Query Match 100.0%; Score 112; DB 2; Length 221;

Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLEQNNLV 22
DB 1 MADNGTITVEELKQLEQNNLV 22

RESULT 40
ID Q6VA74 PRELIMINARY; PRT; 221 AA.
AC Q6VA74;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Putative M protein.
OS SARS coronavirus CUHK-AG03.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxId=239243;
RN [1]
RP SEQUENCE FROM N.A.
RA Chim S.S.C., Tsui S.K.W., Chan K.C.A., Au T.C.C., Hung E.C.W.,
RA Tong Y.K., Chiu R.W.K., Ng E.K.O., Chan P.K.S., Chu C.M., Sung J.J.Y.,
RA Tam J.S., Fung K.P., Waye M.M.Y., Lee C.Y., Yuen K.Y., Chung S.,
RA Au-Yang C., Au K.K.A., Chan A.H., Chan C.W., Kou C.Y.C., Lam W.Y.,
RA Lau S.K., Lau Y.M., Law S.L., Law P.T.W., Li M.L.Y., Wan A.W.K.,
RA Mong C.H., Yiu W.H., Lee N., Wu A., Tse C.H., Chan L.Y.S., Lo Y.M.D.;
RT "Genomic characterisation of the SARS-coronavirus of the Amoy Gardens outbreak in Hong Kong."
RL Lancet 362:1807-1808(2003).
DR EMBL; AY345988; AAP94763.1; -;
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
SQ SEQUENCE 221 AA; 25016 MW; 6658652E2927478E CRC64;

Query Match 100.0%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLEQNNLV 22
DB 1 MADNGTITVEELKQLEQNNLV 22

RESULT 41
ID Q6VA85 PRELIMINARY; PRT; 221 AA.
AC Q6VA85;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Putative M protein.
OS SARS coronavirus CUHK-AG02.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxId=239242;
RN [1]
RP SEQUENCE FROM N.A.
RA Chim S.S.C., Tsui S.K.W., Chan K.C.A., Au T.C.C., Hung E.C.W.,
RA Tong Y.K., Chiu R.W.K., Ng E.K.O., Chan P.K.S., Chu C.M., Sung J.J.Y.,
RA Tam J.S., Fung K.P., Waye M.M.Y., Lee C.Y., Yuen K.Y., Chung S.,
RA Au-Yang C., Au K.K.A., Chan A.H., Chan C.W., Kou C.Y.C., Lam W.Y.,
RA Lau S.K., Lau Y.M., Law S.L., Law P.T.W., Li M.L.Y., Wan A.W.K.,
RA Wong C.H., Yiu W.H., Lee N., Wu A., Tse C.H., Chan L.Y.S., Lo Y.M.D.;
RT "Genomic characterisation of the SARS-coronavirus of the Amoy Gardens outbreak in Hong Kong."
RL Lancet 362:1807-1808(2003).
DR EMBL; AY345987; AAP94752.1; -;
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.

SQ SEQUENCE 221 AA; 25016 MW; 6658652E2927478E CRC64;
Query Match 100.0%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MADNGTITVEELKQLEQNNLV 22
DB 1 MADNGTITVEELKQLEQNNLV 22
RESULT 42
Q6VA96 PRELIMINARY; PRT; 221 AA.
AC 06VA96; 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, last sequence update)
DE Putative M protein.
OS SARS coronavirus CUHK-AG01.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
RN NCBI_TaxID=239241;
[1]
RP SEQUENCE FROM N.A.
RA Chim S.S.C., Tsui S.K.W., Chan K.C.A., Au T.C.C., Hung E.C.W.,
Tong Y.K., Chiu R.W.K., Ng E.K.O., Chan P.K.S., Chu C.M., Sung J.J.Y.,
Tam J.S., Fung K.P., Waye M.M.Y., Lee C.Y., Yuen K.Y., Chung S.,
Au-Yang C., Au K.K.A., Chan A.H., Chan C.W., Kou C.Y.C., Lam W.Y.,
Lau S.K., Lau Y.M., Law S.L., Law P.T.W., Li M.L.Y., Wan A.W.K.,
Wong C.H., Yiu W.H., Lee N., Mu A., Tse C.H., Chan L.Y.S., Lo Y.M.D.,
"Genomic characterisation of the SARS-coronavirus of the Amoy Gardens
outbreak in Hong Kong";
RT Lancet 362:1807-1808(2003).
RL EMBL; AY345986; AAP94741.1; -;
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
SQ SEQUENCE 221 AA; 25016 MW; 6658652E2927478E CRC64;
Query Match 100.0%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MADNGTITVEELKQLEQNNLV 22
DB 1 MADNGTITVEELKQLEQNNLV 22
RESULT 43
Q692E0 PRELIMINARY; PRT; 221 AA.
AC 0692E0; 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, last sequence update)
DE Membrane glycoprotein.
OS SARS coronavirus JUF.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
RN NCBI_TaxID=284672;
[1]
RP SEQUENCE FROM N.A.
RA Chen W., Yan M., Liu M.,
"Isolation and identification of Viruses Related to the SARS
RT Coronavirus from swine in China."
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY54824; AAT76152.1; -;
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
SQ SEQUENCE 221 AA; 25059 MW; 439CD30C104CBFAC CRC64;

Query Match 96.4%; Score 108; DB 2; Length 221;
Best Local Similarity 95.5%; Pred. No. 1.4e-06;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MADNGTITVEELKQLEQNNLV 22
DB 1 MADNGTITVEELKQLEQNNLV 22
RESULT 44
Q6QJ38 PRELIMINARY; PRT; 221 AA.
AC 06QJ38; 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, last sequence update)
DE Membrane protein.
OS SARS coronavirus BJ01.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
RN NCBI_TaxID=228407;
[1]
RP SEQUENCE FROM N.A.
RA Li T., Li X., Chang Z., Liu L.,
RT "Identification of SARS-CoV mRNA leader sequence."
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY536759; AAS48455.1; -;
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
SQ SEQUENCE 221 AA; 25059 MW; 439CD30C104CBFAC CRC64;
Query Match 96.4%; Score 108; DB 2; Length 221;
Best Local Similarity 95.5%; Pred. No. 1.4e-06;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MADNGTITVEELKQLEQNNLV 22
DB 1 MADNGTITVEELKQLEQNNLV 22
RESULT 45
Q6SRK0 PRELIMINARY; PRT; 143 AA.
AC 06SRK0; 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, last sequence update)
DE Membrane glycoprotein M (Fragment).
OS SARS coronavirus TW-YM1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; SARS coronavirus TW.
RN NCBI_TaxID=264383;
[1]
RP SEQUENCE FROM N.A.
RA Ian Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,
Yang J.-Y., Chen H.-Y., Chen Y.-M., Arthur J.,
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY451886; AAS44739.1; -;
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
FT NON_TER 143
SQ SEQUENCE 143 AA; 16435 MW; 2694FA8363B971F7 CRC64;

Query Match 94.6%; Score 106; DB 2; Length 143;
Best Local Similarity 95.5%; Pred. No. 1.6e-06;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MADNGTITVEELKQLEQNNLV 22
DB 1 MADNGTITVEELKQLEQNNLV 22

RESULT 46
HOSC_THET2 STANDARD; PRT; 376 AA.
AC 087198;
DT 30-MAY-2000 (Rel. 39, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Homocitrate synthase (EC 2.3.3.14).
GN Name=lye20; OrderedLocustNames=TTCl550;
OS Thermus thermophilus (Strain HB27 / ATCC BAA-163 / DSM 7039).
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OX NCBI_TaxID=262724;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99085673; PubMed=9866782;
RA Kosuge T., Hoshino T.;
RT "Lysine is synthesized through the alpha-aminoadipate pathway in
RT Thermus thermophilus";
RL FEMS Microbiol. Lett. 169:361-367(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX PubMed=15064768; DOI=10.1038/nbt956;
RA Henne A., Brueggemann H., Raasch C., Wlezer A., Hartsch T.,
RA Liesegang H., Johann A., Lienard T., Gohl O., Martinez-Arias R.,
RA Jacobi C., Starkuviene V., Schlenczek S., Dencker S., Huber R.,
RA Klenk H.-P., Kramer W., Merkl R., Gottschalk G., Fritz H.-U.;
RT "The genome sequence of the extreme thermophile Thermus
RT thermophilus";
RL Nat. Biotechnol. 22:547-553(2004).
CC -1- CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + 2-oxoglutarate = 2-
CC hydroxybutyrate-1,2,4-tricarboxylate + CoA.
CC -1- PATHWAY: Lysine biosynthesis; alpha-aminoadipic acid pathway;
CC first step.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- SIMILARITY: Belongs to the alpha-IPM synthetase / homocitrate
CC synthase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB018379; BAA33785.1; -.
DR EMBL; AE017306; AAS81892.1; -.
DR PIR; T51170; T51170.
DR InterPro; IPR002034; AIPM/HcIt_synth.
DR InterPro; IPR000891; HMGU-like.
DR Pfam; PF00682; HMGU-like; 1.
DR PROSITE; PS00815; AIPM_HOMOCIT_SYNTH_1; 1.
DR PROSITE; PS00816; AIPM_HOMOCIT_SYNTH_2; 1.
DR PROSITE; PS00991; PYR_CT; 1.
KW Complete proteome; Lysine biosynthesis; Transferase.
FT CONFLICT 104 104 A -> P (in Ref. 1).
SQ SEQUENCE 376 AA; 42159 MW; 1B8BEA63C82FCF06 CRC64;

Query Match 51.8%; Score 58; DB 1; Length 376;
Best Local Similarity 47.4%; Pred. No. 15;
Matches 9; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 MADNGTIVVEELKQLEQW 19
DB 355 LADRGQLTLEELDRILREW 373

RESULT 47
Q8PLJ9 PRELIMINARY; PRT; 409 AA.

AC Q8PLJ9;
DT 01-OCT-2002 (TREMblrel. 22, Created)
DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE Two-component system sensor protein.
GN Name=regS; OrderedLocustNames=XAC1798;
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92829;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Canavan F., Cardoso J., Chamberg F., Clapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sene J.A.D., Silva C., de Souza R.F.,
RA Spindola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Secubal J.C., Kitejima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities";
RL Nature 417:459-463(2002).
CC -1- SIMILARITY: Contains 1 histidine kinase domain.
DR EMBL; AE018112; AAM3661.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016301; P:kinase activity; IEA.
DR GO; GO:0001055; P:two-component sensor molecule activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR004358; Bact_sens_pr_C.
DR InterPro; IPR005467; His_Kinase.
DR InterPro; IPR003661; His_kin_N.
DR InterPro; IPR009082; His_kin_homodim.
DR Pfam; PF02518; HATPase_c1; 1.
DR Pfam; PF00512; HSKA; 1.
DR PRINTS; PR00344; BCTRLSENSOR.
DR SMART; SM00387; HATPase_c; 1.
DR SMART; SM00388; HSKA; 1.
DR PROSITE; PS01019; HIS_KIN; 1.
KW Complete proteome; Kinase; Phosphorylation; Sensory transduction;
KW Transferase.
SQ SEQUENCE 409 AA; 44065 MW; F481A6B6FA570BE CRC64;

Query Match 49.6%; Score 55.5; DB 2; Length 409;
Best Local Similarity 54.5%; Pred. No. 35;
Matches 12; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

QY 2 ADNGTIVVE-ELKQLEQWNV 22
DB 258 ADNGHLSREVAVKEVLEQWRLV 279

QY 48
ID Q9LRN6 PRELIMINARY; PRT; 229 AA.

AC Q9LRN6;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE Arabidopsis thaliana genomic DNA, chromosome 3, Pl clone:MU18.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC euroside II; Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20277480; PubMed=10819329;
 RA Nakamura Y.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
 RT features of the regions of 4,504,864 bp covered by sixty p1 and TAC
 RT clones.";
 RL DNA Res. 7:131-135(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB028621; BAB01352.1; -.
 DR HSP; P06787; IFS5.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR InterPro; IPR010983; EF_Hand_Like.
 DR Pfam; PF00036; ehand; 4.
 DR ProDom; PD000012; EF-hand; 1.
 DR SMART; SM00054; Eph; 2.
 DR PROSITE; PS00018; EF_HAND; UNKNOWN 1.
 SQ SEQUENCE 229 AA; 36266 MW; 94C011172CA3740 CRC64;
 Query Match 49.1%; Score 55; DB 2; Length 229;
 Best Local Similarity 61.1%; Pred. No. 23;
 Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 Oy 4 NGTITVEELKQLLEQWNL 21
 Db 70 NGTIDIELKCKCHEKL 87
 RESULT 49
 Q9SE24 PRELIMINARY; PRT; 512 AA.
 AC Q9SE24
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Calcium-dependent protein kinase.
 GN Name=CDPK5;
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OC NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cheong Y.H., Moon B.C., Cho M.U.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ database.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL: AF194414; AAF23901.2; -.
 DR HSSP; PA9137; INXK.
 DR Gramene; Q9SE24; -.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR001751; CABP_S100.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR010983; EF_Hand_Like.
 DR InterPro; IPR011009; Kinase_Like.
 DR InterPro; IPR007719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR InterPro; IPR008271; Ser_thr_kinase.
 DR Pfam; PF00036; ehand; 4.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD0003407; CABP_S100; 1.
 DR ProDom; PD000012; EF-hand; 2.

DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00054; Eph; 4.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS00018; EF_HAND; 4.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Calcium; Calcium-binding; Kinase;
 KW Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 512 AA; 57584 MW; 89B38CFB9537FF6 CRC64;
 Query Match 47.8%; Score 53.5; DB 2; Length 512;
 Best Local Similarity 57.1%; Pred. No. 82;
 Matches 12; Conservative 3; Mismatches 3; Indels 3; Gaps 1;
 Oy 4 NGTITVEELKQLLEQ--WNL 21
 Db 372 NGTISLEELKQALVKVPWRL 392
 RESULT 50
 Q9RCJ0 PRELIMINARY; PRT; 279 AA.
 AC Q9RCJ0
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Bpsq protein (CpsQ).
 GN Name=epsQ; Synonyms=cpsQ;
 OS Streptococcus thermophilus.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OC NCBI_TaxID=1308;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CNR2368;
 RX MEDLINE=98325267; PubMed=9657932; DOI=10.1006/plas.1998.1337;
 RA Bourgoin F., Guedon G., Gintz B., Decaris B.;
 RT "Characterization of a novel insertion sequence, IS1194, in
 RT Streptococcus thermophilus.";
 RL Plasmid 40:44-49(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CNR2368;
 RX MEDLINE=99307153; PubMed=10375631; DOI=10.1016/S0378-1119(99)00144-4;
 RA Bourgoin F., Pluvinet A., Gintz B., Decaris B., Guedon G.;
 RT "Are horizontal transfers involved in the evolution of the
 RT Streptococcus thermophilus exopolysaccharide synthesis loci?";
 RL Gene 233:151-161(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CNR2368;
 RA Schmitt C., Guedon G., Paguer S., Pebay M., Panis C., Decaris B.;
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ database.
 RN [4]
 RP SEQUENCE FROM N.A.
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 RT "Biochemistry, genetics, and applications of exopolysaccharide
 RT production in Streptococcus thermophilus: a review.";
 RL J. Dairy Sci. 86:407-423(2003).
 DR EMBL: Z98171; CAB52237.1; -.
 DR EMBL: AF448249; AAM93399.1; -.
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 DR Pfam; PF00535; Glyco_transf_2; 1.
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OM protein - protein search, using sw model

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Searched: 513545 seqs, 74649064 residues
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Pred. No. is the number of results predicted by chance to have a
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SUMMARIES

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| 167 | 41 | 36.6 | 840 | 4 | US-08-222-617A-12 | Sequence 12, Appl1 | 240 | 39.5 | 35.3 | 855 | 1 | US-08-455-528-28 | Sequence 28, Appl1 |
| 168 | 41 | 36.6 | 840 | 4 | US-08-222-617A-27 | Sequence 27, Appl1 | 241 | 39.5 | 35.3 | 855 | 1 | US-08-455-528-28 | Sequence 28, Appl1 |
| 169 | 41 | 36.6 | 840 | 4 | US-08-222-617A-2 | Sequence 2, Appl1 | 242 | 39.5 | 35.3 | 855 | 1 | US-08-455-528-28 | Sequence 28, Appl1 |
| 170 | 41 | 36.6 | 840 | 4 | US-08-402-804-10 | Sequence 10, Appl1 | 243 | 39.5 | 35.3 | 855 | 1 | US-08-455-528-28 | Sequence 28, Appl1 |
| 171 | 41 | 36.6 | 840 | 4 | US-09-134-001C-4419 | Sequence 4419, Ap | 244 | 39.5 | 35.3 | 855 | 1 | US-08-455-528-28 | Sequence 28, Appl1 |
| 172 | 41 | 36.6 | 840 | 4 | US-09-134-000C-3442 | Sequence 3442, Ap | 245 | 39.5 | 35.3 | 855 | 1 | US-08-455-528-28 | Sequence 28, Appl1 |
| 173 | 41 | 36.6 | 840 | 4 | US-09-022-940-1 | Sequence 1, Appl1 | 246 | 39.5 | 35.3 | 855 | 1 | US-08-455-528-28 | Sequence 28, Appl1 |

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|-----|----|------|-----|---|----------------------|--------------------|-----|------|------|------|---|----------------------|--------------------|
| 247 | 39 | 34.8 | 170 | 4 | US-09-134-000C-4756 | Sequence 4756, Ap | 320 | 39 | 34.8 | 703 | 3 | US-08-910-925-4 | Sequence 4, Appl1 |
| 248 | 39 | 34.8 | 171 | 4 | US-09-328-352-4783 | Sequence 4783, Ap | 321 | 39 | 34.8 | 717 | 3 | US-08-910-925-1 | Sequence 1, Appl1 |
| 249 | 39 | 34.8 | 191 | 4 | US-09-949-016-7105 | Sequence 7105, Ap | 322 | 39 | 34.8 | 743 | 3 | US-08-910-925-3 | Sequence 3, Appl1 |
| 250 | 39 | 34.8 | 205 | 4 | US-09-270-767-42795 | Sequence 42795, A | 323 | 39 | 34.8 | 743 | 4 | US-09-949-016-6261 | Sequence 6261, Ap |
| 251 | 39 | 34.8 | 229 | 4 | US-09-270-767-32090 | Sequence 32090, A | 324 | 39 | 34.8 | 768 | 2 | US-08-222-617A-5 | Sequence 5, Appl1 |
| 252 | 39 | 34.8 | 229 | 4 | US-09-270-767-47307 | Sequence 47307, A | 325 | 39 | 34.8 | 972 | 4 | US-09-710-092-2 | Sequence 2, Appl1 |
| 253 | 39 | 34.8 | 220 | 3 | US-09-516-143A-6 | Sequence 6, Appl1 | 326 | 39 | 34.8 | 989 | 3 | US-09-412-554A-2 | Sequence 2, Appl1 |
| 254 | 39 | 34.8 | 230 | 3 | US-09-984-205-6 | Sequence 6, Appl1 | 327 | 39 | 34.8 | 989 | 4 | US-09-902-540-15948 | Sequence 15948, A |
| 255 | 39 | 34.8 | 241 | 3 | US-08-896-933-32 | Sequence 32, Appl1 | 328 | 39 | 34.8 | 1018 | 4 | US-10-101-464A-909 | Sequence 909, App |
| 256 | 39 | 34.8 | 241 | 3 | US-09-314-235-32 | Sequence 32, Appl1 | 329 | 39 | 34.8 | 1056 | 4 | US-09-710-092-6 | Sequence 6, Appl1 |
| 257 | 39 | 34.8 | 241 | 4 | US-09-708-008A-32 | Sequence 32, Appl1 | 330 | 39 | 34.8 | 1173 | 4 | US-09-543-681A-7965 | Sequence 7965, Ap |
| 258 | 39 | 34.8 | 244 | 4 | US-09-710-279-994 | Sequence 994, App | 331 | 39 | 34.8 | 1270 | 4 | US-09-710-092-10 | Sequence 10, Appl1 |
| 259 | 39 | 34.8 | 250 | 2 | US-08-879-561-8 | Sequence 8, Appl1 | 332 | 39 | 34.8 | 1426 | 4 | US-09-710-092-14 | Sequence 14, Appl1 |
| 260 | 39 | 34.8 | 251 | 4 | US-09-949-016-11398 | Sequence 11398, A | 333 | 39 | 34.8 | 1430 | 3 | US-09-008-172-2 | Sequence 2, Appl1 |
| 261 | 39 | 34.8 | 252 | 4 | US-09-857-498A-6 | Sequence 6, Appl1 | 334 | 39 | 34.8 | 1430 | 3 | US-09-210-361-6 | Sequence 6, Appl1 |
| 262 | 39 | 34.8 | 275 | 4 | US-09-107-532A-6200 | Sequence 6200, Ap | 335 | 39 | 34.8 | 1430 | 4 | US-09-740-274-6 | Sequence 6, Appl1 |
| 263 | 39 | 34.8 | 276 | 4 | US-09-134-000C-4646 | Sequence 4646, Ap | 336 | 39 | 34.8 | 1630 | 4 | US-09-302-540-15591 | Sequence 15591, A |
| 264 | 39 | 34.8 | 288 | 4 | US-09-270-767-46126 | Sequence 46126, A | 337 | 39 | 34.8 | 54 | 4 | US-09-536-977-16 | Sequence 16, Appl1 |
| 265 | 39 | 34.8 | 301 | 4 | US-09-248-796A-26282 | Sequence 26282, A | 338 | 38.5 | 34.4 | 121 | 4 | US-09-248-796A-19888 | Sequence 19888, A |
| 266 | 39 | 34.8 | 320 | 2 | US-09-027-013-1 | Sequence 1, Appl1 | 339 | 38.5 | 34.4 | 121 | 4 | US-09-536-977-44 | Sequence 44, Appl1 |
| 267 | 39 | 34.8 | 320 | 3 | US-09-244-233-1 | Sequence 1, Appl1 | 340 | 38.5 | 34.4 | 210 | 3 | US-09-247-3738-46 | Sequence 46, Appl1 |
| 268 | 39 | 34.8 | 321 | 4 | US-09-328-352-4883 | Sequence 4883, Ap | 341 | 38.5 | 34.4 | 218 | 4 | US-09-583-110-4540 | Sequence 4540, Ap |
| 269 | 39 | 34.8 | 326 | 4 | US-09-489-039A-7348 | Sequence 7348, Ap | 342 | 38.5 | 34.4 | 222 | 4 | US-09-107-433-4007 | Sequence 4007, Ap |
| 270 | 39 | 34.8 | 339 | 4 | US-09-107-532A-4033 | Sequence 4033, Ap | 343 | 38.5 | 34.4 | 227 | 4 | US-09-328-352-6938 | Sequence 6938, Ap |
| 271 | 39 | 34.8 | 358 | 4 | US-09-248-796A-19081 | Sequence 19081, A | 344 | 38.5 | 34.4 | 324 | 4 | US-09-543-681A-6167 | Sequence 6167, Ap |
| 272 | 39 | 34.8 | 360 | 4 | US-09-710-279-2150 | Sequence 2150, Ap | 345 | 38.5 | 34.4 | 358 | 3 | US-09-500-569-18 | Sequence 18, Appl1 |
| 273 | 39 | 34.8 | 367 | 3 | US-09-134-001C-3678 | Sequence 3678, Ap | 346 | 38.5 | 34.4 | 358 | 4 | US-09-971-8238-18 | Sequence 18, Appl1 |
| 274 | 39 | 34.8 | 376 | 4 | US-09-710-279-2106 | Sequence 2106, Ap | 347 | 38.5 | 34.4 | 365 | 3 | US-09-500-569-4 | Sequence 4, Appl1 |
| 275 | 39 | 34.8 | 380 | 4 | US-09-248-796A-17151 | Sequence 17151, A | 348 | 38.5 | 34.4 | 365 | 4 | US-09-971-8238-4 | Sequence 4, Appl1 |
| 276 | 39 | 34.8 | 408 | 1 | US-07-951-715A-21 | Sequence 21, Appl1 | 349 | 38.5 | 34.4 | 425 | 4 | US-09-536-977-46 | Sequence 46, Appl1 |
| 277 | 39 | 34.8 | 408 | 2 | US-08-459-448A-21 | Sequence 21, Appl1 | 350 | 38.5 | 34.4 | 425 | 4 | US-09-536-977-48 | Sequence 48, Appl1 |
| 278 | 39 | 34.8 | 408 | 3 | US-08-459-459A-21 | Sequence 21, Appl1 | 351 | 38.5 | 34.4 | 425 | 4 | US-09-536-977-50 | Sequence 50, Appl1 |
| 279 | 39 | 34.8 | 408 | 3 | US-08-459-504B-21 | Sequence 21, Appl1 | 352 | 38.5 | 34.4 | 425 | 4 | US-09-536-977-52 | Sequence 52, Appl1 |
| 280 | 39 | 34.8 | 408 | 3 | US-08-459-444-21 | Sequence 21, Appl1 | 353 | 38.5 | 34.4 | 450 | 4 | US-09-252-991A-24440 | Sequence 24440, A |
| 281 | 39 | 34.8 | 408 | 3 | US-07-547-422-21 | Sequence 21, Appl1 | 354 | 38.5 | 34.4 | 476 | 4 | US-09-536-977-74 | Sequence 74, Appl1 |
| 282 | 39 | 34.8 | 408 | 4 | US-09-988-462-21 | Sequence 21, Appl1 | 355 | 38.5 | 34.4 | 494 | 4 | US-09-452-991A-28022 | Sequence 28022, A |
| 283 | 39 | 34.8 | 426 | 3 | US-08-676-444-40 | Sequence 40, Appl1 | 356 | 38.5 | 34.4 | 575 | 4 | US-09-248-796A-17643 | Sequence 17643, A |
| 284 | 39 | 34.8 | 453 | 4 | US-09-543-681A-7700 | Sequence 7700, Ap | 357 | 38.5 | 34.4 | 602 | 4 | US-09-540-236-3263 | Sequence 3263, Ap |
| 285 | 39 | 34.8 | 457 | 4 | US-09-248-796A-23295 | Sequence 23295, A | 358 | 38.5 | 34.4 | 635 | 4 | US-09-536-977-68 | Sequence 68, Appl1 |
| 286 | 39 | 34.8 | 463 | 1 | US-07-951-715A-25 | Sequence 25, Appl1 | 359 | 38.5 | 34.4 | 657 | 3 | US-09-256-194-2 | Sequence 2, Appl1 |
| 287 | 39 | 34.8 | 463 | 2 | US-08-459-448A-25 | Sequence 25, Appl1 | 360 | 38.5 | 34.4 | 665 | 2 | US-08-448-603A-32 | Sequence 32, Appl1 |
| 288 | 39 | 34.8 | 463 | 3 | US-08-459-595A-25 | Sequence 25, Appl1 | 361 | 38.5 | 34.4 | 665 | 3 | US-09-134-075-32 | Sequence 32, Appl1 |
| 289 | 39 | 34.8 | 463 | 3 | US-08-459-504B-25 | Sequence 25, Appl1 | 362 | 38.5 | 34.4 | 665 | 3 | US-09-492-739-32 | Sequence 32, Appl1 |
| 290 | 39 | 34.8 | 463 | 3 | US-08-459-444-25 | Sequence 0, Appl1 | 363 | 38.5 | 34.4 | 665 | 4 | US-09-966-931A-32 | Sequence 32, Appl1 |
| 291 | 39 | 34.8 | 463 | 3 | US-09-547-422-25 | Sequence 0, Appl1 | 364 | 38.5 | 34.4 | 675 | 3 | US-09-134-001C-5219 | Sequence 5219, Ap |
| 292 | 39 | 34.8 | 463 | 4 | US-09-988-462-25 | Sequence 25, Appl1 | 365 | 38.5 | 34.4 | 675 | 4 | US-09-536-977-70 | Sequence 70, Appl1 |
| 293 | 39 | 34.8 | 464 | 1 | US-07-951-715A-22 | Sequence 22, Appl1 | 366 | 38.5 | 34.4 | 715 | 4 | US-09-328-352-6830 | Sequence 6830, Ap |
| 294 | 39 | 34.8 | 464 | 2 | US-08-459-448A-22 | Sequence 22, Appl1 | 367 | 38.5 | 34.4 | 820 | 4 | US-09-536-977-72 | Sequence 72, Appl1 |
| 295 | 39 | 34.8 | 464 | 3 | US-08-459-595A-22 | Sequence 22, Appl1 | 368 | 38.5 | 34.4 | 857 | 2 | US-08-448-603A-30 | Sequence 30, Appl1 |
| 296 | 39 | 34.8 | 464 | 3 | US-08-459-504B-22 | Sequence 22, Appl1 | 369 | 38.5 | 34.4 | 857 | 3 | US-09-492-739-30 | Sequence 30, Appl1 |
| 297 | 39 | 34.8 | 464 | 3 | US-08-459-444-22 | Sequence 0, Appl1 | 370 | 38.5 | 34.4 | 857 | 3 | US-09-134-075-30 | Sequence 30, Appl1 |
| 298 | 39 | 34.8 | 464 | 3 | US-09-547-422-22 | Sequence 0, Appl1 | 371 | 38.5 | 34.4 | 857 | 4 | US-09-966-931A-30 | Sequence 30, Appl1 |
| 299 | 39 | 34.8 | 464 | 4 | US-09-988-462-22 | Sequence 22, Appl1 | 372 | 38.5 | 34.4 | 857 | 4 | US-08-887-534A-85 | Sequence 85, Appl1 |
| 300 | 39 | 34.8 | 464 | 4 | US-09-949-016-7399 | Sequence 7399, Ap | 373 | 38.5 | 34.4 | 1048 | 4 | US-09-527-431-85 | Sequence 85, Appl1 |
| 301 | 39 | 34.8 | 491 | 4 | US-09-489-039A-9206 | Sequence 9206, Ap | 374 | 38.5 | 34.4 | 1048 | 4 | US-09-446-861-85 | Sequence 85, Appl1 |
| 302 | 39 | 34.8 | 545 | 2 | US-08-467-822-30 | Sequence 30, Appl1 | 375 | 38 | 33.9 | 37 | 3 | US-08-974-549A-68 | Sequence 68, Appl1 |
| 303 | 39 | 34.8 | 545 | 3 | US-08-432-697-30 | Sequence 30, Appl1 | 376 | 38 | 33.9 | 37 | 3 | US-08-974-549A-210 | Sequence 210, App |
| 304 | 39 | 34.8 | 545 | 3 | US-08-466-248-30 | Sequence 30, Appl1 | 377 | 38 | 33.9 | 37 | 4 | US-08-912-951-68 | Sequence 68, Appl1 |
| 305 | 39 | 34.8 | 545 | 4 | US-09-604-957-4 | Sequence 4, Appl1 | 378 | 38 | 33.9 | 37 | 4 | US-09-402-181B-68 | Sequence 68, Appl1 |
| 306 | 39 | 34.8 | 546 | 3 | US-08-470-260-6 | Sequence 6, Appl1 | 379 | 38 | 33.9 | 37 | 4 | US-09-402-181B-210 | Sequence 210, App |
| 307 | 39 | 34.8 | 546 | 3 | US-08-471-491-6 | Sequence 6, Appl1 | 380 | 38 | 33.9 | 37 | 4 | US-09-721-456-68 | Sequence 68, Appl1 |
| 308 | 39 | 34.8 | 546 | 3 | US-08-466-662-6 | Sequence 6, Appl1 | 381 | 38 | 33.9 | 37 | 4 | US-09-721-456-210 | Sequence 210, App |
| 309 | 39 | 34.8 | 546 | 4 | US-08-256-847C-1 | Sequence 1, Appl1 | 382 | 38 | 33.9 | 40 | 1 | US-08-444-005-27 | Sequence 27, Appl1 |
| 310 | 39 | 34.8 | 546 | 4 | US-08-256-847C-7 | Sequence 7, Appl1 | 383 | 38 | 33.9 | 45 | 2 | US-08-219-237B-10 | Sequence 10, Appl1 |
| 311 | 39 | 34.8 | 555 | 1 | US-08-039-777-3 | Sequence 3, Appl1 | 384 | 38 | 33.9 | 54 | 3 | US-08-851-843A-21 | Sequence 21, Appl1 |
| 312 | 39 | 34.8 | 555 | 1 | US-08-611-361A-3 | Sequence 3, Appl1 | 385 | 38 | 33.9 | 54 | 3 | US-08-854-050-21 | Sequence 21, Appl1 |
| 313 | 39 | 34.8 | 561 | 1 | US-09-640-305-2 | Sequence 2, Appl1 | 386 | 38 | 33.9 | 54 | 3 | US-09-430-323-21 | Sequence 21, Appl1 |
| 314 | 39 | 34.8 | 561 | 1 | US-08-360-673-2 | Sequence 2, Appl1 | 387 | 38 | 33.9 | 54 | 4 | US-09-766-253-21 | Sequence 21, Appl1 |
| 315 | 39 | 34.8 | 604 | 4 | US-09-949-016-6585 | Sequence 6585, Ap | 388 | 38 | 33.9 | 63 | 3 | US-08-894-626-1 | Sequence 1, Appl1 |
| 316 | 39 | 34.8 | 604 | 4 | US-09-949-016-10250 | Sequence 10250, A | 389 | 38 | 33.9 | 64 | 4 | US-09-248-796A-24105 | Sequence 24105, A |
| 317 | 39 | 34.8 | 657 | 4 | US-09-949-016-10426 | Sequence 10426, A | 390 | 38 | 33.9 | 65 | 2 | US-08-867-087B-31 | Sequence 31, Appl1 |
| 318 | 39 | 34.8 | 657 | 4 | US-09-949-016-6174 | Sequence 6174, Ap | 391 | 38 | 33.9 | 68 | 3 | US-09-527-236A-22 | Sequence 22, Appl1 |
| 319 | 39 | 34.8 | 678 | 4 | US-09-949-016-10001 | Sequence 10001, A | 392 | 38 | 33.9 | 68 | 4 | US-09-756-854-22 | Sequence 22, Appl1 |

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|-----|----|------|-----|---|----------------------|--------------------|-----|----|------|-----|---|----------------------|--------------------|
| 393 | 38 | 33.9 | 70 | 4 | US-09-159-277A-5 | Sequence 5, Appl1 | 466 | 38 | 33.9 | 314 | 1 | US-08-152-443A-19 | Sequence 19, Appl1 |
| 394 | 38 | 33.9 | 70 | 4 | US-08-844-691A-5 | Sequence 5, Appl1 | 467 | 38 | 33.9 | 314 | 2 | US-08-389-459A-6 | Sequence 6, Appl1 |
| 395 | 38 | 33.9 | 72 | 4 | US-09-583-110-4899 | Sequence 4899, Ap | 468 | 38 | 33.9 | 314 | 2 | US-08-987-867A-6 | Sequence 6, Appl1 |
| 396 | 38 | 33.9 | 72 | 4 | US-09-107-433-2938 | Sequence 2938, Ap | 469 | 38 | 33.9 | 314 | 5 | PCT-US95-1708B-4 | Sequence 4, Appl1 |
| 397 | 38 | 33.9 | 77 | 4 | US-08-828-683A-24 | Sequence 24, Appl | 470 | 38 | 33.9 | 323 | 3 | US-09-134-001C-3339 | Sequence 3339, Ap |
| 398 | 38 | 33.9 | 84 | 4 | US-09-069-827A-119 | Sequence 119, Ap | 471 | 38 | 33.9 | 327 | 3 | US-08-679-493A-71 | Sequence 71, Appl |
| 399 | 38 | 33.9 | 85 | 4 | US-09-042-785A-26 | Sequence 26, Appl | 472 | 38 | 33.9 | 327 | 4 | US-08-679-493A-72 | Sequence 72, Appl |
| 400 | 38 | 33.9 | 95 | 1 | US-07-987-272A-9 | Sequence 9, Appl1 | 473 | 38 | 33.9 | 327 | 4 | US-09-585-858-53 | Sequence 53, Appl |
| 401 | 38 | 33.9 | 97 | 4 | US-09-461-912A-48 | Sequence 48, Appl | 474 | 38 | 33.9 | 327 | 4 | US-10-270-878A-53 | Sequence 53, Appl |
| 402 | 38 | 33.9 | 99 | 4 | US-09-270-767-31885 | Sequence 31885, A | 475 | 38 | 33.9 | 331 | 2 | US-08-564-972-9 | Sequence 9, Appl1 |
| 403 | 38 | 33.9 | 99 | 4 | US-09-270-767-47102 | Sequence 47102, A | 476 | 38 | 33.9 | 331 | 4 | US-09-086-483A-3 | Sequence 3, Appl1 |
| 404 | 38 | 33.9 | 120 | 1 | US-08-233-788A-57 | Sequence 57, Appl | 477 | 38 | 33.9 | 331 | 4 | US-09-580-212-3 | Sequence 3, Appl1 |
| 405 | 38 | 33.9 | 124 | 4 | US-09-328-352-5521 | Sequence 5521, Ap | 478 | 38 | 33.9 | 331 | 4 | US-09-769-402-3 | Sequence 3, Appl1 |
| 406 | 38 | 33.9 | 127 | 4 | US-09-614-912-146 | Sequence 146, Ap | 479 | 38 | 33.9 | 335 | 1 | US-07-947-130-2 | Sequence 2, Appl1 |
| 407 | 38 | 33.9 | 134 | 4 | US-10-000-489-2 | Sequence 2, Appl1 | 480 | 38 | 33.9 | 335 | 1 | US-08-421-822-2 | Sequence 2, Appl1 |
| 408 | 38 | 33.9 | 137 | 3 | US-09-446-504-34 | Sequence 34, Appl | 481 | 38 | 33.9 | 335 | 1 | US-08-421-823-2 | Sequence 2, Appl1 |
| 409 | 38 | 33.9 | 137 | 3 | US-09-712-266-34 | Sequence 34, Appl | 482 | 38 | 33.9 | 335 | 2 | US-08-319-237B-2 | Sequence 2, Appl1 |
| 410 | 38 | 33.9 | 137 | 3 | US-09-328-352-7316 | Sequence 7316, Ap | 483 | 38 | 33.9 | 335 | 2 | US-08-409-338-1 | Sequence 1, Appl1 |
| 411 | 38 | 33.9 | 151 | 1 | US-08-233-788A-59 | Sequence 59, Appl | 484 | 38 | 33.9 | 335 | 3 | US-08-815-469-6 | Sequence 6, Appl1 |
| 412 | 38 | 33.9 | 152 | 4 | US-09-248-796A-15593 | Sequence 15593, A | 485 | 38 | 33.9 | 335 | 3 | US-09-290-640-2 | Sequence 2, Appl1 |
| 413 | 38 | 33.9 | 153 | 4 | US-09-107-532A-5159 | Sequence 5159, Ap | 486 | 38 | 33.9 | 335 | 3 | US-09-006-353A-7 | Sequence 7, Appl1 |
| 414 | 38 | 33.9 | 156 | 4 | US-09-710-279-2848 | Sequence 2848, Ap | 487 | 38 | 33.9 | 335 | 3 | US-08-468-560C-2 | Sequence 2, Appl1 |
| 415 | 38 | 33.9 | 156 | 4 | US-09-540-236-3123 | Sequence 3123, Ap | 488 | 38 | 33.9 | 335 | 3 | US-09-180-100-20 | Sequence 20, Appl |
| 416 | 38 | 33.9 | 157 | 4 | US-09-710-279-408 | Sequence 408, Ap | 489 | 38 | 33.9 | 335 | 4 | US-09-565-918-3 | Sequence 3, Appl1 |
| 417 | 38 | 33.9 | 157 | 4 | US-08-564-972-62 | Sequence 62, Appl | 490 | 38 | 33.9 | 335 | 4 | US-09-573-986-7 | Sequence 7, Appl1 |
| 418 | 38 | 33.9 | 175 | 4 | US-09-107-433-3909 | Sequence 3909, Ap | 491 | 38 | 33.9 | 335 | 4 | US-09-665-615B-2 | Sequence 2, Appl1 |
| 419 | 38 | 33.9 | 189 | 4 | US-09-270-767-31816 | Sequence 31816, A | 492 | 38 | 33.9 | 335 | 4 | US-09-557-908-6 | Sequence 6, Appl1 |
| 420 | 38 | 33.9 | 189 | 4 | US-09-270-767-47033 | Sequence 47033, A | 493 | 38 | 33.9 | 335 | 4 | US-09-874-138-4 | Sequence 4, Appl1 |
| 421 | 38 | 33.9 | 192 | 2 | US-09-107-532A-6870 | Sequence 6870, Ap | 494 | 38 | 33.9 | 335 | 4 | US-09-333-966-6 | Sequence 6, Appl1 |
| 422 | 38 | 33.9 | 200 | 2 | US-08-531-525-33 | Sequence 33, Appl | 495 | 38 | 33.9 | 335 | 4 | US-09-949-016-5877 | Sequence 5877, Ap |
| 423 | 38 | 33.9 | 200 | 2 | US-08-718-270A-33 | Sequence 33, Appl | 496 | 38 | 33.9 | 335 | 5 | PCT-US95-1708B-2 | Sequence 2, Appl1 |
| 424 | 38 | 33.9 | 205 | 4 | US-09-107-532A-4830 | Sequence 4830, Ap | 497 | 38 | 33.9 | 338 | 4 | US-09-248-796A-15934 | Sequence 15934, A |
| 425 | 38 | 33.9 | 208 | 3 | US-09-134-001C-4697 | Sequence 4697, Ap | 498 | 38 | 33.9 | 345 | 3 | US-09-120-365-73 | Sequence 73, Appl |
| 426 | 38 | 33.9 | 215 | 4 | US-09-902-540-11802 | Sequence 11802, A | 499 | 38 | 33.9 | 345 | 3 | US-09-515-039-73 | Sequence 73, Appl |
| 427 | 38 | 33.9 | 222 | 3 | US-09-134-001C-4254 | Sequence 4264, Ap | 500 | 38 | 33.9 | 345 | 3 | US-08-827-1718-7 | Sequence 7, Appl1 |
| 428 | 38 | 33.9 | 223 | 4 | US-09-543-681A-5667 | Sequence 5667, Ap | 501 | 38 | 33.9 | 345 | 4 | US-09-598-062-7 | Sequence 7, Appl1 |
| 429 | 38 | 33.9 | 228 | 4 | US-09-710-279-3190 | Sequence 3190, Ap | 502 | 38 | 33.9 | 347 | 4 | US-09-543-681A-5315 | Sequence 5315, Ap |
| 430 | 38 | 33.9 | 230 | 2 | US-08-844-120-3 | Sequence 3, Appl1 | 503 | 38 | 33.9 | 351 | 1 | US-09-500-651-2 | Sequence 2, Appl1 |
| 431 | 38 | 33.9 | 230 | 2 | US-09-022-940-5 | Sequence 5, Appl1 | 504 | 38 | 33.9 | 351 | 2 | US-08-813-591-2 | Sequence 2, Appl1 |
| 432 | 38 | 33.9 | 230 | 3 | US-09-216-001-3 | Sequence 3, Appl1 | 505 | 38 | 33.9 | 355 | 4 | US-09-489-039A-12174 | Sequence 12174, A |
| 433 | 38 | 33.9 | 220 | 3 | US-09-216-386-5 | Sequence 5, Appl1 | 506 | 38 | 33.9 | 361 | 4 | US-09-252-991A-30426 | Sequence 30426, A |
| 434 | 38 | 33.9 | 220 | 3 | US-08-878-862-3 | Sequence 3, Appl1 | 507 | 38 | 33.9 | 365 | 4 | US-09-270-767-58705 | Sequence 58705, A |
| 435 | 38 | 33.9 | 220 | 3 | US-09-213-394-3 | Sequence 3, Appl1 | 508 | 38 | 33.9 | 369 | 4 | US-09-328-352-5567 | Sequence 5567, Ap |
| 436 | 38 | 33.9 | 220 | 4 | US-09-988-982-3 | Sequence 3, Appl1 | 509 | 38 | 33.9 | 375 | 4 | US-09-107-532A-3754 | Sequence 3754, Ap |
| 437 | 38 | 33.9 | 234 | 3 | US-09-503-391-22 | Sequence 22, Appl | 510 | 38 | 33.9 | 377 | 2 | US-08-839-581A-31 | Sequence 31, Appl |
| 438 | 38 | 33.9 | 236 | 4 | US-09-489-039A-11850 | Sequence 11850, A | 511 | 38 | 33.9 | 377 | 3 | US-09-023-591A-31 | Sequence 31, Appl |
| 439 | 38 | 33.9 | 246 | 3 | US-09-451-117-2 | Sequence 2, Appl1 | 512 | 38 | 33.9 | 383 | 3 | US-09-134-001C-3701 | Sequence 3701, Ap |
| 440 | 38 | 33.9 | 246 | 4 | US-09-888-555-2 | Sequence 2, Appl1 | 513 | 38 | 33.9 | 383 | 4 | US-09-710-279-3110 | Sequence 3110, Ap |
| 441 | 38 | 33.9 | 246 | 4 | US-09-888-501-2 | Sequence 2, Appl1 | 514 | 38 | 33.9 | 384 | 4 | US-09-452-991A-19333 | Sequence 19333, A |
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| 552 | 38 | 33.9 | 513 | 3 | US-09-134-001C-4629 | Sequence 4629, Ap | 625 | 37.5 | 33.5 | 293 | 4 | US-09-323-998B-15 | Sequence 15, Appl |
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| 554 | 38 | 33.9 | 535 | 3 | US-09-171-969-9 | Sequence 9, Appl | 627 | 37.5 | 33.5 | 305 | 1 | US-08-524-125-14 | Sequence 14, Appl |
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| 685 | 37 | 33.0 | 82 | 1 | US-07-881-075-19 | Sequence 19, Appl | 758 | 37 | 33.0 | 344 | 4 | US-09-809-665A-101 | Sequence 101, App |
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| 687 | 37 | 33.0 | 82 | 1 | US-08-478-675-19 | Sequence 19, Appl | 760 | 37 | 33.0 | 352 | 3 | US-08-630-915A-12 | Sequence 12, Appl |
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| 692 | 37 | 33.0 | 116 | 4 | US-09-328-352-5161 | Sequence 5161, Ap | 765 | 37 | 33.0 | 355 | 4 | US-09-248-796A-14612 | Sequence 14612, A |
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| 702 | 37 | 33.0 | 142 | 4 | US-09-601-729-5 | Sequence 5, Appl | 775 | 37 | 33.0 | 367 | 4 | US-09-949-016-9627 | Sequence 9627, Ap |
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| 707 | 37 | 33.0 | 147 | 3 | US-08-361-441B-5 | Sequence 5, Appl | 780 | 37 | 33.0 | 380 | 4 | US-09-949-016-7167 | Sequence 7167, Ap |
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| 714 | 37 | 33.0 | 172 | 4 | US-09-513-999C-7983 | Sequence 7983, Ap | 787 | 37 | 33.0 | 413 | 4 | US-09-614-066-14 | Sequence 14, Appl |
| 715 | 37 | 33.0 | 174 | 4 | US-09-710-279-1938 | Sequence 1938, Ap | 788 | 37 | 33.0 | 413 | 4 | US-09-821-802A-7 | Sequence 7, Appl |
| 716 | 37 | 33.0 | 176 | 4 | US-09-107-532A-4940 | Sequence 4940, Ap | 789 | 37 | 33.0 | 413 | 4 | US-09-821-802A-8 | Sequence 8, Appl |
| 717 | 37 | 33.0 | 187 | 4 | US-09-248-796A-19162 | Sequence 19162, A | 790 | 37 | 33.0 | 413 | 3 | US-08-852-936C-1 | Sequence 1, Appl |
| 718 | 37 | 33.0 | 190 | 1 | US-08-393-985-25 | Sequence 25, Appl | 791 | 37 | 33.0 | 416 | 3 | US-09-257-721-2 | Sequence 2, Appl |
| 719 | 37 | 33.0 | 190 | 4 | US-09-134-000C-6075 | Sequence 6075, Ap | 792 | 37 | 33.0 | 416 | 3 | US-09-311-760-2 | Sequence 2, Appl |
| 720 | 37 | 33.0 | 203 | 3 | US-08-852-936C-4 | Sequence 4, Appl | 793 | 37 | 33.0 | 416 | 3 | US-09-300-328-1 | Sequence 1, Appl |
| 721 | 37 | 33.0 | 203 | 3 | US-09-300-328-4 | Sequence 4, Appl | 794 | 37 | 33.0 | 416 | 3 | US-09-069-023-23 | Sequence 23, Appl |
| 722 | 37 | 33.0 | 209 | 4 | US-09-508-710-14 | Sequence 12992, A | 795 | 37 | 33.0 | 416 | 3 | US-09-561-756-30 | Sequence 30, Appl |
| 723 | 37 | 33.0 | 222 | 4 | US-09-508-710-14 | Sequence 12992, A | 796 | 37 | 33.0 | 416 | 3 | US-08-865-579-2 | Sequence 2, Appl |
| 724 | 37 | 33.0 | 228 | 4 | US-09-710-279-970 | Sequence 970, App | 797 | 37 | 33.0 | 416 | 4 | US-10-059-742-2 | Sequence 2, Appl |
| 725 | 37 | 33.0 | 231 | 4 | US-09-248-796A-25146 | Sequence 25146, A | 798 | 37 | 33.0 | 416 | 4 | US-09-954-697-102 | Sequence 102, App |
| 726 | 37 | 33.0 | 234 | 3 | US-09-134-001C-3195 | Sequence 3195, A | 799 | 37 | 33.0 | 416 | 4 | US-09-851-877-130 | Sequence 130, App |
| 727 | 37 | 33.0 | 234 | 4 | US-09-134-000C-6036 | Sequence 6036, Ap | 800 | 37 | 33.0 | 416 | 4 | US-09-328-092-4114 | Sequence 123, Ap |
| 728 | 37 | 33.0 | 254 | 4 | US-09-949-016-10670 | Sequence 10670, A | 801 | 37 | 33.0 | 416 | 4 | US-09-538-092-244 | Sequence 244, App |
| 729 | 37 | 33.0 | 259 | 4 | US-09-509-738C-25 | Sequence 25, Appl | 802 | 37 | 33.0 | 418 | 4 | US-09-107-532A-5939 | Sequence 5939, Ap |
| 730 | 37 | 33.0 | 263 | 1 | US-08-393-985-23 | Sequence 23, Appl | 803 | 37 | 33.0 | 436 | 4 | US-09-328-092-4114 | Sequence 6114, Ap |
| 731 | 37 | 33.0 | 263 | 4 | US-09-902-540-11627 | Sequence 11627, A | 804 | 37 | 33.0 | 444 | 4 | US-09-248-796A-16216 | Sequence 16216, A |
| 732 | 37 | 33.0 | 271 | 4 | US-09-809-665A-6 | Sequence 6, Appl | 805 | 37 | 33.0 | 445 | 4 | US-09-328-092-4114 | Sequence 123, Ap |
| 733 | 37 | 33.0 | 273 | 4 | US-09-134-000C-3441 | Sequence 3441, Ap | 806 | 37 | 33.0 | 455 | 4 | US-09-538-092-244 | Sequence 244, App |
| 734 | 37 | 33.0 | 277 | 6 | 5164481-2 | Patent No. 5164481 | 807 | 37 | 33.0 | 465 | 4 | US-09-252-991A-23099 | Sequence 23099, A |
| 735 | 37 | 33.0 | 277 | 6 | 5164481-2 | Patent No. 5164481 | 808 | 37 | 33.0 | 469 | 4 | US-09-538-092-244 | Sequence 244, App |
| 736 | 37 | 33.0 | 285 | 1 | US-08-393-985-2 | Sequence 2, Appl | 809 | 37 | 33.0 | 469 | 4 | US-09-538-092-244 | Sequence 244, App |
| 737 | 37 | 33.0 | 285 | 4 | US-08-311-731A-34 | Sequence 34, Appl | 810 | 37 | 33.0 | 479 | 4 | US-09-543-681A-6605 | Sequence 6605, Ap |
| 738 | 37 | 33.0 | 285 | 4 | US-08-311-731A-36 | Sequence 36, Appl | 811 | 37 | 33.0 | 490 | 2 | US-08-687-916-24 | Sequence 24, Appl |
| 739 | 37 | 33.0 | 286 | 4 | US-09-370-767-44940 | Sequence 44940, A | 812 | 37 | 33.0 | 490 | 3 | US-09-138-61A-24 | Sequence 24, Appl |
| 740 | 37 | 33.0 | 288 | 1 | US-08-337-602-4 | Sequence 4, Appl | 813 | 37 | 33.0 | 493 | 4 | US-09-252-991A-30722 | Sequence 30722, A |
| 741 | 37 | 33.0 | 288 | 3 | US-08-558-135-4 | Sequence 4, Appl | 814 | 37 | 33.0 | 497 | 3 | US-08-882-164D-32 | Sequence 32, Appl |
| 742 | 37 | 33.0 | 288 | 3 | US-08-819-286-3 | Sequence 3, Appl | 815 | 37 | 33.0 | 499 | 3 | US-09-090-793-11 | Sequence 11, Appl |
| 743 | 37 | 33.0 | 291 | 2 | US-08-531-927B-4 | Sequence 4, Appl | 816 | 37 | 33.0 | 508 | 4 | US-09-231-899-11 | Sequence 11, Appl |
| 744 | 37 | 33.0 | 296 | 4 | US-09-902-540-14392 | Sequence 14392, A | 817 | 37 | 33.0 | 508 | 4 | US-09-270-767-44071 | Sequence 45071, A |
| 745 | 37 | 33.0 | 298 | 4 | US-09-134-001C-4569 | Sequence 4569, Ap | 818 | 37 | 33.0 | 512 | 4 | US-09-902-540-13924 | Sequence 13924, A |
| 746 | 37 | 33.0 | 300 | 4 | US-09-248-796A-14770 | Sequence 14770, A | 819 | 37 | 33.0 | 522 | 1 | US-08-375-709-19 | Sequence 1096, Ap |
| 747 | 37 | 33.0 | 303 | 4 | US-09-352-991A-28605 | Sequence 28605, A | 820 | 37 | 33.0 | 525 | 1 | US-08-375-709-19 | Sequence 19, Appl |
| 748 | 37 | 33.0 | 307 | 3 | US-09-475-316A-70 | Sequence 70, Appl | 821 | 37 | 33.0 | 525 | 1 | US-08-752-929-19 | Sequence 19, Appl |
| 749 | 37 | 33.0 | 307 | 3 | US-09-704-640-70 | Sequence 70, Appl | 822 | 37 | 33.0 | 530 | 3 | US-08-979-608A-8 | Sequence 8, Appl |
| 750 | 37 | 33.0 | 309 | 3 | US-09-475-316A-72 | Sequence 72, Appl | 823 | 37 | 33.0 | 530 | 4 | US-09-517-848-8 | Sequence 8, Appl |
| 751 | 37 | 33.0 | 309 | 3 | US-09-134-001C-4952 | Sequence 4952, Ap | 824 | 37 | 33.0 | 530 | 4 | US-09-616-288-8 | Sequence 8, Appl |
| 752 | 37 | 33.0 | 309 | 3 | US-09-704-640-72 | Sequence 72, Appl | 825 | 37 | 33.0 | 532 | 4 | US-09-710-279-546 | Sequence 546, Appl |
| 753 | 37 | 33.0 | 325 | 4 | US-09-949-016-9168 | Sequence 9168, Ap | 826 | 37 | 33.0 | 533 | 4 | US-09-252-991A-20633 | Sequence 20633, A |
| 754 | 37 | 33.0 | 325 | 4 | US-09-949-016-9168 | Sequence 9168, Ap | 827 | 37 | 33.0 | 543 | 1 | US-08-375-709-17 | Sequence 17, Appl |
| 755 | 37 | 33.0 | 339 | 4 | US-09-107-532A-5514 | Sequence 5514, Ap | 828 | 37 | 33.0 | 543 | 1 | US-08-752-929-17 | Sequence 17, Appl |
| 756 | 37 | 33.0 | 341 | 4 | US-09-710-279-226 | Sequence 226, App | 829 | 37 | 33.0 | 543 | 3 | US-09-090-793-10 | Sequence 10, Appl |
| 757 | 37 | 33.0 | 342 | 4 | US-09-991-258-10 | Sequence 10, Appl | 830 | 37 | 33.0 | 543 | 4 | US-09-231-899-10 | Sequence 10, Appl |

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| 831 | 37 | 33.0 | 544 | 4 | US-09-248-796A-18637 | Sequence 18637, A | 904 | 37 | 33.0 | 1533 | 3 | US-09-534-242-9 | Sequence 9, Appl1 |
| 832 | 37 | 33.0 | 546 | 4 | US-09-616-289-44 | Sequence 44, Appl1 | 905 | 37 | 33.0 | 1533 | 3 | US-09-454-854-9 | Sequence 9, Appl1 |
| 833 | 37 | 33.0 | 548 | 4 | US-09-902-540-12604 | Sequence 12604, A | 906 | 37 | 33.0 | 1533 | 3 | US-09-164-671-9 | Sequence 9, Appl1 |
| 834 | 37 | 33.0 | 553 | 4 | US-09-902-540-9807 | Sequence 9807, Ap | 907 | 37 | 33.0 | 1533 | 4 | US-09-182-113-9 | Sequence 9, Appl1 |
| 835 | 37 | 33.0 | 557 | 3 | US-08-979-608A-5 | Sequence 5, Appl1 | 908 | 37 | 33.0 | 1533 | 4 | US-08-862-442-9 | Sequence 1033, Ap |
| 836 | 37 | 33.0 | 557 | 4 | US-09-517-849-5 | Sequence 5, Appl1 | 909 | 37 | 33.0 | 1222 | 4 | US-09-538-092-1033 | Sequence 45587, A |
| 837 | 37 | 33.0 | 557 | 4 | US-09-616-289-5 | Sequence 16908, A | 910 | 37 | 33.0 | 1165 | 4 | US-09-270-767-45587 | Sequence 15978, A |
| 838 | 37 | 33.0 | 558 | 4 | US-09-252-991A-16908 | Sequence 20658, A | 911 | 37 | 33.0 | 1803 | 4 | US-09-902-540-15978 | Sequence 94, Appl1 |
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| 840 | 37 | 33.0 | 576 | 3 | US-09-347-801-19 | Sequence 19, Appl1 | 913 | 37 | 33.0 | 1998 | 2 | US-08-800-644-94 | Sequence 1280, Ap |
| 841 | 37 | 33.0 | 576 | 4 | US-09-854-731-19 | Sequence 439, App | 914 | 37 | 33.0 | 1598 | 2 | US-09-538-092-1280 | Sequence 23, Appl1 |
| 842 | 37 | 33.0 | 653 | 4 | US-09-198-452A-439 | Sequence 6748, Ap | 915 | 37 | 33.0 | 2186 | 2 | US-08-822-445-2 | Sequence 2, Appl1 |
| 843 | 37 | 33.0 | 661 | 4 | US-09-328-352-6748 | Sequence 6983, Ap | 916 | 37 | 33.0 | 2471 | 3 | US-09-396-540-2 | Sequence 4, Appl1 |
| 844 | 37 | 33.0 | 665 | 4 | US-09-328-352-6983 | Sequence 421, App | 917 | 37 | 33.0 | 2471 | 3 | US-09-112-450-4 | Sequence 4, Appl1 |
| 845 | 37 | 33.0 | 674 | 3 | US-09-160-119-42 | Sequence 421, App | 918 | 37 | 33.0 | 2471 | 4 | US-09-119-291A-4 | Sequence 4, Appl1 |
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| 847 | 37 | 33.0 | 604 | 4 | US-09-252-991A-22481 | Sequence 24140, A | 920 | 36.5 | 32.6 | 59 | 3 | US-08-468-011A-23 | Sequence 23, Appl1 |
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| 849 | 37 | 33.0 | 716 | 4 | US-09-248-796A-24140 | Sequence 1178, Ap | 922 | 36.5 | 32.6 | 248 | 1 | US-08-500-222-4 | Sequence 4, Appl1 |
| 850 | 37 | 33.0 | 741 | 4 | US-09-710-279-1178 | Sequence 2921, Ap | 923 | 36.5 | 32.6 | 248 | 1 | US-08-500-125-4 | Sequence 4, Appl1 |
| 851 | 37 | 33.0 | 751 | 4 | US-09-540-236-2921 | Sequence 3689, Ap | 924 | 36.5 | 32.6 | 248 | 2 | US-07-779-704B-4 | Sequence 4, Appl1 |
| 852 | 37 | 33.0 | 766 | 3 | US-09-134-001C-3689 | Sequence 17675, A | 925 | 36.5 | 32.6 | 251 | 4 | US-09-270-767-44812 | Sequence 5453, Ap |
| 853 | 37 | 33.0 | 775 | 4 | US-09-248-796A-17675 | Sequence 5192, Ap | 926 | 36.5 | 32.6 | 266 | 3 | US-09-134-001C-5453 | Sequence 2850, Ap |
| 854 | 37 | 33.0 | 784 | 4 | US-09-583-110-5192 | Sequence 2, Appl1 | 927 | 36.5 | 32.6 | 295 | 3 | US-09-134-001C-2850 | Sequence 3, Appl1 |
| 855 | 37 | 33.0 | 787 | 3 | US-09-721-383-2 | Sequence 2, Appl1 | 928 | 36.5 | 32.6 | 307 | 4 | US-09-197-970B-3 | Sequence 4330, Ap |
| 856 | 37 | 33.0 | 787 | 3 | US-09-721-337-2 | Sequence 2, Appl1 | 929 | 36.5 | 32.6 | 326 | 4 | US-09-583-110-4330 | Sequence 4, Appl1 |
| 857 | 37 | 33.0 | 787 | 4 | US-09-721-251-2 | Sequence 2, Appl1 | 930 | 36.5 | 32.6 | 335 | 4 | US-09-222-938A-4 | Sequence 4, Appl1 |
| 858 | 37 | 33.0 | 787 | 4 | US-10-114-764-2 | Sequence 4612, Ap | 931 | 36.5 | 32.6 | 336 | 1 | US-07-641-143B-2 | Sequence 2, Appl1 |
| 859 | 37 | 33.0 | 787 | 4 | US-09-107-433-4612 | Sequence 17457, A | 932 | 36.5 | 32.6 | 336 | 1 | US-08-124-290-2 | Sequence 2, Appl1 |
| 860 | 37 | 33.0 | 823 | 4 | US-09-252-991A-17457 | Sequence 4302, Ap | 933 | 36.5 | 32.6 | 336 | 3 | US-08-696-372A-2 | Sequence 52, Appl1 |
| 861 | 37 | 33.0 | 860 | 4 | US-09-368-989A-2 | Sequence 25237, A | 934 | 36.5 | 32.6 | 336 | 3 | US-08-235-836C-52 | Sequence 54, Appl1 |
| 862 | 37 | 33.0 | 866 | 4 | US-09-252-991A-25237 | Sequence 2, Appl1 | 935 | 36.5 | 32.6 | 336 | 3 | US-08-235-836C-54 | Sequence 128, App |
| 863 | 37 | 33.0 | 911 | 4 | US-09-336-989A-6 | Sequence 39, Appl1 | 936 | 36.5 | 32.6 | 336 | 3 | US-08-858-003-34 | Sequence 34, Appl1 |
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| 867 | 37 | 33.0 | 953 | 4 | US-09-419-291A-2 | Sequence 2, Appl1 | 940 | 36.5 | 32.6 | 434 | 4 | US-09-328-352-7167 | Sequence 29241, A |
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| 869 | 37 | 33.0 | 971 | 4 | US-09-540-236-2304 | Sequence 1, Appl1 | 942 | 36.5 | 32.6 | 494 | 4 | US-08-500-125-2 | Sequence 2, Appl1 |
| 870 | 37 | 33.0 | 975 | 4 | US-08-127-499A-1 | Sequence 19450, A | 943 | 36.5 | 32.6 | 498 | 1 | US-07-779-704B-2 | Sequence 7370, Ap |
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| 872 | 37 | 33.0 | 992 | 1 | US-09-248-796A-20908 | Sequence 46, Appl1 | 945 | 36.5 | 32.6 | 513 | 3 | US-08-472-240A-14 | Sequence 14, Appl1 |
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| 878 | 37 | 33.0 | 1063 | 1 | US-08-482-847-8 | Sequence 7696, Ap | 951 | 36.5 | 32.6 | 545 | 4 | US-09-489-039A-11980 | Sequence 140, App |
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| 891 | 37 | 33.0 | 1533 | 3 | US-08-933-774-9 | Sequence 9, Appl1 | 964 | 36.5 | 32.6 | 856 | 1 | US-08-647-714-2 | Sequence 2, Appl1 |
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| 893 | 37 | 33.0 | 1533 | 3 | | | 966 | 36.5 | 32.6 | | | | |
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977 36.5 32.6 856 3 US-07-556-483-11 Sequence 11, Appl
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989 36.5 32.6 1769 4 US-09-949-016-8280 Sequence 8280, Ap
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1000 36.5 32.6 2813 4 US-09-381-261A-1 Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-206-551-11
; Sequence 11, Application US/09206551B
; Patent No. 6521739
; GENERAL INFORMATION:
; APPLICANT: Hahn, Beatrice H.
; APPLICANT: Gao, Feng
; APPLICANT: Marx, Preston A.
; APPLICANT: Shaw, George M.
; APPLICANT: Smith, Stephen M.
; APPLICANT: Georges-Courbot, Marie Claude
; APPLICANT: Lu, Chang Yong
; TITLE OF INVENTION: Complete Genome Sequences of a Simian
; TITLE OF INVENTION: Immunodeficiency Virus from a Red-Capped
; TITLE OF INVENTION: Mangabey
; FILE REFERENCE: D6286
; CURRENT APPLICATION NUMBER: US/09/206,551B
; CURRENT FILING DATE: 1998-12-07
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 11
; LENGTH: 855
; TYPE: PRT
; ORGANISM: Simian immunodeficiency virus
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of homologous region of
; US-09-206-551-11

Query Match 46.0%; Score 51.5; DB 4; Length 855;
Best Local Similarity 43.5%; Pred. No. 31;
Matches 10; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

QY 1 MADNGTIVE-ELKQLEQNLV 22
DB 401 MGPNGTITLCRIKQIINMWQRV 423

RESULT 2
US-09-206-551-12
; Sequence 12, Application US/09206551B
; Patent No. 6521739
; GENERAL INFORMATION:
; APPLICANT: Hahn, Beatrice H.
; APPLICANT: Gao, Feng

; APPLICANT: Marx, Preston A.
; APPLICANT: Shaw, George M.
; APPLICANT: Smith, Stephen M.
; APPLICANT: Georges-Courbot, Marie Claude
; APPLICANT: Lu, Chang Yong
; TITLE OF INVENTION: Complete Genome Sequences of a Simian
; TITLE OF INVENTION: Immunodeficiency Virus from a Red-Capped
; TITLE OF INVENTION: Mangabey
; FILE REFERENCE: D6286
; CURRENT APPLICATION NUMBER: US/09/206,551B
; CURRENT FILING DATE: 1998-12-07
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 12
; LENGTH: 855
; TYPE: PRT
; ORGANISM: Simian immunodeficiency virus
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of homologous region of
; US-09-206-551-12

Query Match 46.0%; Score 51.5; DB 4; Length 855;
Best Local Similarity 43.5%; Pred. No. 31;
Matches 10; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

QY 1 MADNGTIVE-ELKQLEQNLV 22
DB 401 MGPNGTITLCRIKQIINMWQRV 423

RESULT 3
US-08-531-525-31
; Sequence 31, Application US/08531525
; Patent No. 5840683
; GENERAL INFORMATION:
; APPLICANT: Hlavka, Joseph J.
; APPLICANT: Pincus, Matthew R.
; APPLICANT: No. 58406831e, John F.
; APPLICANT: Adajian, Henry B.
; APPLICANT: Kende, Andrew S.
; TITLE OF INVENTION: Peptides Inhibiting the Oncogenic Action
; TITLE OF INVENTION: of P21 Ras
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Greenlee and Winner, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: Colorado
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/531,525
; FILING DATE: 21-SEP-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 37-94
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 205 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-531-525-31

Query Match 45.5%; Score 51; DB 2; Length 205;
Best Local Similarity 42.9%; Pred. No. 7.3;
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 MADNGTIVBELKQLEQWNL 21
DB 131 LEDKQVSEAKRAEQWNV 151

RESULT 4

US-08-718-270A-31
Sequence 31, Application US/08718270A
Patent No. 5910478
GENERAL INFORMATION:
APPLICANT: Hlavka, Joseph J.
APPLICANT: Placus, Matthew R.
APPLICANT: No. 59104781e, John F.
APPLICANT: Abajian, Henry B.
TITLE OF INVENTION: Peptidomimetics Inhibiting
TITLE OF INVENTION: the Oncogenic Action of p21 Ras
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,270A
FILING DATE: 20-SEP-1996
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/531,525
FILING DATE: 21-SEP-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/004,091
FILING DATE: 21-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 78-95
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 205 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-718-270A-31

Query Match 45.5%; Score 51; DB 2; Length 205;
Best Local Similarity 42.9%; Pred. No. 7.3;
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
QY 1 MADNGTIVBELKQLEQWNL 21

DB 131 LEDKQVSEAKRAEQWNV 151

RESULT 5

US-09-078-317-15
Sequence 15, Application US/09078317
Patent No. 6017710
GENERAL INFORMATION:
APPLICANT: Allen, Maxine J.
APPLICANT: Rutter, Marc
APPLICANT: Buckler, Alan J.
TITLE OF INVENTION: RAG Genes and Their Uses
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bozicevic & Reed, LLP
STREET: 285 Hamilton Ave, Suite 200
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/078,317
FILING DATE: 13-MAY-1998
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Francis, Carol L
REGISTRATION NUMBER: 36,513
REFERENCE/DOCKET NUMBER: SEQ-18P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-327-3400
TELEFAX: 650-327-3231
TELEX:
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 206 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6017710e
US-09-078-317-15

Query Match 45.5%; Score 51; DB 3; Length 206;
Best Local Similarity 42.9%; Pred. No. 7.4;
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 MADNGTIVBELKQLEQWNL 21
DB 131 LEDKQVSEAKRAEQWNV 151

RESULT 6

US-09-454-818-15
Sequence 15, Application US/09454818
Patent No. 638792
GENERAL INFORMATION:
APPLICANT: Allen, Maxine J.
APPLICANT: Rutter, Marc
APPLICANT: Buckler, Alan J.
TITLE OF INVENTION: RAG Genes and Their Uses
FILE REFERENCE: AXYS-018DIV
CURRENT APPLICATION NUMBER: US/09/454,818
CURRENT FILING DATE: 1999-12-03
PRIORITY APPLICATION NUMBER: 09/078,317
PRIORITY FILING DATE: 1998-05-13

NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 15
LENGTH: 206
TYPE: PRT
ORGANISM: Homo sapiens
US-09-454-818-15

Query Match 45.5%; Score 51; DB 3; Length 206;
Best Local Similarity 42.9%; Pred. No. 7.4;
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 MADNGTIVTEELKQLEQWNL 21
DB 131 LEDKROVSVEAKNRAEQWNV 151

RESULT 7
US-09-709-103-48
Sequence 48, Application US/09709103
Patent No. 6733991
GENERAL INFORMATION:
APPLICANT: Cismowski, Mary
APPLICANT: Duzic, Emir
TITLE OF INVENTION: AGS Proteins and Nucleic Acid Molecules and Uses Therefor
FILE REFERENCE: 60388-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/709,103
CURRENT FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 73
SOFTWARE: Patentin version 3.1
SEQ ID NO: 48
LENGTH: 206
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-709-103-48

Query Match 45.5%; Score 51; DB 4; Length 206;
Best Local Similarity 42.9%; Pred. No. 7.4;
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 MADNGTIVTEELKQLEQWNL 21
DB 131 LEDKROVSVEAKNRAEQWNV 151

RESULT 8
US-09-439-410A-48
Sequence 48, Application US/09439410A
Patent No. 6746852
GENERAL INFORMATION:
APPLICANT: Cismowski, Mary
APPLICANT: Duzic, Emir
TITLE OF INVENTION: AGS PROTEIN AND NUCLEIC ACID MOLECULES AND USES THEREOF
FILE REFERENCE: 1919/60388-B
CURRENT APPLICATION NUMBER: US/09/439,410A
CURRENT FILING DATE: 1999-11-11
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin version 3.1
SEQ ID NO: 48
LENGTH: 206
TYPE: PRT
ORGANISM: Homo sapiens
US-09-439-410A-48

Query Match 45.5%; Score 51; DB 4; Length 206;
Best Local Similarity 42.9%; Pred. No. 7.4;
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 MADNGTIVTEELKQLEQWNL 21
DB 131 LEDKROVSVEAKNRAEQWNV 151

RESULT 9
US-09-266-965-132
Sequence 132, Application US/09266965
Patent No. 6495348
GENERAL INFORMATION:
APPLICANT: Sherman, D
APPLICANT: Mao, Y
APPLICANT: Varoglu, M
APPLICANT: He, M
APPLICANT: Sheldon, P
TITLE OF INVENTION: Mitomycin biosynthetic gene cluster
FILE REFERENCE: 600.456US1
CURRENT APPLICATION NUMBER: US/09/266,965
CURRENT FILING DATE: 1999-03-12
EARLIER APPLICATION NUMBER: US 08/624,447
EARLIER FILING DATE: 1996-08-19
EARLIER APPLICATION NUMBER: PCT/US94/11279
EARLIER FILING DATE: 1994-10-06
EARLIER APPLICATION NUMBER: US 08/133,963
EARLIER FILING DATE: 1993-10-07
NUMBER OF SEQ ID NOS: 145
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 132
LENGTH: 123
TYPE: PRT
ORGANISM: Streptomyces lavendulae
US-09-266-965-132

Query Match 43.8%; Score 49; DB 4; Length 123;
Best Local Similarity 57.1%; Pred. No. 8.1;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 NGTIVTEELKQLE 17
DB 86 NGTVPEELREWVE 99

RESULT 10
US-09-538-092-241
Sequence 241, Application US/09538092
Patent No. 6753314
GENERAL INFORMATION:
APPLICANT: Giot, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuratPatSegFormatter Version 0.9
SEQ ID NO: 241
LENGTH: 218
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number YER063W
US-09-538-092-241

Query Match 43.8%; Score 49; DB 4; Length 218;
Best Local Similarity 52.4%; Pred. No. 15;
Matches 11; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 MADNGTIVTEELKQLEQWNL 21
DB 1 MADYSLTVVQKDLITKRL 21

RESULT 11
US-09-543-681A-7926
; Sequence 7926, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709, 1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 7926
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-7926

Query Match 42.9%; Score 48; DB 4; Length 300;
Best Local Similarity 45.0%; Pred. No. 31;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 MADNGTIVVELKQLLEQNM 20
DB 60 LPTDGAIVYEHAKQIILQAFN 79

RESULT 12
US-09-538-092-769
; Sequence 769, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Glot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurataseqFormatter Version 0.9
; SEQ ID NO 769
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number YPL003W
US-09-538-092-769

Query Match 42.9%; Score 48; DB 4; Length 462;
Best Local Similarity 43.8%; Pred. No. 50;
Matches 7; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

QY 3 DNGTIVVELKQLLEQ 18
DB 213 NNGRITIDOKKVVDDQ 228

RESULT 13
US-09-538-092-266
; Sequence 266, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Glot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same

; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurataseqFormatter Version 0.9
; SEQ ID NO 266
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number YPL017C
US-09-538-092-266

Query Match 42.0%; Score 47; DB 4; Length 159;
Best Local Similarity 50.0%; Pred. No. 21;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 5 GTTIVVELKQLLEQNM 20
DB 31 GTTPESFSKILKVMN 46

RESULT 14
US-09-513-999C-6125
; Sequence 6125, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclet, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59, US2, REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 6125
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-6125

Query Match 41.1%; Score 46; DB 4; Length 100;
Best Local Similarity 60.0%; Pred. No. 18;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 DNGTIVVELKQLLE 17
DB 47 ENEGINIVELKQYLE 61

RESULT 15
US-09-270-767-45884
; Sequence 45884, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 45884

LENGTH: 149
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-270-767-45884

Query Match 41.1%; Score 46; DB 4; Length 149;
Best Local Similarity 41.2%; Pred. No. 27;
Matches 7; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 3 DNGTIVEELKQLEOM 19
DB 92 NKGTSARQRLNLCNW 108

RESULT 16
US-09-710-279-2624
Sequence 2624, Application US/09710279
Patent No. 6703492
GENERAL INFORMATION:
APPLICANT: KIMBERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 2624
LENGTH: 216
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-710-279-2624

Query Match 41.1%; Score 46; DB 4; Length 216;
Best Local Similarity 60.0%; Pred. No. 42;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 NGTIVEELKQLEO 18
DB 59 NGMTLEAKYQLE 73

RESULT 17
US-09-134-001C-5279
Sequence 5279, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 5279
LENGTH: 274
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5279

Query Match 41.1%; Score 46; DB 3; Length 274;
Best Local Similarity 60.0%; Pred. No. 54;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 NGTIVEELKQLEO 18

DB 117 NGMTLEAKYQLE 131

RESULT 18
US-09-648-004-26
Sequence 26, Application US/09648004
Patent No. 6498242
GENERAL INFORMATION:
APPLICANT: CHEN, QIONG
APPLICANT: THOMAS, STUART
APPLICANT: NAGARAJAN, VASANTHA
TITLE OF INVENTION: BIOLOGICAL METHOD FOR THE PRODUCTION OF ADIPIC ACID AND
FILE REFERENCE: CL-1341-A
CURRENT APPLICATION NUMBER: US/09/648,004
CURRENT FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/252,553
PRIOR FILING DATE: 1999-02-19
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Microsoft Office 97
SEQ ID NO 26
LENGTH: 300
TYPE: PRT
ORGANISM: Acinetobacter sp.
US-09-648-004-26

Query Match 41.1%; Score 46; DB 4; Length 300;
Best Local Similarity 25.0%; Pred. No. 60;
Matches 5; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

QY 1 MADNGTIVEELKQLEOMN 20
DB 22 MOENPMTEEDFRSMFDEWH 41

RESULT 19
US-10-272-419-26
Sequence 26, Application US/10272419
Patent No. 6794165
GENERAL INFORMATION:
APPLICANT: CHEN, QIONG
APPLICANT: THOMAS, STUART
APPLICANT: NAGARAJAN, VASANTHA
TITLE OF INVENTION: BIOLOGICAL METHOD FOR THE PRODUCTION OF ADIPIC ACID AND
FILE REFERENCE: CL1341-A
CURRENT APPLICATION NUMBER: US/10/272,419
CURRENT FILING DATE: 2002-10-16
PRIOR APPLICATION NUMBER: 09/252,553
PRIOR FILING DATE: 1999-02-19
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Microsoft Office 97
SEQ ID NO 26
LENGTH: 300
TYPE: PRT
ORGANISM: Acinetobacter sp.
US-10-272-419-26

Query Match 41.1%; Score 46; DB 4; Length 300;
Best Local Similarity 25.0%; Pred. No. 60;
Matches 5; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

QY 1 MADNGTIVEELKQLEOMN 20
DB 22 MOENPMTEEDFRSMFDEWH 41

RESULT 20
US-09-248-796A-14232
Sequence 14232, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
PRIORITY FILING DATE: 1999-02-12
PRIORITY APPLICATION NUMBER: US 60/074,725
PRIORITY FILING DATE: 1998-02-13
PRIORITY APPLICATION NUMBER: US 60/096,409
PRIORITY FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 14232
LENGTH: 415
TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-14232

Query Match 41.1%; Score 46; DB 4; Length 415;
Best Local Similarity 46.7%; Pred. No. 87;
Matches 7; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 7 ITVEELKQLEQNL 21
DB 106 ITPKCLKRAIDQWNI 120

RESULT 21
US-09-489-039A-10011
Sequence 10011, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
PRIORITY FILING DATE: 2000-01-27
PRIORITY APPLICATION NUMBER: US 60/117,747
PRIORITY FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 10011
LENGTH: 532
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-10011

Query Match 41.1%; Score 46; DB 4; Length 532;
Best Local Similarity 53.3%; Pred. No. 1,1e+02;
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 MADNGTIVEELKQL 15
DB 293 MADNGTLFDEIGEL 307

RESULT 22
US-08-940-332-2
Sequence 2, Application US/08940332
Patent No. 5885834
GENERAL INFORMATION:
APPLICANT: Epestein, Paul M.
TITLE OF INVENTION: SYNTHESIS OF ANTISENSE
TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE OF PHOSPHODIESTERASE AND
TITLE OF INVENTION: INDUCEMENT OF APOPTOSIS IN HUMAN LYMPHOBLASTOID CELLS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESSES:
ADDRESSEE: ALIX, YALE & RISTAS, LLP
STREET: 750 MAIN STREET
CITY: HARTFORD
STATE: CT
COUNTRY: USA
ZIP: 06103-2721
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,332
FILING DATE: 30-SEP-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/027,207
FILING DATE: 30-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Alix, James B.
REGISTRATION NUMBER: 20,736
REFERENCE/DOCKET NUMBER: UCON/137/US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (860)527-9211
TELEFAX: (860)527-5029
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 536 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-940-332-2

Query Match 41.1%; Score 46; DB 2; Length 536;
Best Local Similarity 60.0%; Pred. No. 1,2e+02;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 DNGTIVEELKQLE 17
DB 47 ENGEMINEELKQLE 61

RESULT 23
US-09-543-681A-4729
Sequence 4729, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
PRIORITY FILING DATE: 2000-04-05
PRIORITY APPLICATION NUMBER: US 60/128,706
PRIORITY FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 4729
LENGTH: 537
TYPE: PRT
ORGANISM: Proteus mirabilis
US-09-543-681A-4729

Query Match 41.1%; Score 46; DB 4; Length 537;
Best Local Similarity 36.8%; Pred. No. 1,2e+02;
Matches 7; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 3 DNGTIVEELKQLEQNL 21
DB 114 DNGSASLEDEPDELLEDKWL 132

RESULT 24
US-09-949-016-7536
Sequence 7536, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016

;; CURRENT FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: 60/241,755
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 7536
;; LENGTH: 542
;; TYPE: PRT
;; ORGANISM: Human
US-09-949-016-7536

Query Match 41.1%; Score 46; DB 4; Length 542;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 3 DNGTIVTEELKQLE 17
Db 53 ENGKINIEELKNLE 67

RESULT 25
US-09-540-236-2256
; Sequence 2256, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2256
; LENGTH: 119
; TYPE: PRT
; ORGANISM: M. catarrhalis
US-09-540-236-2256

Query Match 40.2%; Score 45; DB 4; Length 119;
Best Local Similarity 45.5%; Pred. No. 30;
Matches 10; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MADNGTIVTEELKQLE 22
Db 78 VASNGDITEELSLVEKTHV 99

RESULT 26
US-09-248-796A-21680
; Sequence 21680, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 21680
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-21680

Query Match 40.2%; Score 45; DB 4; Length 292;
Best Local Similarity 47.4%; Pred. No. 82;
Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 3 DNGTIVTEELKQLE 21
Db 84 DHIDIKVNLKQIKQINQWNI 102

RESULT 27
US-07-872-644-27
; Sequence 27, Application US/07872644
; Patent No. 5389527
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
ZIP: 60603

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/872,644
; FILING DATE: 19920420
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5389527and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 534 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-872-644-27

Query Match 40.2%; Score 45; DB 1; Length 534;
Best Local Similarity 53.3%; Pred. No. 1.6e+02;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 3 DNGTIVTEELKQLE 17
Db 46 ENGKINIEELKNLE 60

RESULT 28
US-08-297-494-27
; Sequence 27, Application US/08297494
; Patent No. 5560771
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.

APPLICANT: Bentley, Kelley
APPLICANT: Charbonneau, Harry
APPLICANT: Sonnenburg, William K.
TITLE OF INVENTION: DNA Encoding Mammalian
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
Bicknell
STREET: Two First National Plaza, 20 South Clark
Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/297,494
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5580771and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30822
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 534 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-297-494-27

Query Match 40.2%; Score 45; DB 1; Length 534;
Best Local Similarity 53.3%; Pred. No. 1.6e+02;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 DNGITVEELKKOLE 17
DB 46 ENGEVNIIEELKKOLE 60

RESULT 29
US-08-297-510-27
Sequence 27, Application US/08297510
Patent No. 5602019
GENERAL INFORMATION:
APPLICANT: Beavo, Joseph A.
APPLICANT: Bentley, Kelley
APPLICANT: Charbonneau, Harry
APPLICANT: Sonnenburg, William K.
TITLE OF INVENTION: DNA Encoding Mammalian
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
Bicknell
STREET: Two First National Plaza, 20 South Clark
Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/297,510
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5602019and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30822
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 534 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-297-510-27

Query Match 40.2%; Score 45; DB 1; Length 534;
Best Local Similarity 53.3%; Pred. No. 1.6e+02;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 DNGITVEELKKOLE 17
DB 46 ENGEVNIIEELKKOLE 60

RESULT 30
US-08-479-532-27
Sequence 27, Application US/08479532
Patent No. 5776752
GENERAL INFORMATION:
APPLICANT: Beavo, Joseph A.
APPLICANT: Bentley, Kelley
APPLICANT: Charbonneau, Harry
APPLICANT: Sonnenburg, William K.
TITLE OF INVENTION: DNA Encoding Mammalian
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
Bicknell
STREET: Two First National Plaza, 20 South Clark
Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,532
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/297,494
FILING DATE:
APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:

NAME: No. 5776752and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30822
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 534 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-479-532-27

Query Match
Best Local Similarity 53.3%; Score 45; DB 1; Length 534;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 DNGTIVBELKQLLE 17
: ||| : ||||| : ||
Db 46 ENGQVNIIEBLKKNLE 60

RESULT 31
US-08-455-526-27
; Sequence 27, Application US/08455526
; Patent No. 5789553
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; TITLE OF INVENTION: Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,526
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/297,494
; FILING DATE: 29-AUG-1994
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5789553and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 534 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-455-526-27

Query Match
Best Local Similarity 53.3%; Score 45; DB 1; Length 534;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 DNGTIVBELKQLLE 17
: ||| : ||||| : ||
Db 46 ENGQVNIIEBLKKNLE 60

RESULT 32
US-08-455-525-27
; Sequence 27, Application US/08455525
; Patent No. 5800987
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; TITLE OF INVENTION: Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,525
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/297,494
; FILING DATE:
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5800987and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 534 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-455-525-27

Query Match
Best Local Similarity 53.3%; Score 45; DB 1; Length 534;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 DNGTIVBELKQLLE 17
: ||| : ||||| : ||
Db 46 ENGQVNIIEBLKKNLE 60

RESULT 33
US-08-139-491-27

Sequence 27, Application US/09139491
Patent No. 6015677
GENERAL INFORMATION:
APPLICANT: Beavo, Joseph A.
APPLICANT: Bentley, Kelley
APPLICANT: Charbonneau, Harry
APPLICANT: Sonnenburg, William K.
TITLE OF INVENTION: DNA Encoding Mammalian
TITLE OF INVENTION: Phosphodiesterases
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/139,491
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/455,525
FILING DATE: 31-MAY-1995
APPLICATION NUMBER: 08/297,494
FILING DATE:
APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 6015677and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30822
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 984-9740
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 534 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-139-491-27

Query Match 40.2%; Score 45; DB 3; Length 534;
Best Local Similarity 53.3%; Pred. No. 1.6e+02;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 DNGTIVEEIKKLE 17
DB 46 ENGEVNIIEIKKLE 60

RESULT 34
US-09-883-825-27
Sequence 27, Application US/09883825
Patent No. 6642040
GENERAL INFORMATION:
APPLICANT: Beavo, Joseph A.
APPLICANT: Bentley, Kelley
APPLICANT: Charbonneau, William K.
APPLICANT: Sonnenburg, William K.
TITLE OF INVENTION: DNA Encoding Mammalian
TITLE OF INVENTION: Phosphodiesterases
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/883,825
FILING DATE: 18-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/123,783
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/297,494
FILING DATE: <Unknown>
APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 6642040and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30822
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 534 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-09-883-825-27

Query Match 40.2%; Score 45; DB 4; Length 534;
Best Local Similarity 53.3%; Pred. No. 1.6e+02;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 DNGTIVEEIKKLE 17
DB 46 ENGEVNIIEIKKLE 60

RESULT 35
PCT-US92-03222-27
Sequence 27, Application PC/TUS9203222
GENERAL INFORMATION:
APPLICANT: Beavo, Joseph A.
APPLICANT: Bentley, Kelley
APPLICANT: Charbonneau, Harry
APPLICANT: Sonnenburg, William K.
TITLE OF INVENTION: DNA Encoding Mammalian
TITLE OF INVENTION: Phosphodiesterases
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/03222
FILING DATE: 19920420
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta B.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30822
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 534 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US92-03222-27

Query Match 40.2%; Score 45; DB 5; Length 534;
Best Local Similarity 53.3%; Pred. No. 1.6e+02;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 DNGTIVEELKOLLEQNL 17
Db 46 ENGEVNEIEELKNLE 60

RESULT 36
US-09-248-796A-18997
Sequence 18997, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 18997
LENGTH: 714
TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-18997

Query Match 40.2%; Score 45; DB 4; Length 714;
Best Local Similarity 46.7%; Pred. No. 2.2e+02;
Matches 7; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 7 ITVEELKOLLEQNL 21
Db 87 ITLENKKGDKKNI 101

RESULT 37
US-09-255-502-7
Sequence 7, Application US/09255502
Patent No. 6218165
GENERAL INFORMATION:
APPLICANT: Estell, David
APPLICANT: Harding, Fiona
TITLE OF INVENTION: Mutant Proteins Having Lower Allergenic Responses in

TITLE OF INVENTION: Humans and Methods for Constructing, Identifying and
TITLE OF INVENTION: Producing Such Proteins
FILE REFERENCE: GC 527-D2
CURRENT APPLICATION NUMBER: US/09/255,502
CURRENT FILING DATE: 1999-02-23
PRIOR APPLICATION NUMBER: 09/060,872
PRIOR FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 1052
TYPE: PRT
ORGANISM: Homo sapiens
US-09-255-502-7

Query Match 40.2%; Score 45; DB 3; Length 1052;
Best Local Similarity 38.1%; Pred. No. 3.4e+02;
Matches 8; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 MADNGTIVEELKOLLEQNL 21
Db 747 MPDTGANIPALNELSVNM 767

RESULT 38
US-09-360-237-1
Sequence 1, Application US/09360237
Patent No. 6322962
GENERAL INFORMATION:
APPLICANT: BROWN, MICHAEL S.
APPLICANT: CHENG, DONG
APPLICANT: ESPENSHADE, PETER J.
APPLICANT: GOLDSTEIN, JOSEPH L.
APPLICANT: RAMSON, ROBERT B.
APPLICANT: SAKAI, JURO
TITLE OF INVENTION: STEROL-REGULATED SITE-1 PROTEASE AND ASSAYS OF
TITLE OF INVENTION: MODULATORS THEREOF
FILE REFERENCE: UTXD:567
CURRENT APPLICATION NUMBER: US/09/360,237
CURRENT FILING DATE: 1999-07-23
EARLIER APPLICATION NUMBER: 60/096,571
EARLIER FILING DATE: 1998-08-14
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 1052
TYPE: PRT
ORGANISM: Cricetus griseus
US-09-360-237-1

Query Match 40.2%; Score 45; DB 3; Length 1052;
Best Local Similarity 38.1%; Pred. No. 3.4e+02;
Matches 8; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 MADNGTIVEELKOLLEQNL 21
Db 747 MPDTGANIPALNELSVNM 767

RESULT 39
US-09-360-237-3
Sequence 3, Application US/09360237
Patent No. 6322962
GENERAL INFORMATION:
APPLICANT: BROWN, MICHAEL S.
APPLICANT: CHENG, DONG
APPLICANT: ESPENSHADE, PETER J.
APPLICANT: GOLDSTEIN, JOSEPH L.
APPLICANT: RAMSON, ROBERT B.
APPLICANT: SAKAI, JURO
TITLE OF INVENTION: STEROL-REGULATED SITE-1 PROTEASE AND ASSAYS OF
TITLE OF INVENTION: MODULATORS THEREOF
FILE REFERENCE: UTXD:567

CURRENT APPLICATION NUMBER: US/09/360,237
CURRENT FILING DATE: 1999-07-23
EARLIER APPLICATION NUMBER: 60/096,571
EARLIER FILING DATE: 1998-08-14
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 1052
TYPE: PRT
ORGANISM: Human
US-09-360-237-3

Query Match 40.2%; Score 45; DB 3; Length 1052;
Best Local Similarity 38.1%; Pred. No. 3.4e+02;
Matches 8; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 MADNGTIVEELKOLLEQNL 21
DB 747 MPDTGANIPALNELLSVNM 767

RESULT 40
US-09-255-501-208
Sequence 208, Application US/09255501
Patent No. 6596525
GENERAL INFORMATION:
APPLICANT: Estell, David
APPLICANT: Harding, Fiona
TITLE OF INVENTION: MUTANT PROTEINS HAVING LOWER ALLERGENIC RESPONSE IN
TITLE OF INVENTION: HUMANS AND METHODS FOR CONSTRUCTING, IDENTIFYING AND
FILE REFERENCE: GC527
CURRENT APPLICATION NUMBER: US/09/255,501
CURRENT FILING DATE: 1999-02-23
NUMBER OF SEQ ID NOS: 211
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 208
LENGTH: 1052
TYPE: PRT
ORGANISM: Homo sapiens
US-09-255-501-208

Query Match 40.2%; Score 45; DB 4; Length 1052;
Best Local Similarity 38.1%; Pred. No. 3.4e+02;
Matches 8; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 MADNGTIVEELKOLLEQNL 21
DB 747 MPDTGANIPALNELLSVNM 767

RESULT 41
US-09-060-854B-7
Sequence 7, Application US/09060854B
Patent No. 6642011
GENERAL INFORMATION:
APPLICANT: Betell, David Aaron
TITLE OF INVENTION: Human Protease and Use of Such Protease for Pharmaceutical
TITLE OF INVENTION: Applications and for Reducing the Allergenicity of No. 6642011-H
FILE REFERENCE: GC532
CURRENT APPLICATION NUMBER: US/09/060,854B
CURRENT FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 7
LENGTH: 1052
TYPE: PRT
ORGANISM: Homo sapien
US-09-060-854B-7

Query Match 40.2%; Score 45; DB 4; Length 1052;
Best Local Similarity 38.1%; Pred. No. 3.4e+02;

Matches 8; Conservative 3; Mismatches 10; Indels 0; Gaps 0;
QY 1 MADNGTIVEELKOLLEQNL 21
DB 747 MPDTGANIPALNELLSVNM 767

RESULT 42
US-09-891-711-4
Sequence 4, Application US/09891711
Patent No. 6723553
GENERAL INFORMATION:
APPLICANT: Pharmacia AB
TITLE OF INVENTION: Promoter Sequences
FILE REFERENCE: 00130
CURRENT APPLICATION NUMBER: US/09/891,711
CURRENT FILING DATE: 2001-06-26
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 1052
TYPE: PRT
ORGANISM: Homo sapiens
US-09-891-711-4

Query Match 40.2%; Score 45; DB 4; Length 1052;
Best Local Similarity 38.1%; Pred. No. 3.4e+02;
Matches 8; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 MADNGTIVEELKOLLEQNL 21
DB 747 MPDTGANIPALNELLSVNM 767

RESULT 43
US-09-891-711-6
Sequence 6, Application US/09891711
Patent No. 6723553
GENERAL INFORMATION:
APPLICANT: Pharmacia AB
TITLE OF INVENTION: Promoter Sequences
FILE REFERENCE: 00130
CURRENT APPLICATION NUMBER: US/09/891,711
CURRENT FILING DATE: 2001-06-26
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 1052
TYPE: PRT
ORGANISM: Cricetus griseus
US-09-891-711-6

Query Match 40.2%; Score 45; DB 4; Length 1052;
Best Local Similarity 38.1%; Pred. No. 3.4e+02;
Matches 8; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 MADNGTIVEELKOLLEQNL 21
DB 747 MPDTGANIPALNELLSVNM 767

RESULT 44
US-09-949-016-6413
Sequence 6413, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755

;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 6413
;; LENGTH: 1052
;; TYPE: PRT
;; ORGANISM: Human
US-09-949-016-6413

Query Match 40.2%; Score 45; DB 4; Length 1052;
Best Local Similarity 38.1%; Pred. No. 3.4e+02;
Matches 8; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 MADNGTIVTEELKOLLEQNL 21
DB 747 MPDTGANIPALNELLSVNM 767

RESULT 45
US-09-060-872A-208
; Sequence 208, Application US/09060872A
; Patent No. 6835550
; GENERAL INFORMATION:
; APPLICANT: Estell, David
; TITLE OF INVENTION: MUTANT PROTEINS HAVING LOWER ALLERGENIC RESPONSE IN
; TITLE OF INVENTION: HUMANS AND METHODS FOR CONSTRUCTING, IDENTIFYING AND
; FILE REFERENCE: GC527
; CURRENT APPLICATION NUMBER: US/09/060,872A
; CURRENT FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 211
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 208
; LENGTH: 1052
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-060-872A-208

Query Match 40.2%; Score 45; DB 4; Length 1052;
Best Local Similarity 38.1%; Pred. No. 3.4e+02;
Matches 8; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 MADNGTIVTEELKOLLEQNL 21
DB 747 MPDTGANIPALNELLSVNM 767

RESULT 46
US-09-500-135C-208
; Sequence 208, Application US/09500135C
; Patent No. 6838269
; GENERAL INFORMATION:
; APPLICANT: Estell, David A.
; APPLICANT: Harding, Fiona A.
; TITLE OF INVENTION: PROTEINS PRODUCING AN ALTERED IMMUNOGENIC RESPONSE AND
; FILE REFERENCE: A-68893/DJB/DAY
; CURRENT APPLICATION NUMBER: US/09/500,135C
; CURRENT FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: US 09/060,872
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 236
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 208
; LENGTH: 1052
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-500-135C-208

Query Match 40.2%; Score 45; DB 4; Length 1052;
Best Local Similarity 38.1%; Pred. No. 3.4e+02;
Matches 8; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 MADNGTIVTEELKOLLEQNL 21
DB 747 MPDTGANIPALNELLSVNM 767

RESULT 47
US-09-949-016-10687
; Sequence 10687, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10687
; LENGTH: 1058
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10687

Query Match 40.2%; Score 45; DB 4; Length 1058;
Best Local Similarity 38.1%; Pred. No. 3.5e+02;
Matches 8; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 MADNGTIVTEELKOLLEQNL 21
DB 753 MPDTGANIPALNELLSVNM 773

RESULT 48
US-09-476-242-2
; Sequence 2, Application US/09476242
; Patent No. 6889879
; GENERAL INFORMATION:
; APPLICANT: BARNETT, Susan
; APPLICANT: HARTEG, Karin
; APPLICANT: MARTIN, Eric
; TITLE OF INVENTION: MODIFIED HIV ENV POLYPEPTIDES
; FILE REFERENCE: 1605.002
; CURRENT APPLICATION NUMBER: US/09/476,242
; CURRENT FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 847
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-09-476-242-2

Query Match 39.7%; Score 44.5; DB 4; Length 847;
Best Local Similarity 45.0%; Pred. No. 3.2e+02;
Matches 9; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

QY 4 NGTIVTEELKOLLEQNL 22
DB 401 NGTIVTEELKOLLEQNL 420

RESULT 49
US-09-621-976-4009
Sequence 4009, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jober, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO: 4009
LENGTH: 93
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: -58..-1
US-09-621-976-4009

Query Match 39.3%; Score 44; DB 4; Length 93;
Best Local Similarity 37.5%; Pred. No. 32;
Matches 9; Conservative 7; Mismatches 6; Indels 2; Gaps 1;

QY 1 MADNGTITVEE-LKOLLEQNLV 22
DB 9 LSAQGTVTFFEDVAVKFTQEEML 32

RESULT 50
US-09-107-532A-6600
Sequence 6600, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucet-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Atinello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 6600:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...114
SEQUENCE DESCRIPTION: SEQ ID NO: 6600:
US-09-107-532A-6600

Query Match 39.3%; Score 44; DB 4; Length 114;
Best Local Similarity 42.9%; Pred. No. 40;
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKOLLEQNL 21
DB 49 LIDSGAETVGEVSMILDYFNL 69

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OM protein - protein search, using sw model

Run on: May 11, 2005, 21:23:25 ; Search time 85.6596 Seconds

(without alignments)
85.795 Million cell updates/sec

Title: US-10-712-812-5

Sequence: 1 MADNGRTYBELKQLLEQNNLV 22

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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20: /cgn2_6/prodata/2/pubppa/US88_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 4 | 112 | 100.0 | 221 | 16 | US-10-839-729-6 |
| 5 | 112 | 100.0 | 221 | 16 | US-10-839-729-6 |
| 6 | 112 | 100.0 | 221 | 16 | US-10-839-729-6 |
| 7 | 112 | 100.0 | 221 | 16 | US-10-839-729-6 |
| 8 | 112 | 100.0 | 221 | 16 | US-10-839-729-6 |
| 9 | 112 | 100.0 | 221 | 16 | US-10-839-729-6 |
| 10 | 112 | 100.0 | 221 | 16 | US-10-839-729-6 |
| 11 | 112 | 100.0 | 221 | 16 | US-10-839-729-6 |
| 12 | 112 | 100.0 | 221 | 16 | US-10-839-729-6 |
| 13 | 112 | 100.0 | 221 | 16 | US-10-839-729-6 |

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| 14 | 53.5 | 47.8 | 523 | 15 | US-10-425-114-57880 | Sequence 57880, A |
| 15 | 51.5 | 46.0 | 855 | 14 | US-10-369-294-11 | Sequence 11, App1 |
| 16 | 51.5 | 46.0 | 855 | 14 | US-10-369-294-11 | Sequence 12, App1 |
| 17 | 51 | 45.5 | 54 | 9 | US-09-864-761-39008 | Sequence 39008, A |
| 18 | 51 | 45.5 | 206 | 10 | US-09-873-546-10 | Sequence 10, App1 |
| 19 | 51 | 45.5 | 206 | 10 | US-10-153-668-214 | Sequence 214, App |
| 20 | 51 | 45.5 | 206 | 14 | US-10-021-660-132 | Sequence 132, App |
| 21 | 51 | 45.5 | 206 | 15 | US-10-231-913-64 | Sequence 64, App1 |
| 22 | 51 | 45.5 | 206 | 15 | US-10-211-462-79 | Sequence 79, App1 |
| 23 | 51 | 45.5 | 206 | 16 | US-10-408-765A-7022 | Sequence 2022, Ap |
| 24 | 51 | 45.5 | 206 | 16 | US-10-804-493-48 | Sequence 48, App1 |
| 25 | 51 | 45.5 | 209 | 15 | US-10-231-913-66 | Sequence 66, App1 |
| 26 | 51 | 45.5 | 351 | 15 | US-10-282-1122A-51593 | Sequence 51593, A |
| 27 | 50 | 44.6 | 92 | 15 | US-10-424-599-219887 | Sequence 219887, |
| 28 | 50 | 44.6 | 174 | 16 | US-10-437-963-186189 | Sequence 186189, |
| 29 | 50 | 44.6 | 469 | 15 | US-10-417-700A-49 | Sequence 49, App1 |
| 30 | 50 | 44.6 | 546 | 15 | US-10-424-599-203557 | Sequence 203557, |
| 31 | 50 | 44.6 | 549 | 15 | US-10-425-114-54704 | Sequence 54704, A |
| 32 | 50 | 44.6 | 673 | 15 | US-10-282-1122A-76721 | Sequence 76721, A |
| 33 | 49 | 43.8 | 123 | 10 | US-09-953-348-132 | Sequence 132, App |
| 34 | 49 | 43.8 | 123 | 14 | US-10-267-255-132 | Sequence 63, App1 |
| 35 | 48 | 42.9 | 206 | 15 | US-10-231-913-63 | Sequence 63, App1 |
| 36 | 48 | 42.9 | 206 | 15 | US-10-231-913-65 | Sequence 65, App1 |
| 37 | 48 | 42.9 | 206 | 15 | US-10-231-913-67 | Sequence 67, App1 |
| 38 | 48 | 42.9 | 299 | 16 | US-10-437-963-124248 | Sequence 124248, |
| 39 | 48 | 42.9 | 401 | 15 | US-10-369-493-10440 | Sequence 10440, A |
| 40 | 48 | 42.9 | 4437 | 14 | US-10-314-657-45 | Sequence 45, App1 |
| 41 | 48 | 42.9 | 4437 | 17 | US-10-473-193-45 | Sequence 45, App1 |
| 42 | 47 | 42.0 | 159 | 15 | US-10-429-812-4 | Sequence 4, App1 |
| 43 | 47 | 42.0 | 159 | 15 | US-10-612-779-30 | Sequence 30, App1 |
| 44 | 47 | 42.0 | 159 | 17 | US-10-823-397-33 | Sequence 33, App1 |
| 45 | 47 | 42.0 | 508 | 16 | US-10-686-947-238 | Sequence 238, App |
| 46 | 47 | 42.0 | 508 | 16 | US-10-686-947-266 | Sequence 266, App |
| 47 | 47 | 42.0 | 509 | 16 | US-10-686-947-240 | Sequence 240, App |
| 48 | 47 | 42.0 | 659 | 15 | US-10-369-493-2600 | Sequence 2600, Ap |
| 49 | 47 | 42.0 | 987 | 14 | US-10-156-761-14515 | Sequence 14515, A |
| 50 | 46.5 | 41.5 | 428 | 15 | US-10-282-1122A-77230 | Sequence 77230, A |
| 51 | 46.5 | 41.5 | 849 | 10 | US-09-899-575-23 | Sequence 23, App1 |
| 52 | 46.5 | 41.5 | 849 | 14 | US-10-190-435-148 | Sequence 148, App |
| 53 | 46 | 41.1 | 183 | 15 | US-10-425-114-49684 | Sequence 49684, A |
| 54 | 46 | 41.1 | 216 | 17 | US-10-470-048B-286 | Sequence 286, App |
| 55 | 46 | 41.1 | 224 | 16 | US-10-767-701-39143 | Sequence 39143, A |
| 56 | 46 | 41.1 | 300 | 14 | US-10-272-419-26 | Sequence 26, App1 |
| 57 | 46 | 41.1 | 513 | 16 | US-10-437-963-173217 | Sequence 173217, |
| 58 | 46 | 41.1 | 516 | 17 | US-10-781-102-1 | Sequence 1, App1 |
| 59 | 46 | 41.1 | 525 | 15 | US-10-425-114-64587 | Sequence 64587, A |
| 60 | 46 | 41.1 | 536 | 17 | US-10-781-102-3 | Sequence 3, App1 |
| 61 | 46 | 41.1 | 536 | 17 | US-10-815-392-1 | Sequence 1, App1 |
| 62 | 46 | 41.1 | 545 | 15 | US-10-282-1122A-54546 | Sequence 54546, A |
| 63 | 46 | 41.1 | 572 | 9 | US-09-986-632-10 | Sequence 10, App1 |
| 64 | 46 | 41.1 | 792 | 13 | US-10-025-380-1127 | Sequence 1127, Ap |
| 65 | 45.5 | 40.6 | 175 | 15 | US-10-425-114-44519 | Sequence 44519, A |
| 66 | 45.5 | 40.6 | 202 | 15 | US-10-424-599-213143 | Sequence 213143, |
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| 68 | 45 | 40.2 | 60 | 17 | US-10-781-102-13 | Sequence 13, App1 |
| 69 | 45 | 40.2 | 126 | 15 | US-10-424-599-147399 | Sequence 147399, |
| 70 | 45 | 40.2 | 137 | 15 | US-10-425-114-51360 | Sequence 51360, A |
| 71 | 45 | 40.2 | 138 | 15 | US-10-424-599-188811 | Sequence 188811, |
| 72 | 45 | 40.2 | 259 | 15 | US-10-424-599-277269 | Sequence 277269, |
| 73 | 45 | 40.2 | 339 | 14 | US-10-029-386-3201 | Sequence 3201, A |
| 74 | 45 | 40.2 | 336 | 15 | US-10-424-599-165657 | Sequence 165657, |
| 75 | 45 | 40.2 | 462 | 15 | US-10-282-1122A-53097 | Sequence 53097, A |
| 76 | 45 | 40.2 | 467 | 15 | US-10-104-047-2347 | Sequence 2347, Ap |
| 77 | 45 | 40.2 | 508 | 16 | US-10-686-947-174 | Sequence 174, App |
| 78 | 45 | 40.2 | 534 | 9 | US-09-883-825-27 | Sequence 27, App1 |
| 79 | 45 | 40.2 | 547 | 16 | US-10-437-963-179668 | Sequence 179668, |
| 80 | 45 | 40.2 | 636 | 15 | US-10-282-1122A-60575 | Sequence 60575, A |
| 81 | 45 | 40.2 | 633 | 9 | US-09-815-242-11334 | Sequence 11334, A |
| 82 | 45 | 40.2 | 643 | 15 | US-10-282-1122A-58503 | Sequence 58503, A |
| 83 | 45 | 40.2 | 666 | 15 | US-10-264-231-2631 | Sequence 2631, Ap |
| 84 | 45 | 40.2 | 808 | 15 | US-10-104-047-23224 | Sequence 23224, Ap |
| 85 | 45 | 40.2 | 1052 | 9 | US-09-060-8545-7 | Sequence 7, App1 |

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| 87 | 45 | 40.2 | 1052 | 9 | US-09-891-711-4 | Sequence 4, Appli |
| 88 | 45 | 40.2 | 1052 | 9 | US-09-891-711-6 | Sequence 6, Appli |
| 89 | 45 | 40.2 | 1052 | 15 | US-10-665-689-6 | Sequence 6, Appli |
| 90 | 45 | 40.2 | 1052 | 16 | US-10-829-118-4 | Sequence 4, Appli |
| 91 | 45 | 40.2 | 1052 | 16 | US-10-829-118-6 | Sequence 6, Appli |
| 92 | 45 | 40.2 | 1696 | 16 | US-10-408-765A-822 | Sequence 822, App |
| 93 | 45 | 40.2 | 1720 | 15 | US-10-161-927-8 | Sequence 8, Appli |
| 94 | 44.5 | 39.7 | 159 | 15 | US-10-425-114-43153 | Sequence 43153, A |
| 95 | 44.5 | 39.7 | 171 | 15 | US-10-425-114-47363 | Sequence 47363, A |
| 96 | 44.5 | 39.7 | 258 | 15 | US-10-424-599-218227 | Sequence 218227, A |
| 97 | 44.5 | 39.7 | 417 | 15 | US-10-425-114-38139 | Sequence 38139, A |
| 98 | 44.5 | 39.7 | 417 | 15 | US-10-369-493-21136 | Sequence 21136, A |
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| 101 | 44.5 | 39.7 | 502 | 15 | US-10-425-114-40675 | Sequence 40675, A |
| 102 | 44.5 | 39.7 | 542 | 15 | US-10-424-599-218225 | Sequence 218225, A |
| 103 | 44.5 | 39.7 | 549 | 9 | US-09-828-313-39 | Sequence 39, Appli |
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| 105 | 44.5 | 39.7 | 619 | 9 | US-09-891-609-4 | Sequence 4, Appli |
| 106 | 44.5 | 39.7 | 646 | 9 | US-09-891-609-2 | Sequence 2, Appli |
| 107 | 44.5 | 39.7 | 842 | 14 | US-10-190-435-2 | Sequence 2, Appli |
| 108 | 44.5 | 39.7 | 842 | 14 | US-10-241-009-2 | Sequence 2, Appli |
| 109 | 44.5 | 39.7 | 842 | 14 | US-10-190-434B-2 | Sequence 2, Appli |
| 110 | 44.5 | 39.7 | 842 | 14 | US-10-190-305A-2 | Sequence 2, Appli |
| 111 | 44.5 | 39.7 | 847 | 9 | US-09-476-242-2 | Sequence 2, Appli |
| 112 | 44 | 39.3 | 68 | 15 | US-10-424-599-161357 | Sequence 161357, A |
| 113 | 44 | 39.3 | 74 | 15 | US-10-424-599-146899 | Sequence 146899, A |
| 114 | 44 | 39.3 | 143 | 11 | US-09-978-360A-641 | Sequence 641, App |
| 115 | 44 | 39.3 | 157 | 15 | US-10-369-493-207 | Sequence 207, App |
| 116 | 44 | 39.3 | 182 | 15 | US-10-424-599-199507 | Sequence 199507, A |
| 117 | 44 | 39.3 | 196 | 16 | US-10-437-963-102544 | Sequence 102544, A |
| 118 | 44 | 39.3 | 196 | 16 | US-10-437-963-200009 | Sequence 200009, A |
| 119 | 44 | 39.3 | 200 | 15 | US-10-424-599-236486 | Sequence 236486, A |
| 120 | 44 | 39.3 | 206 | 15 | US-10-231-913-6 | Sequence 6, Appli |
| 121 | 44 | 39.3 | 257 | 15 | US-10-425-114-44806 | Sequence 44806, A |
| 122 | 44 | 39.3 | 273 | 17 | US-10-729-571B-48 | Sequence 48, Appli |
| 123 | 44 | 39.3 | 277 | 15 | US-10-282-122A-57733 | Sequence 57733, A |
| 124 | 44 | 39.3 | 286 | 16 | US-10-437-963-201175 | Sequence 201175, A |
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| 126 | 44 | 39.3 | 308 | 15 | US-10-369-493-23066 | Sequence 23066, A |
| 127 | 44 | 39.3 | 316 | 15 | US-10-425-114-55782 | Sequence 55782, A |
| 128 | 44 | 39.3 | 331 | 15 | US-10-424-599-276035 | Sequence 276035, A |
| 129 | 44 | 39.3 | 428 | 16 | US-10-437-963-141938 | Sequence 141938, A |
| 130 | 44 | 39.3 | 473 | 14 | US-10-354-358-96 | Sequence 96, Appli |
| 131 | 44 | 39.3 | 476 | 15 | US-10-264-049-22925 | Sequence 22925, Ap |
| 132 | 44 | 39.3 | 480 | 16 | US-10-437-963-201442 | Sequence 201442, A |
| 133 | 44 | 39.3 | 491 | 9 | US-09-815-242-5671 | Sequence 5671, Ap |
| 134 | 44 | 39.3 | 504 | 9 | US-09-815-242-12692 | Sequence 12692, A |
| 135 | 44 | 39.3 | 511 | 15 | US-10-282-122A-44428 | Sequence 44428, A |
| 136 | 44 | 39.3 | 533 | 16 | US-10-437-963-200006 | Sequence 200006, A |
| 137 | 44 | 39.3 | 545 | 14 | US-10-192-419-2 | Sequence 2, Appli |
| 138 | 44 | 39.3 | 553 | 15 | US-10-369-493-17467 | Sequence 17467, A |
| 139 | 44 | 39.3 | 553 | 15 | US-10-424-599-236485 | Sequence 236485, A |
| 140 | 44 | 39.3 | 571 | 15 | US-10-369-493-39 | Sequence 39, Appli |
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| 143 | 43.5 | 38.8 | 429 | 15 | US-10-282-122A-75835 | Sequence 75835, A |
| 144 | 43.5 | 38.8 | 477 | 9 | US-09-815-242-13991 | Sequence 13991, A |
| 145 | 43.5 | 38.8 | 500 | 17 | US-10-866-527-38 | Sequence 38, Appli |
| 146 | 43.5 | 38.8 | 530 | 16 | US-10-437-963-153480 | Sequence 153480, A |
| 147 | 43.5 | 38.8 | 619 | 15 | US-10-369-493-19203 | Sequence 19203, A |
| 148 | 43.5 | 38.8 | 673 | 14 | US-10-156-761-11243 | Sequence 11243, A |
| 149 | 43.5 | 38.8 | 999 | 16 | US-10-437-963-117353 | Sequence 117353, A |
| 150 | 43 | 38.4 | 42 | 14 | US-10-029-386-31644 | Sequence 31644, A |
| 151 | 43 | 38.4 | 83 | 15 | US-10-424-599-194945 | Sequence 194945, A |
| 152 | 43 | 38.4 | 90 | 15 | US-10-335-977-8761 | Sequence 8761, Ap |
| 153 | 43 | 38.4 | 172 | 15 | US-10-369-493-21205 | Sequence 21205, A |
| 154 | 43 | 38.4 | 172 | 15 | US-10-282-122A-68573 | Sequence 68573, A |
| 155 | 43 | 38.4 | 196 | 9 | US-09-764-877-1830 | Sequence 1830, Ap |
| 156 | 43 | 38.4 | 196 | 15 | US-10-242-515-1830 | Sequence 1830, Ap |
| 157 | 43 | 38.4 | 210 | 15 | US-10-425-114-40176 | Sequence 40176, A |
| 158 | 43 | 38.4 | 210 | 15 | US-10-767-701-36983 | Sequence 36983, A |
| 159 | 43 | 38.4 | 263 | 15 | US-10-335-977-8763 | Sequence 8763, Ap |
| 160 | 43 | 38.4 | 304 | 15 | US-10-424-599-280749 | Sequence 280749, A |
| 161 | 43 | 38.4 | 311 | 14 | US-10-219-810-49 | Sequence 49, Appli |
| 162 | 43 | 38.4 | 325 | 15 | US-10-424-599-198782 | Sequence 198782, A |
| 163 | 43 | 38.4 | 394 | 16 | US-10-451-467A-510 | Sequence 510, App |
| 164 | 43 | 38.4 | 407 | 15 | US-10-108-260A-6092 | Sequence 4092, Ap |
| 165 | 43 | 38.4 | 453 | 14 | US-10-156-761-12790 | Sequence 12790, A |
| 166 | 43 | 38.4 | 467 | 15 | US-10-417-700A-39 | Sequence 39, Appli |
| 167 | 43 | 38.4 | 469 | 15 | US-10-369-493-2943 | Sequence 2943, Ap |
| 168 | 43 | 38.4 | 490 | 8 | US-08-781-986A-5212 | Sequence 5212, Ap |
| 169 | 43 | 38.4 | 490 | 15 | US-10-329-624-5212 | Sequence 5212, Ap |
| 170 | 43 | 38.4 | 492 | 15 | US-10-424-599-272777 | Sequence 272777, A |
| 171 | 43 | 38.4 | 510 | 15 | US-10-369-493-56 | Sequence 56, Appli |
| 172 | 43 | 38.4 | 521 | 15 | US-09-820-843A-93 | Sequence 93, Appli |
| 173 | 43 | 38.4 | 555 | 15 | US-10-282-122A-67921 | Sequence 67921, A |
| 174 | 43 | 38.4 | 567 | 15 | US-10-425-114-69463 | Sequence 69463, A |
| 175 | 43 | 38.4 | 587 | 15 | US-10-282-122A-57731 | Sequence 57731, A |
| 176 | 43 | 38.4 | 594 | 15 | US-10-369-493-3337 | Sequence 3337, Ap |
| 177 | 43 | 38.4 | 1893 | 15 | US-10-296-734-39 | Sequence 399, App |
| 178 | 43 | 38.4 | 1896 | 15 | US-10-326-734-333 | Sequence 393, App |
| 179 | 43 | 38.4 | 5245 | 14 | US-10-329-079-45 | Sequence 11, Appli |
| 180 | 43 | 38.4 | 5245 | 14 | US-10-329-079-45 | Sequence 405, App |
| 181 | 43 | 38.4 | 5747 | 15 | US-10-296-734-405 | Sequence 221216, A |
| 182 | 42.5 | 37.9 | 114 | 15 | US-10-424-599-221216 | Sequence 221216, A |
| 183 | 42.5 | 37.9 | 424 | 15 | US-10-369-493-232 | Sequence 232, App |
| 184 | 42.5 | 37.9 | 429 | 9 | US-09-815-242-10098 | Sequence 10098, A |
| 185 | 42.5 | 37.9 | 429 | 15 | US-10-369-493-770 | Sequence 770, App |
| 186 | 42.5 | 37.9 | 429 | 15 | US-10-282-122A-56485 | Sequence 56485, A |
| 187 | 42.5 | 37.9 | 435 | 15 | US-10-282-122A-59565 | Sequence 59565, A |
| 188 | 42.5 | 37.9 | 437 | 14 | US-10-156-761-14620 | Sequence 14620, A |
| 189 | 42.5 | 37.9 | 506 | 17 | US-10-866-527-118 | Sequence 118, App |
| 190 | 42.5 | 37.9 | 546 | 11 | US-09-764-875-1182 | Sequence 112, Ap |
| 191 | 42.5 | 37.9 | 568 | 11 | US-09-764-875-8122 | Sequence 833, App |
| 192 | 42.5 | 37.9 | 883 | 16 | US-10-441-926-2 | Sequence 2, Appli |
| 193 | 42.5 | 37.9 | 883 | 16 | US-10-441-949-2 | Sequence 2, Appli |
| 194 | 42 | 37.5 | 44 | 10 | US-09-877-843-84 | Sequence 84, Appli |
| 195 | 42 | 37.5 | 78 | 15 | US-10-369-493-20021 | Sequence 20021, A |
| 196 | 42 | 37.5 | 82 | 15 | US-10-424-599-180924 | Sequence 180924, A |
| 197 | 42 | 37.5 | 94 | 15 | US-10-424-599-228445 | Sequence 228445, A |
| 198 | 42 | 37.5 | 117 | 15 | US-10-335-977-8014 | Sequence 8014, Ap |
| 199 | 42 | 37.5 | 127 | 15 | US-10-424-599-161942 | Sequence 161942, A |
| 200 | 42 | 37.5 | 155 | 16 | US-10-437-963-166917 | Sequence 166917, A |
| 201 | 42 | 37.5 | 163 | 15 | US-10-424-599-148963 | Sequence 148963, A |
| 202 | 42 | 37.5 | 169 | 16 | US-10-767-701-52386 | Sequence 52386, A |
| 203 | 42 | 37.5 | 189 | 16 | US-10-767-701-32627 | Sequence 32627, A |
| 204 | 42 | 37.5 | 202 | 15 | US-10-424-599-271745 | Sequence 271745, A |
| 205 | 42 | 37.5 | 207 | 15 | US-10-424-599-249257 | Sequence 249257, A |
| 206 | 42 | 37.5 | 208 | 16 | US-10-767-701-33537 | Sequence 33537, A |
| 207 | 42 | 37.5 | 225 | 15 | US-10-282-122A-78029 | Sequence 78029, A |
| 208 | 42 | 37.5 | 244 | 15 | US-10-369-493-2951 | Sequence 2951, Ap |
| 209 | 42 | 37.5 | 295 | 15 | US-10-425-114-53449 | Sequence 53449, A |
| 210 | 42 | 37.5 | 305 | 15 | US-10-425-114-70080 | Sequence 70080, A |
| 211 | 42 | 37.5 | 305 | 16 | US-10-767-701-44602 | Sequence 44602, A |
| 212 | 42 | 37.5 | 315 | 16 | US-10-437-963-116503 | Sequence 116503, A |
| 213 | 42 | 37.5 | 324 | 15 | US-10-282-122A-57090 | Sequence 57090, A |
| 214 | 42 | 37.5 | 331 | 15 | US-10-424-599-238604 | Sequence 238604, A |
| 215 | 42 | 37.5 | 347 | 15 | US-10-425-114-38844 | Sequence 38844, A |
| 216 | 42 | 37.5 | 351 | 14 | US-10-033-585-7371 | Sequence 7371, Ap |
| 217 | 42 | 37.5 | 357 | 15 | US-10-424-599-226137 | Sequence 226137, A |
| 218 | 42 | 37.5 | 397 | 16 | US-10-437-963-143589 | Sequence 143589, A |
| 219 | 42 | 37.5 | 423 | 15 | US-10-369-493-6746 | Sequence 6746, Ap |
| 220 | 42 | 37.5 | 450 | 15 | US-10-282-122A-69508 | Sequence 69508, A |
| 221 | 42 | 37.5 | 451 | 15 | US-10-282-122A-67651 | Sequence 67651, A |
| 222 | 42 | 37.5 | 460 | 15 | US-10-417-700A-133 | Sequence 133, App |
| 223 | 42 | 37.5 | 464 | 15 | US-10-369-493-7005 | Sequence 7005, Ap |
| 224 | 42 | 37.5 | 467 | 9 | US-09-875-573-17 | Sequence 17, Appli |
| 225 | 42 | 37.5 | 467 | 9 | US-09-875-573-19 | Sequence 19, Appli |
| 226 | 42 | 37.5 | 467 | 9 | US-09-875-573-21 | Sequence 21, Appli |
| 227 | 42 | 37.5 | 468 | 9 | US-09-875-573-23 | Sequence 23, Appli |
| 228 | 42 | 37.5 | 468 | 9 | US-09-875-573-25 | Sequence 25, Appli |
| 229 | 42 | 37.5 | 468 | 9 | US-09-875-573-27 | Sequence 27, Appli |
| 230 | 42 | 37.5 | 481 | 15 | US-10-425-114-53209 | Sequence 53209, A |
| 231 | 42 | 37.5 | 481 | 15 | US-10-425-114-59273 | Sequence 59273, A |
| 232 | 42 | 37.5 | 481 | 16 | US-10-767-701-46495 | Sequence 46495, A |

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|-----|------|------|------|----|----------------------|--------------------|-----|------|------|------|----|----------------------|---------------------|
| 233 | 42 | 37.5 | 485 | 15 | US-10-425-114-46975 | Sequence 46975, A | 306 | 41 | 36.6 | 329 | 15 | US-10-627-476-306 | Sequence 306, App |
| 234 | 42 | 37.5 | 485 | 15 | US-10-425-114-47502 | Sequence 47502, A | 307 | 41 | 36.6 | 336 | 15 | US-10-425-114-38903 | Sequence 38903, A |
| 235 | 42 | 37.5 | 485 | 15 | US-10-425-114-47600 | Sequence 47600, A | 308 | 41 | 36.6 | 367 | 16 | US-10-786-720-48 | Sequence 48, App1 |
| 236 | 42 | 37.5 | 485 | 15 | US-10-425-114-53351 | Sequence 53351, A | 309 | 41 | 36.6 | 416 | 15 | US-10-335-977-8816 | Sequence 8816, Ap |
| 237 | 42 | 37.5 | 485 | 15 | US-10-425-114-53175 | Sequence 53175, A | 310 | 41 | 36.6 | 421 | 15 | US-10-335-977-8817 | Sequence 8817, Ap |
| 238 | 42 | 37.5 | 485 | 15 | US-10-425-114-59189 | Sequence 59189, A | 311 | 41 | 36.6 | 421 | 15 | US-10-335-977-8818 | Sequence 8818, Ap |
| 239 | 42 | 37.5 | 485 | 15 | US-10-425-114-55993 | Sequence 55993, A | 312 | 41 | 36.6 | 430 | 15 | US-10-320-797-3201 | Sequence 3201, Ap |
| 240 | 42 | 37.5 | 485 | 15 | US-10-425-114-62688 | Sequence 62688, A | 313 | 41 | 36.6 | 455 | 15 | US-10-369-493-18160 | Sequence 18160, Ap |
| 241 | 42 | 37.5 | 485 | 15 | US-10-425-114-66115 | Sequence 66115, A | 314 | 41 | 36.6 | 459 | 15 | US-10-627-476-302 | Sequence 302, App |
| 242 | 42 | 37.5 | 485 | 15 | US-10-425-114-72073 | Sequence 72073, A | 315 | 41 | 36.6 | 465 | 15 | US-10-282-122A-66168 | Sequence 66168, A |
| 243 | 42 | 37.5 | 485 | 15 | US-10-425-114-72092 | Sequence 72092, A | 316 | 41 | 36.6 | 471 | 15 | US-10-425-114-55771 | Sequence 55771, A |
| 244 | 42 | 37.5 | 485 | 15 | US-10-425-114-72099 | Sequence 72099, A | 317 | 41 | 36.6 | 477 | 15 | US-10-335-977-9400 | Sequence 9400, Ap |
| 245 | 42 | 37.5 | 490 | 15 | US-10-369-493-16459 | Sequence 16459, A | 318 | 41 | 36.6 | 479 | 9 | US-09-738-626-3765 | Sequence 3765, Ap |
| 246 | 42 | 37.5 | 488 | 16 | US-10-767-701-46009 | Sequence 46009, A | 319 | 41 | 36.6 | 489 | 15 | US-10-282-122A-55280 | Sequence 45280, A |
| 247 | 42 | 37.5 | 518 | 16 | US-10-437-963-195842 | Sequence 195842, A | 320 | 41 | 36.6 | 490 | 14 | US-10-074-155-26 | Sequence 26, App1 |
| 248 | 42 | 37.5 | 531 | 15 | US-10-425-114-70256 | Sequence 70256, A | 321 | 41 | 36.6 | 495 | 10 | US-09-848-806-1 | Sequence 1, App1 |
| 249 | 42 | 37.5 | 537 | 15 | US-10-425-114-70196 | Sequence 70196, A | 322 | 41 | 36.6 | 495 | 15 | US-10-369-493-6635 | Sequence 6635, Ap |
| 250 | 42 | 37.5 | 539 | 15 | US-10-425-114-37249 | Sequence 37249, A | 323 | 41 | 36.6 | 501 | 10 | US-09-848-806-3 | Sequence 3, App1 |
| 251 | 42 | 37.5 | 549 | 16 | US-10-437-963-164372 | Sequence 164372, A | 324 | 41 | 36.6 | 503 | 15 | US-10-424-599-274943 | Sequence 274943, A |
| 252 | 42 | 37.5 | 574 | 16 | US-10-437-963-102998 | Sequence 102998, A | 325 | 41 | 36.6 | 505 | 15 | US-10-282-122A-46385 | Sequence 46385, A |
| 253 | 42 | 37.5 | 608 | 15 | US-10-282-122A-71442 | Sequence 71442, A | 326 | 41 | 36.6 | 542 | 16 | US-10-437-963-196998 | Sequence 196998, A |
| 254 | 42 | 37.5 | 643 | 15 | US-10-282-122A-67033 | Sequence 67033, A | 327 | 41 | 36.6 | 559 | 16 | US-10-437-963-184089 | Sequence 184089, A |
| 255 | 42 | 37.5 | 684 | 15 | US-10-282-122A-47915 | Sequence 47915, A | 328 | 41 | 36.6 | 579 | 17 | US-10-802-682-6 | Sequence 6, App1 |
| 256 | 42 | 37.5 | 689 | 15 | US-10-424-599-187294 | Sequence 187294, A | 329 | 41 | 36.6 | 581 | 16 | US-10-437-963-197001 | Sequence 197001, A |
| 257 | 42 | 37.5 | 698 | 15 | US-10-369-493-13572 | Sequence 13572, A | 330 | 41 | 36.6 | 585 | 15 | US-10-282-122A-71330 | Sequence 71330, A |
| 258 | 42 | 37.5 | 698 | 15 | US-10-369-493-18198 | Sequence 18198, A | 331 | 41 | 36.6 | 596 | 9 | US-09-815-242-5244 | Sequence 5244, Ap |
| 259 | 42 | 37.5 | 703 | 16 | US-10-437-963-166914 | Sequence 166914, A | 332 | 41 | 36.6 | 604 | 9 | US-09-815-242-12525 | Sequence 12525, A |
| 260 | 42 | 37.5 | 722 | 16 | US-10-437-963-166911 | Sequence 166911, A | 333 | 41 | 36.6 | 604 | 15 | US-10-282-122A-43977 | Sequence 43977, A |
| 261 | 42 | 37.5 | 909 | 17 | US-10-826-812-13 | Sequence 13, App1 | 334 | 41 | 36.6 | 608 | 16 | US-10-148-884-2 | Sequence 2, App1 |
| 262 | 42 | 37.5 | 1238 | 16 | US-10-408-765A-2450 | Sequence 2450, Ap | 335 | 41 | 36.6 | 611 | 15 | US-10-369-493-5204 | Sequence 5204, App1 |
| 263 | 42 | 37.5 | 1297 | 14 | US-10-289-776-17 | Sequence 17, App1 | 336 | 41 | 36.6 | 618 | 16 | US-10-437-963-197005 | Sequence 197005, A |
| 264 | 42 | 37.5 | 1297 | 17 | US-10-826-812-6 | Sequence 6, App1 | 337 | 41 | 36.6 | 630 | 15 | US-10-282-122A-60647 | Sequence 60647, A |
| 265 | 42 | 37.5 | 1409 | 15 | US-10-369-493-5387 | Sequence 5387, Ap | 338 | 41 | 36.6 | 695 | 10 | US-09-305-924-13 | Sequence 13, App1 |
| 266 | 42 | 37.5 | 1973 | 16 | US-10-661-809-22 | Sequence 22, App1 | 339 | 41 | 36.6 | 719 | 15 | US-10-425-114-70174 | Sequence 70174, A |
| 267 | 42 | 37.5 | 1973 | 16 | US-10-661-809-24 | Sequence 24, App1 | 340 | 41 | 36.6 | 754 | 15 | US-10-282-122A-66762 | Sequence 66762, A |
| 268 | 42 | 37.5 | 98 | 16 | US-10-437-963-162000 | Sequence 162000, A | 341 | 41 | 36.6 | 831 | 15 | US-10-369-493-18676 | Sequence 18676, A |
| 269 | 41.5 | 37.1 | 85 | 16 | US-10-767-701-53086 | Sequence 53086, A | 342 | 41 | 36.6 | 883 | 17 | US-10-472-928-4222 | Sequence 4222, Ap |
| 270 | 41.5 | 37.1 | 122 | 15 | US-10-424-599-146448 | Sequence 146448, A | 343 | 41 | 36.6 | 887 | 9 | US-09-815-242-13179 | Sequence 13179, A |
| 271 | 41.5 | 37.1 | 121 | 16 | US-10-437-963-137765 | Sequence 137765, A | 344 | 41 | 36.6 | 890 | 15 | US-10-282-122A-74187 | Sequence 74187, A |
| 272 | 41.5 | 37.1 | 261 | 15 | US-10-424-599-16446 | Sequence 146446, A | 345 | 41 | 36.6 | 890 | 16 | US-10-474-776-393 | Sequence 393, App |
| 273 | 41.5 | 37.1 | 368 | 15 | US-10-469-993-12 | Sequence 12, App1 | 346 | 41 | 36.6 | 953 | 10 | US-09-884-696-3 | Sequence 3, App1 |
| 274 | 41.5 | 37.1 | 374 | 16 | US-10-437-963-118336 | Sequence 118336, A | 347 | 41 | 36.6 | 953 | 16 | US-10-148-884-5 | Sequence 5, App1 |
| 275 | 41.5 | 37.1 | 425 | 15 | US-10-282-122A-68661 | Sequence 68661, A | 348 | 41 | 36.6 | 1100 | 17 | US-10-741-849-7239 | Sequence 7239, Ap |
| 276 | 41.5 | 37.1 | 470 | 15 | US-10-425-114-70198 | Sequence 70198, A | 349 | 41 | 36.6 | 1110 | 16 | US-10-437-963-197003 | Sequence 197003, A |
| 277 | 41.5 | 37.1 | 472 | 15 | US-10-437-963-137763 | Sequence 67, App1 | 350 | 41 | 36.6 | 1217 | 16 | US-10-437-963-183891 | Sequence 183891, A |
| 278 | 41.5 | 37.1 | 500 | 16 | US-10-437-963-137763 | Sequence 137763, A | 351 | 41 | 36.6 | 1346 | 16 | US-10-437-963-121131 | Sequence 121131, A |
| 279 | 41.5 | 37.1 | 518 | 16 | US-10-437-963-168927 | Sequence 168927, A | 352 | 41 | 36.6 | 1396 | 15 | US-10-282-122A-69535 | Sequence 69535, A |
| 280 | 41.5 | 37.1 | 561 | 14 | US-10-032-585-7306 | Sequence 7306, Ap | 353 | 40.5 | 36.2 | 111 | 15 | US-10-424-599-265776 | Sequence 265776, A |
| 281 | 41.5 | 37.1 | 603 | 16 | US-10-437-963-161888 | Sequence 161888, A | 354 | 40.5 | 36.2 | 251 | 15 | US-10-369-493-14215 | Sequence 14215, A |
| 282 | 41.5 | 37.1 | 639 | 9 | US-09-854-731-17 | Sequence 17, App1 | 355 | 40.5 | 36.2 | 251 | 15 | US-10-369-493-14944 | Sequence 14944, A |
| 283 | 41 | 36.6 | 40 | 17 | US-10-781-102-9 | Sequence 9, App1 | 356 | 40.5 | 36.2 | 252 | 15 | US-10-369-493-14589 | Sequence 14589, A |
| 284 | 41 | 36.6 | 55 | 15 | US-10-424-599-235854 | Sequence 235854, A | 357 | 40.5 | 36.2 | 257 | 15 | US-10-369-493-11551 | Sequence 11551, A |
| 285 | 41 | 36.6 | 60 | 17 | US-10-781-102-8 | Sequence 8, App1 | 358 | 40.5 | 36.2 | 345 | 16 | US-10-437-963-204556 | Sequence 204556, A |
| 286 | 41 | 36.6 | 63 | 16 | US-10-437-963-182278 | Sequence 182278, A | 359 | 40.5 | 36.2 | 404 | 16 | US-10-437-963-110927 | Sequence 110927, A |
| 287 | 41 | 36.6 | 71 | 9 | US-09-982-809-2 | Sequence 2, App1 | 360 | 40.5 | 36.2 | 459 | 15 | US-10-369-493-2334 | Sequence 2334, Ap |
| 288 | 41 | 36.6 | 71 | 14 | US-10-161-941-11 | Sequence 11, App1 | 361 | 40.5 | 36.2 | 459 | 15 | US-10-369-493-2336 | Sequence 2336, Ap |
| 289 | 41 | 36.6 | 99 | 16 | US-10-437-963-168376 | Sequence 168376, A | 362 | 40.5 | 36.2 | 470 | 16 | US-10-728-195-17 | Sequence 17, App1 |
| 290 | 41 | 36.6 | 133 | 16 | US-10-286-421-28 | Sequence 28, App1 | 363 | 40.5 | 36.2 | 487 | 17 | US-10-866-527-50 | Sequence 50, App1 |
| 291 | 41 | 36.6 | 135 | 16 | US-10-767-701-55426 | Sequence 55426, A | 364 | 40.5 | 36.2 | 493 | 17 | US-10-866-527-130 | Sequence 130, App |
| 292 | 41 | 36.6 | 140 | 15 | US-10-335-977-9398 | Sequence 9398, Ap | 365 | 40.5 | 36.2 | 503 | 9 | US-09-759-841-4 | Sequence 4, App1 |
| 293 | 41 | 36.6 | 147 | 15 | US-10-282-122A-77767 | Sequence 77767, A | 366 | 40.5 | 36.2 | 512 | 17 | US-10-866-527-108 | Sequence 108, App |
| 294 | 41 | 36.6 | 148 | 15 | US-10-424-599-155154 | Sequence 155154, A | 367 | 40 | 35.7 | 39 | 17 | US-10-781-102-11 | Sequence 11, App1 |
| 295 | 41 | 36.6 | 149 | 15 | US-10-369-493-2146 | Sequence 2146, Ap | 368 | 40 | 35.7 | 48 | 17 | US-10-476-447-2 | Sequence 2, App1 |
| 296 | 41 | 36.6 | 157 | 15 | US-10-424-599-236576 | Sequence 236576, A | 369 | 40 | 35.7 | 52 | 13 | US-10-102-265-13 | Sequence 13, App1 |
| 297 | 41 | 36.6 | 158 | 15 | US-10-389-566-511 | Sequence 511, App | 370 | 40 | 35.7 | 53 | 9 | US-09-799-514-16 | Sequence 16, App1 |
| 298 | 41 | 36.6 | 160 | 15 | US-10-108-260A-3318 | Sequence 3318, Ap | 371 | 40 | 35.7 | 71 | 15 | US-10-424-599-176074 | Sequence 176074, A |
| 299 | 41 | 36.6 | 161 | 15 | US-10-369-493-22406 | Sequence 22406, A | 372 | 40 | 35.7 | 90 | 14 | US-10-106-698-5022 | Sequence 5022, Ap |
| 300 | 41 | 36.6 | 164 | 10 | US-09-443-218-2 | Sequence 2, App1 | 373 | 40 | 35.7 | 120 | 15 | US-10-424-599-241329 | Sequence 241329, A |
| 301 | 41 | 36.6 | 164 | 10 | US-09-443-218-4 | Sequence 4, App1 | 374 | 40 | 35.7 | 138 | 15 | US-10-425-114-64012 | Sequence 64012, A |
| 302 | 41 | 36.6 | 164 | 10 | US-09-443-218-5 | Sequence 5, App1 | 375 | 40 | 35.7 | 139 | 15 | US-10-425-114-64012 | Sequence 64012, A |
| 303 | 41 | 36.6 | 164 | 10 | US-09-443-218-7 | Sequence 7, App1 | 376 | 40 | 35.7 | 140 | 15 | US-10-425-114-64012 | Sequence 64012, A |
| 304 | 41 | 36.6 | 264 | 15 | US-10-425-114-38904 | Sequence 38904, A | 377 | 40 | 35.7 | 142 | 16 | US-10-437-963-204004 | Sequence 204004, A |
| 305 | 41 | 36.6 | 309 | 15 | US-10-369-493-10903 | Sequence 10903, A | 378 | 40 | 35.7 | 156 | 15 | US-10-424-599-184133 | Sequence 184133, A |

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| 379 | 40 | 35.7 | 158 | 13 | US-10-102-265-3 | Sequence 3, Appl1 |
| 380 | 40 | 35.7 | 158 | 13 | US-10-102-265-6 | Sequence 6, Appl1 |
| 381 | 40 | 35.7 | 158 | 13 | US-10-424-599-234231 | Sequence 234231, A |
| 382 | 40 | 35.7 | 159 | 13 | US-10-102-265-4 | Sequence 4, Appl1 |
| 383 | 40 | 35.7 | 159 | 13 | US-10-102-265-7 | Sequence 7, Appl1 |
| 384 | 40 | 35.7 | 159 | 13 | US-10-102-265-7 | Sequence 7, Appl1 |
| 385 | 40 | 35.7 | 160 | 15 | US-10-424-599-245344 | Sequence 245344, A |
| 386 | 40 | 35.7 | 166 | 14 | US-10-237-271-18 | Sequence 18, Appl1 |
| 387 | 40 | 35.7 | 166 | 14 | US-10-408-765A-2060 | Sequence 2060, Ap |
| 388 | 40 | 35.7 | 170 | 15 | US-10-425-114-46390 | Sequence 46390, A |
| 389 | 40 | 35.7 | 171 | 16 | US-10-767-701-45361 | Sequence 45361, A |
| 390 | 40 | 35.7 | 176 | 15 | US-10-424-599-242860 | Sequence 242860, A |
| 391 | 40 | 35.7 | 179 | 13 | US-10-102-265-2 | Sequence 2, Appl1 |
| 392 | 40 | 35.7 | 179 | 13 | US-10-102-265-5 | Sequence 5, Appl1 |
| 393 | 40 | 35.7 | 179 | 13 | US-10-102-265-14 | Sequence 14, Appl1 |
| 394 | 40 | 35.7 | 181 | 16 | US-10-102-265-15 | Sequence 15, Appl1 |
| 395 | 40 | 35.7 | 181 | 16 | US-10-767-701-34753 | Sequence 34753, A |
| 396 | 40 | 35.7 | 187 | 9 | US-09-815-153-3 | Sequence 3, Appl1 |
| 397 | 40 | 35.7 | 187 | 9 | US-10-428-487-3 | Sequence 3, Appl1 |
| 398 | 40 | 35.7 | 187 | 15 | US-10-424-599-283060 | Sequence 283060, A |
| 399 | 40 | 35.7 | 191 | 16 | US-10-767-701-45179 | Sequence 45179, A |
| 400 | 40 | 35.7 | 196 | 9 | US-09-815-153-7 | Sequence 7, Appl1 |
| 401 | 40 | 35.7 | 197 | 16 | US-10-437-963-144209 | Sequence 144209, A |
| 402 | 40 | 35.7 | 198 | 9 | US-09-815-153-5 | Sequence 5, Appl1 |
| 403 | 40 | 35.7 | 198 | 15 | US-10-428-487-22 | Sequence 22, Appl1 |
| 404 | 40 | 35.7 | 199 | 15 | US-10-282-122A-52399 | Sequence 52399, A |
| 405 | 40 | 35.7 | 203 | 16 | US-10-767-701-37332 | Sequence 37332, A |
| 406 | 40 | 35.7 | 206 | 16 | US-10-363-829-311 | Sequence 311, App |
| 407 | 40 | 35.7 | 208 | 9 | US-09-988-982-1 | Sequence 1, Appl1 |
| 408 | 40 | 35.7 | 208 | 15 | US-10-131-487A-185 | Sequence 185, App |
| 409 | 40 | 35.7 | 211 | 16 | US-10-767-701-55874 | Sequence 55874, A |
| 410 | 40 | 35.7 | 216 | 9 | US-09-853-450-34 | Sequence 34, Appl |
| 411 | 40 | 35.7 | 217 | 16 | US-10-424-599-184045 | Sequence 184045, A |
| 412 | 40 | 35.7 | 218 | 15 | US-10-478-245-4 | Sequence 4, Appl1 |
| 413 | 40 | 35.7 | 222 | 14 | US-10-296-115-772 | Sequence 772, App |
| 414 | 40 | 35.7 | 222 | 15 | US-10-106-698-5793 | Sequence 5793, Ap |
| 415 | 40 | 35.7 | 223 | 15 | US-10-425-599-254434 | Sequence 254434, A |
| 416 | 40 | 35.7 | 224 | 15 | US-10-425-114-42487 | Sequence 42487, A |
| 417 | 40 | 35.7 | 224 | 15 | US-10-425-114-36966 | Sequence 36966, A |
| 418 | 40 | 35.7 | 224 | 16 | US-10-437-963-200588 | Sequence 200588, A |
| 419 | 40 | 35.7 | 230 | 14 | US-10-237-271-17 | Sequence 17, Appl |
| 420 | 40 | 35.7 | 230 | 15 | US-10-210-130-56 | Sequence 60, Appl |
| 421 | 40 | 35.7 | 230 | 15 | US-10-236-417-60 | Sequence 60, Appl |
| 422 | 40 | 35.7 | 230 | 15 | US-10-236-417-64 | Sequence 64, Appl |
| 423 | 40 | 35.7 | 233 | 16 | US-10-699-156-18 | Sequence 18, Appl |
| 424 | 40 | 35.7 | 234 | 13 | US-10-102-265-1 | Sequence 1, Appl1 |
| 425 | 40 | 35.7 | 234 | 15 | US-10-428-487-1 | Sequence 1, Appl1 |
| 426 | 40 | 35.7 | 234 | 15 | US-10-302-172-950 | Sequence 950, App |
| 427 | 40 | 35.7 | 235 | 9 | US-09-815-153-6 | Sequence 6, Appl1 |
| 428 | 40 | 35.7 | 235 | 14 | US-10-314-657-27 | Sequence 27, Appl |
| 429 | 40 | 35.7 | 235 | 15 | US-10-428-487-84 | Sequence 84, Appl |
| 430 | 40 | 35.7 | 235 | 17 | US-10-473-193-27 | Sequence 27, Appl |
| 431 | 40 | 35.7 | 244 | 15 | US-10-424-599-210083 | Sequence 210083, A |
| 432 | 40 | 35.7 | 244 | 15 | US-10-425-114-39990 | Sequence 39990, A |
| 433 | 40 | 35.7 | 247 | 15 | US-10-369-493-448 | Sequence 448, App |
| 434 | 40 | 35.7 | 248 | 16 | US-10-437-963-169185 | Sequence 169185, A |
| 435 | 40 | 35.7 | 250 | 15 | US-10-282-122A-68953 | Sequence 68953, A |
| 436 | 40 | 35.7 | 254 | 15 | US-10-369-493-20963 | Sequence 20963, A |
| 437 | 40 | 35.7 | 254 | 16 | US-10-767-701-43819 | Sequence 43819, A |
| 438 | 40 | 35.7 | 258 | 15 | US-10-424-599-229486 | Sequence 229486, A |
| 439 | 40 | 35.7 | 263 | 9 | US-09-925-899-991 | Sequence 991, App |
| 440 | 40 | 35.7 | 263 | 10 | US-09-925-299-991 | Sequence 991, App |
| 441 | 40 | 35.7 | 265 | 10 | US-09-975-719-31 | Sequence 31, Appl |
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| 443 | 40 | 35.7 | 268 | 16 | US-10-437-963-192778 | Sequence 192778, A |
| 444 | 40 | 35.7 | 270 | 16 | US-10-437-963-171875 | Sequence 171875, A |
| 445 | 40 | 35.7 | 273 | 15 | US-10-369-493-12865 | Sequence 12865, A |
| 446 | 40 | 35.7 | 282 | 15 | US-10-282-122A-62789 | Sequence 62789, A |
| 447 | 40 | 35.7 | 282 | 15 | US-10-282-122A-64811 | Sequence 64811, A |
| 448 | 40 | 35.7 | 283 | 16 | US-10-437-963-165776 | Sequence 165776, A |
| 449 | 40 | 35.7 | 291 | 9 | US-09-864-761-37074 | Sequence 37074, A |
| 450 | 40 | 35.7 | 294 | 15 | US-10-369-493-18390 | Sequence 18390, A |
| 451 | 40 | 35.7 | 300 | 15 | US-10-424-599-211071 | Sequence 211071, A |
| | 40 | 35.7 | 314 | 15 | US-10-425-114-65717 | Sequence 65717, A |
| 452 | 40 | 35.7 | 316 | 9 | US-09-799-514-11 | Sequence 11, Appl |
| 453 | 40 | 35.7 | 324 | 15 | US-10-094-749-1930 | Sequence 1930, Ap |
| 454 | 40 | 35.7 | 326 | 15 | US-10-282-122A-53226 | Sequence 53226, A |
| 455 | 40 | 35.7 | 326 | 15 | US-10-425-114-51354 | Sequence 51354, A |
| 456 | 40 | 35.7 | 326 | 15 | US-10-425-114-51354 | Sequence 51354, A |
| 457 | 40 | 35.7 | 336 | 15 | US-10-316-223-104617 | Sequence 104617, A |
| 458 | 40 | 35.7 | 340 | 16 | US-10-437-963-104617 | Sequence 104617, A |
| 459 | 40 | 35.7 | 344 | 9 | US-09-925-300-1360 | Sequence 1360, Ap |
| 460 | 40 | 35.7 | 344 | 15 | US-10-369-493-16716 | Sequence 16716, A |
| 461 | 40 | 35.7 | 345 | 14 | US-10-033-201B-263 | Sequence 263, App |
| 462 | 40 | 35.7 | 351 | 15 | US-10-369-493-17093 | Sequence 17093, A |
| 463 | 40 | 35.7 | 351 | 15 | US-10-425-114-63151 | Sequence 63151, A |
| 464 | 40 | 35.7 | 352 | 15 | US-10-425-114-63151 | Sequence 63151, A |
| 465 | 40 | 35.7 | 362 | 15 | US-10-425-114-63151 | Sequence 63151, A |
| 466 | 40 | 35.7 | 379 | 15 | US-10-424-599-274676 | Sequence 274676, A |
| 467 | 40 | 35.7 | 383 | 15 | US-10-425-114-53577 | Sequence 53577, A |
| 468 | 40 | 35.7 | 391 | 15 | US-10-289-762-921 | Sequence 921, App |
| 469 | 40 | 35.7 | 394 | 15 | US-10-108-260A-2699 | Sequence 2699, Ap |
| 470 | 40 | 35.7 | 397 | 14 | US-10-156-761-7779 | Sequence 7779, Ap |
| 471 | 40 | 35.7 | 400 | 16 | US-10-437-963-165037 | Sequence 165037, A |
| 472 | 40 | 35.7 | 408 | 15 | US-10-282-122A-55471 | Sequence 55471, A |
| 473 | 40 | 35.7 | 419 | 16 | US-10-437-963-108808 | Sequence 108808, A |
| 474 | 40 | 35.7 | 444 | 9 | US-09-805-020-53 | Sequence 53, Appl |
| 475 | 40 | 35.7 | 446 | 15 | US-10-424-599-151497 | Sequence 151497, A |
| 476 | 40 | 35.7 | 450 | 15 | US-10-282-122A-71596 | Sequence 71596, A |
| 477 | 40 | 35.7 | 457 | 16 | US-10-437-963-200116 | Sequence 200116, A |
| 478 | 40 | 35.7 | 459 | 15 | US-10-437-963-200116 | Sequence 200116, A |
| 479 | 40 | 35.7 | 463 | 13 | US-10-037-860-13 | Sequence 13, Appl |
| 480 | 40 | 35.7 | 466 | 15 | US-10-417-700A-51 | Sequence 51, Appl |
| 481 | 40 | 35.7 | 469 | 16 | US-10-322-281-834 | Sequence 834, App |
| 482 | 40 | 35.7 | 478 | 15 | US-10-468-406-10 | Sequence 10, Appl |
| 483 | 40 | 35.7 | 484 | 15 | US-10-282-122A-64268 | Sequence 64268, A |
| 484 | 40 | 35.7 | 487 | 15 | US-10-282-122A-52836 | Sequence 52836, A |
| 485 | 40 | 35.7 | 488 | 15 | US-10-425-114-56442 | Sequence 56442, A |
| 486 | 40 | 35.7 | 490 | 17 | US-10-424-599-280137 | Sequence 280137, A |
| 487 | 40 | 35.7 | 490 | 17 | US-10-675-086-24 | Sequence 24, Appl |
| 488 | 40 | 35.7 | 491 | 16 | US-10-282-122A-48421 | Sequence 48421, A |
| 489 | 40 | 35.7 | 494 | 16 | US-10-437-963-180232 | Sequence 180232, A |
| 490 | 40 | 35.7 | 500 | 15 | US-10-424-599-283059 | Sequence 283059, A |
| 491 | 40 | 35.7 | 505 | 15 | US-10-425-114-47312 | Sequence 47312, A |
| 492 | 40 | 35.7 | 508 | 16 | US-10-437-963-155126 | Sequence 155126, A |
| 493 | 40 | 35.7 | 509 | 14 | US-10-097-559-11 | Sequence 11, Appl |
| 494 | 40 | 35.7 | 511 | 15 | US-10-424-599-202766 | Sequence 202766, A |
| 495 | 40 | 35.7 | 521 | 16 | US-10-437-963-200463 | Sequence 200463, A |
| 496 | 40 | 35.7 | 526 | 15 | US-10-424-599-283059 | Sequence 283059, A |
| 497 | 40 | 35.7 | 533 | 16 | US-10-437-963-127855 | Sequence 127855, A |
| 498 | 40 | 35.7 | 535 | 14 | US-10-106-698-5101 | Sequence 5101, Ap |
| 499 | 40 | 35.7 | 538 | 15 | US-10-425-114-53814 | Sequence 53814, A |
| 500 | 40 | 35.7 | 538 | 15 | US-10-424-599-248196 | Sequence 248196, A |
| 501 | 40 | 35.7 | 541 | 15 | US-10-282-122A-77047 | Sequence 77047, A |
| 502 | 40 | 35.7 | 544 | 9 | US-09-841-133-400 | Sequence 400, App |
| 503 | 40 | 35.7 | 544 | 9 | US-09-759-272B-5 | Sequence 5, Appl1 |
| 504 | 40 | 35.7 | 544 | 11 | US-09-809-745-3 | Sequence 3, Appl1 |
| 505 | 40 | 35.7 | 544 | 11 | US-10-289-762-153 | Sequence 153, App |
| 506 | 40 | 35.7 | 544 | 15 | US-10-282-122A-54855 | Sequence 54855, A |
| 507 | 40 | 35.7 | 544 | 16 | US-10-282-122A-55161 | Sequence 55161, A |
| 508 | 40 | 35.7 | 549 | 15 | US-10-470-093-5 | Sequence 5, Appl1 |
| 509 | 40 | 35.7 | 551 | 15 | US-10-259-194A-258 | Sequence 258, App |
| 510 | 40 | 35.7 | 551 | 15 | US-10-369-493-18994 | Sequence 18994, A |
| 511 | 40 | 35.7 | 551 | 15 | US-10-369-493-20184 | Sequence 20184, A |
| 512 | 40 | 35.7 | 553 | 15 | US-10-425-114-37251 | Sequence 37251, A |
| 513 | 40 | 35.7 | 553 | 15 | US-10-425-114-67049 | Sequence 67049, A |
| 514 | 40 | 35.7 | 553 | 15 | US-10-425-114-68488 | Sequence 68488, A |
| 515 | 40 | 35.7 | 555 | 15 | US-10-425-114-37250 | Sequence 37250, A |
| 516 | 40 | 35.7 | 555 | 15 | US-10-425-114-49942 | Sequence 49942, A |
| 517 | 40 | 35.7 | 555 | 15 | US-10-425-114-49943 | Sequence 49943, A |
| 518 | 40 | 35.7 | 555 | 15 | US-10-425-114-63129 | Sequence 63129, A |
| 519 | 40 | 35.7 | 555 | 15 | US-10-425-114-68181 | Sequence 68181, A |
| 520 | 40 | 35.7 | 564 | 15 | US-10-425-114-67773 | Sequence 67773, A |
| 521 | 40 | 35.7 | 572 | 9 | US-09-986-633-8 | Sequence 8, Appl1 |
| 522 | 40 | 35.7 | 572 | 9 | US-09-736-457-1815 | Sequence 1815, Ap |
| 523 | 40 | 35.7 | 572 | 9 | US-09-902-941-1815 | Sequence 1815, Ap |
| 524 | 40 | 35.7 | 572 | 14 | US-10-017-754-1815 | Sequence 1815, Ap |

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| 525 | 40 | 35.7 | 572 | 14 | US-10-180-198-2 | Sequence 2, Appl1 | 598 | 39.5 | 35.3 | 278 | 15 | US-10-282-122A-71303 | Sequence 71303, A |
| 526 | 40 | 35.7 | 572 | 14 | US-10-113-872-1815 | Sequence 1815, Ap | 599 | 39.5 | 35.3 | 221 | 15 | US-10-369-493-114 | Sequence 154, App |
| 527 | 40 | 35.7 | 572 | 14 | US-10-283-017-1815 | Sequence 1815, Ap | 600 | 39.5 | 35.3 | 307 | 15 | US-10-156-761-11788 | Sequence 11788, A |
| 528 | 40 | 35.7 | 580 | 16 | US-10-437-963-199601 | Sequence 199601, | 601 | 39.5 | 35.3 | 335 | 16 | US-10-332-413-32 | Sequence 32, Appl |
| 529 | 40 | 35.7 | 584 | 17 | US-10-472-928-1034 | Sequence 1034, Ap | 602 | 39.5 | 35.3 | 340 | 14 | US-10-177-293-116 | Sequence 116, App |
| 530 | 40 | 35.7 | 600 | 16 | US-10-437-963-104086 | Sequence 104086, | 603 | 39.5 | 35.3 | 376 | 9 | US-09-934-060A-28 | Sequence 28, Appl |
| 531 | 40 | 35.7 | 609 | 15 | US-10-108-260A-3971 | Sequence 3971, Ap | 604 | 39.5 | 35.3 | 460 | 17 | US-10-866-527-42 | Sequence 42, Appl |
| 532 | 40 | 35.7 | 622 | 15 | US-10-282-122A-60827 | Sequence 60827, A | 605 | 39.5 | 35.3 | 474 | 16 | US-10-728-195-18 | Sequence 18, Appl |
| 533 | 40 | 35.7 | 627 | 15 | US-10-425-114-59660 | Sequence 59660, A | 606 | 39.5 | 35.3 | 483 | 15 | US-10-424-599-258507 | Sequence 258507, |
| 534 | 40 | 35.7 | 629 | 14 | US-10-128-714-3099 | Sequence 3099, Ap | 607 | 39.5 | 35.3 | 506 | 9 | US-09-934-060A-24 | Sequence 24, Appl |
| 535 | 40 | 35.7 | 641 | 16 | US-10-437-963-188700 | Sequence 188700, | 608 | 39.5 | 35.3 | 506 | 9 | US-09-934-060A-30 | Sequence 30, Appl |
| 536 | 40 | 35.7 | 647 | 15 | US-10-369-493-23040 | Sequence 23040, A | 609 | 39.5 | 35.3 | 528 | 15 | US-10-371-472-44 | Sequence 44, Appl |
| 537 | 40 | 35.7 | 651 | 16 | US-10-408-765A-1578 | Sequence 1578, Ap | 610 | 39.5 | 35.3 | 554 | 17 | US-10-855-581-18 | Sequence 18, Appl |
| 538 | 40 | 35.7 | 685 | 14 | US-10-128-714-8099 | Sequence 8099, Ap | 611 | 39.5 | 35.3 | 556 | 9 | US-09-934-060A-6 | Sequence 6, Appl1 |
| 539 | 40 | 35.7 | 687 | 16 | US-10-437-963-174167 | Sequence 174167, | 612 | 39.5 | 35.3 | 587 | 14 | US-10-335-394-50 | Sequence 50, Appl |
| 540 | 40 | 35.7 | 703 | 17 | US-10-480-988-2 | Sequence 2, Appl1 | 613 | 39.5 | 35.3 | 585 | 14 | US-10-335-394-56 | Sequence 13, Appl |
| 541 | 40 | 35.7 | 776 | 15 | US-10-424-599-200232 | Sequence 200232, | 614 | 39.5 | 35.3 | 590 | 9 | US-10-425-114-56605 | Sequence 56, Appl |
| 542 | 40 | 35.7 | 809 | 15 | US-10-369-493-16530 | Sequence 16530, A | 615 | 39.5 | 35.3 | 601 | 14 | US-10-335-394-52 | Sequence 52, Appl |
| 543 | 40 | 35.7 | 811 | 15 | US-10-282-122A-45773 | Sequence 45773, A | 616 | 39.5 | 35.3 | 608 | 16 | US-09-738-626-3609 | Sequence 3609, Ap |
| 544 | 40 | 35.7 | 822 | 16 | US-10-645-250A-8 | Sequence 8, Appl1 | 617 | 39.5 | 35.3 | 618 | 17 | US-10-494-672-272 | Sequence 272, App |
| 545 | 40 | 35.7 | 829 | 9 | US-09-925-298-602 | Sequence 602, App | 618 | 39.5 | 35.3 | 625 | 15 | US-10-494-541-60 | Sequence 60, Appl |
| 546 | 40 | 35.7 | 829 | 14 | US-10-102-806-602 | Sequence 602, App | 619 | 39.5 | 35.3 | 625 | 15 | US-10-369-493-19782 | Sequence 19782, A |
| 547 | 40 | 35.7 | 839 | 15 | US-10-424-599-200231 | Sequence 200231, | 620 | 39.5 | 35.3 | 637 | 9 | US-09-815-242-5280 | Sequence 5280, Ap |
| 548 | 40 | 35.7 | 859 | 16 | US-10-437-963-165313 | Sequence 169313, | 621 | 39.5 | 35.3 | 662 | 9 | US-09-815-242-12140 | Sequence 12140, A |
| 549 | 40 | 35.7 | 1004 | 16 | US-10-473-276-3 | Sequence 3, Appl1 | 622 | 39.5 | 35.3 | 662 | 15 | US-10-282-122A-43842 | Sequence 43842, A |
| 550 | 40 | 35.7 | 1024 | 14 | US-10-211-962-41 | Sequence 41, Appl | 623 | 39.5 | 35.3 | 662 | 15 | US-10-282-122A-71137 | Sequence 71137, A |
| 551 | 40 | 35.7 | 1024 | 14 | US-10-211-962-44 | Sequence 44, Appl | 624 | 39.5 | 35.3 | 669 | 15 | US-10-282-122A-48909 | Sequence 48909, A |
| 552 | 40 | 35.7 | 1036 | 16 | US-10-322-281-160 | Sequence 160, App | 625 | 39.5 | 35.3 | 720 | 9 | US-09-934-060A-2 | Sequence 2, Appl1 |
| 553 | 40 | 35.7 | 1038 | 16 | US-10-322-281-157 | Sequence 157, App | 626 | 39.5 | 35.3 | 720 | 9 | US-09-934-060A-4 | Sequence 4, Appl1 |
| 554 | 40 | 35.7 | 1050 | 15 | US-10-425-114-55722 | Sequence 55722, A | 627 | 39.5 | 35.3 | 722 | 15 | US-10-369-493-5651 | Sequence 5651, Ap |
| 555 | 40 | 35.7 | 1253 | 15 | US-10-161-927-32 | Sequence 32, App | 628 | 39.5 | 35.3 | 748 | 15 | US-10-282-122A-48709 | Sequence 48709, A |
| 556 | 40 | 35.7 | 1256 | 16 | US-10-437-963-130209 | Sequence 130209, | 629 | 39.5 | 35.3 | 751 | 15 | US-10-369-493-19004 | Sequence 19004, A |
| 557 | 40 | 35.7 | 1287 | 16 | US-10-437-963-112735 | Sequence 112735, | 630 | 39.5 | 35.3 | 844 | 9 | US-09-991-258-19 | Sequence 19, Appl |
| 558 | 40 | 35.7 | 1394 | 16 | US-10-471-762-9 | Sequence 9, Appl1 | 631 | 39.5 | 35.3 | 844 | 16 | US-10-332-413-6 | Sequence 6, Appl1 |
| 559 | 40 | 35.7 | 1444 | 16 | US-10-609-113-11 | Sequence 11, Appl | 632 | 39.5 | 35.3 | 852 | 16 | US-10-332-413-12 | Sequence 12, Appl |
| 560 | 40 | 35.7 | 1518 | 16 | US-10-383-930-40 | Sequence 40, Appl | 633 | 39.5 | 35.3 | 858 | 16 | US-10-332-413-15 | Sequence 14, Appl |
| 561 | 40 | 35.7 | 1518 | 17 | US-10-797-821-40 | Sequence 40, Appl | 634 | 39.5 | 35.3 | 860 | 14 | US-10-190-435-145 | Sequence 145, App |
| 562 | 40 | 35.7 | 1548 | 16 | US-10-437-963-113738 | Sequence 113738, | 635 | 39.5 | 35.3 | 860 | 14 | US-10-190-435-146 | Sequence 146, App |
| 563 | 40 | 35.7 | 1568 | 14 | US-10-156-761-10037 | Sequence 10037, A | 636 | 39.5 | 35.3 | 14 | 9 | US-09-883-825-28 | Sequence 28, Appl |
| 564 | 40 | 35.7 | 1987 | 14 | US-10-132-382-6 | Sequence 6, Appl1 | 637 | 39.5 | 35.3 | 14 | 16 | US-10-697-894-28 | Sequence 28, Appl |
| 565 | 40 | 35.7 | 2013 | 14 | US-10-132-382-2 | Sequence 2, Appl1 | 638 | 39.5 | 35.3 | 52 | 9 | US-09-764-887-187 | Sequence 187, App |
| 566 | 40 | 35.7 | 2014 | 14 | US-10-132-382-8 | Sequence 8, Appl1 | 639 | 39.5 | 35.3 | 52 | 14 | US-10-073-961-167 | Sequence 167, App |
| 567 | 40 | 35.7 | 2014 | 15 | US-10-220-955-18 | Sequence 18, Appl | 640 | 39.5 | 35.3 | 64 | 9 | US-09-864-761-36928 | Sequence 36928, A |
| 568 | 40 | 35.7 | 2014 | 15 | US-10-415-011-8 | Sequence 8, Appl1 | 641 | 39.5 | 35.3 | 66 | 11 | US-09-864-408A-8998 | Sequence 8998, Ap |
| 569 | 40 | 35.7 | 2040 | 14 | US-10-132-382-4 | Sequence 4, Appl1 | 642 | 39.5 | 35.3 | 74 | 15 | US-10-424-599-144538 | Sequence 144538, |
| 570 | 40 | 35.7 | 2420 | 16 | US-10-437-963-165599 | Sequence 165599, | 643 | 39.5 | 35.3 | 88 | 11 | US-09-864-408A-7318 | Sequence 7318, Ap |
| 571 | 40 | 35.7 | 2477 | 14 | US-10-360-053-28 | Sequence 28, Appl | 644 | 39.5 | 35.3 | 97 | 15 | US-10-335-977-7642 | Sequence 7642, Ap |
| 572 | 40 | 35.7 | 2477 | 16 | US-10-408-765A-238 | Sequence 238, App | 645 | 39.5 | 35.3 | 98 | 15 | US-10-335-977-7641 | Sequence 7641, Ap |
| 573 | 40 | 35.7 | 2541 | 14 | US-10-177-293-470 | Sequence 470, App | 646 | 39.5 | 35.3 | 100 | 16 | US-10-658-834A-290 | Sequence 290, App |
| 574 | 40 | 35.7 | 2541 | 15 | US-10-454-351-30 | Sequence 30, Appl | 647 | 39.5 | 35.3 | 100 | 16 | US-10-658-834A-295 | Sequence 295, App |
| 575 | 40 | 35.7 | 2828 | 9 | US-09-802-318-21 | Sequence 21, Appl | 648 | 39.5 | 35.3 | 100 | 16 | US-10-658-834A-299 | Sequence 299, App |
| 576 | 40 | 35.7 | 2828 | 9 | US-09-905-129-21 | Sequence 21, Appl | 649 | 39.5 | 35.3 | 101 | 15 | US-10-424-599-246719 | Sequence 246719, |
| 577 | 40 | 35.7 | 2828 | 9 | US-09-991-630-21 | Sequence 21, Appl | 650 | 39.5 | 35.3 | 119 | 9 | US-09-764-868-637 | Sequence 637, App |
| 578 | 40 | 35.7 | 2828 | 14 | US-10-176-847-54 | Sequence 54, Appl | 651 | 39.5 | 35.3 | 119 | 9 | US-09-955-999-84 | Sequence 84, Appl |
| 579 | 40 | 35.7 | 2828 | 14 | US-10-177-293-110 | Sequence 110, App | 652 | 39.5 | 35.3 | 119 | 11 | US-09-764-867-1152 | Sequence 1152, Ap |
| 580 | 40 | 35.7 | 2828 | 14 | US-10-301-823-49 | Sequence 49, Appl | 653 | 39.5 | 35.3 | 119 | 11 | US-10-158-057-321 | Sequence 321, App |
| 581 | 40 | 35.7 | 2828 | 14 | US-10-032-189-126 | Sequence 126, App | 654 | 39.5 | 35.3 | 121 | 15 | US-10-282-122A-48956 | Sequence 48956, A |
| 582 | 40 | 35.7 | 2828 | 15 | US-10-295-027-58 | Sequence 58, Appl | 655 | 39.5 | 35.3 | 122 | 14 | US-10-194-885-21 | Sequence 21, Appl |
| 583 | 40 | 35.7 | 2828 | 15 | US-10-295-027-115 | Sequence 115, Ap | 656 | 39.5 | 35.3 | 122 | 14 | US-10-032-201B-89 | Sequence 89, Appl |
| 584 | 40 | 35.7 | 2828 | 15 | US-10-072-012-607 | Sequence 607, App | 657 | 39.5 | 35.3 | 124 | 15 | US-10-424-599-163334 | Sequence 163334, |
| 585 | 40 | 35.7 | 2828 | 15 | US-10-072-012-608 | Sequence 608, App | 658 | 39.5 | 35.3 | 127 | 15 | US-10-424-599-13334 | Sequence 13334, A |
| 586 | 40 | 35.7 | 2828 | 15 | US-10-454-351-21 | Sequence 21, Appl | 659 | 39.5 | 35.3 | 129 | 16 | US-10-767-701-53518 | Sequence 53518, A |
| 587 | 40 | 35.7 | 2845 | 15 | US-10-093-463-21 | Sequence 21, Appl | 660 | 39.5 | 35.3 | 132 | 16 | US-10-424-599-226031 | Sequence 226031, |
| 588 | 40 | 35.7 | 3432 | 15 | US-10-282-122A-68849 | Sequence 68849, A | 661 | 39.5 | 35.3 | 135 | 16 | US-10-437-963-16532 | Sequence 16532, |
| 589 | 40 | 35.7 | 5149 | 15 | US-10-282-122A-46333 | Sequence 46333, A | 662 | 39.5 | 35.3 | 146 | 14 | US-10-149-759-34 | Sequence 9502, Ap |
| 590 | 40 | 35.3 | 139 | 16 | US-10-437-963-138425 | Sequence 138425, | 663 | 39.5 | 35.3 | 156 | 14 | US-10-156-761-9502 | Sequence 9502, Ap |
| 591 | 40 | 35.3 | 180 | 16 | US-10-767-701-60185 | Sequence 60185, A | 664 | 39.5 | 35.3 | 158 | 15 | US-10-424-599-206082 | Sequence 206082, |
| 592 | 39.5 | 35.3 | 196 | 15 | US-10-424-599-222287 | Sequence 222287, | 665 | 39.5 | 35.3 | 163 | 16 | US-10-437-963-192466 | Sequence 192466, |
| 593 | 39.5 | 35.3 | 202 | 15 | US-10-364-397-12 | Sequence 12, Appl | 666 | 39.5 | 35.3 | 166 | 15 | US-10-425-114-56605 | Sequence 56605, A |
| 594 | 39.5 | 35.3 | 214 | 15 | US-10-425-114-55256 | Sequence 52526, A | 667 | 39.5 | 35.3 | 167 | 16 | US-10-437-963-137652 | Sequence 137652, |
| 595 | 39.5 | 35.3 | 258 | 16 | US-10-437-963-152423 | Sequence 152423, | 668 | 39.5 | 35.3 | 169 | 15 | US-10-282-122A-44822 | Sequence 44822, A |
| 596 | 39.5 | 35.3 | 269 | 16 | US-10-437-963-203722 | Sequence 203722, | 669 | 39.5 | 35.3 | 172 | 15 | US-10-425-114-40972 | Sequence 40972, A |
| 597 | 39.5 | 35.3 | 272 | 15 | US-10-369-493-13506 | Sequence 13506, A | 670 | 39.5 | 35.3 | 174 | 15 | US-10-425-114-66809 | Sequence 66809, A |

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| 671 | 39 | 34.8 | 176 | 15 | US-10-425-114-73069 | Sequence 73069, A |
| 672 | 39 | 34.8 | 183 | 15 | US-10-424-599-256423 | Sequence 256423, A |
| 673 | 39 | 34.8 | 184 | 15 | US-09-873-546-15 | Sequence 15, App1 |
| 674 | 39 | 34.8 | 185 | 16 | US-10-437-963-201054 | Sequence 201054, A |
| 675 | 39 | 34.8 | 187 | 15 | US-10-425-114-49529 | Sequence 49529, A |
| 676 | 39 | 34.8 | 187 | 15 | US-10-425-114-57345 | Sequence 57345, A |
| 677 | 39 | 34.8 | 187 | 15 | US-10-302-172-949 | Sequence 949, App |
| 678 | 39 | 34.8 | 188 | 16 | US-10-767-701-40973 | Sequence 40973, A |
| 679 | 39 | 34.8 | 190 | 14 | US-10-032-585-7287 | Sequence 7287, App |
| 680 | 39 | 34.8 | 201 | 15 | US-10-424-599-282990 | Sequence 282990, A |
| 681 | 39 | 34.8 | 214 | 11 | US-09-764-875-870 | Sequence 870, App |
| 682 | 39 | 34.8 | 214 | 11 | US-10-158-057-247 | Sequence 247, App |
| 683 | 39 | 34.8 | 218 | 15 | US-10-424-599-163668 | Sequence 163668, A |
| 684 | 39 | 34.8 | 227 | 15 | US-10-424-599-268627 | Sequence 268627, A |
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| 688 | 39 | 34.8 | 230 | 16 | US-10-759-277-6 | Sequence 6, App1 |
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| 690 | 39 | 34.8 | 238 | 15 | US-10-282-122A-43083 | Sequence 43083, A |
| 691 | 39 | 34.8 | 239 | 15 | US-10-369-493-20567 | Sequence 20567, A |
| 692 | 39 | 34.8 | 249 | 16 | US-10-437-963-184335 | Sequence 184335, A |
| 693 | 39 | 34.8 | 258 | 15 | US-10-424-599-259680 | Sequence 259680, A |
| 694 | 39 | 34.8 | 260 | 15 | US-10-282-122A-75932 | Sequence 75932, A |
| 695 | 39 | 34.8 | 260 | 16 | US-10-408-765A-408 | Sequence 408, App |
| 696 | 39 | 34.8 | 260 | 17 | US-10-791-155-1 | Sequence 1, App1 |
| 697 | 39 | 34.8 | 260 | 17 | US-10-791-155-5 | Sequence 5, App1 |
| 698 | 39 | 34.8 | 262 | 16 | US-10-437-963-147300 | Sequence 147300, A |
| 699 | 39 | 34.8 | 263 | 16 | US-10-767-701-45057 | Sequence 45057, A |
| 699 | 39 | 34.8 | 263 | 16 | US-10-767-701-45057 | Sequence 45057, A |
| 700 | 39 | 34.8 | 265 | 15 | US-10-425-114-45439 | Sequence 45439, A |
| 701 | 39 | 34.8 | 269 | 15 | US-10-282-122A-77449 | Sequence 77449, A |
| 702 | 39 | 34.8 | 270 | 16 | US-10-437-963-178643 | Sequence 178643, A |
| 703 | 39 | 34.8 | 271 | 9 | US-09-815-242-14072 | Sequence 14072, A |
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| 705 | 39 | 34.8 | 283 | 15 | US-10-282-122A-75079 | Sequence 75079, A |
| 706 | 39 | 34.8 | 303 | 15 | US-10-424-599-208863 | Sequence 208863, A |
| 707 | 39 | 34.8 | 304 | 9 | US-09-738-628-3743 | Sequence 3743, App |
| 708 | 39 | 34.8 | 305 | 15 | US-10-424-599-208862 | Sequence 208862, A |
| 709 | 39 | 34.8 | 306 | 15 | US-10-425-114-49629 | Sequence 49629, A |
| 710 | 39 | 34.8 | 315 | 15 | US-10-282-122A-57816 | Sequence 57816, A |
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| 712 | 39 | 34.8 | 318 | 15 | US-10-425-114-47355 | Sequence 47355, A |
| 713 | 39 | 34.8 | 318 | 15 | US-10-425-114-53382 | Sequence 53382, A |
| 714 | 39 | 34.8 | 318 | 15 | US-10-425-114-53396 | Sequence 53396, A |
| 715 | 39 | 34.8 | 324 | 15 | US-10-282-122A-48373 | Sequence 48373, A |
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| 717 | 39 | 34.8 | 343 | 14 | US-10-223-084-12 | Sequence 12, App1 |
| 718 | 39 | 34.8 | 343 | 14 | US-10-223-088-12 | Sequence 12, App1 |
| 719 | 39 | 34.8 | 343 | 14 | US-10-223-090-12 | Sequence 12, App1 |
| 720 | 39 | 34.8 | 343 | 14 | US-10-223-087-12 | Sequence 12, App1 |
| 721 | 39 | 34.8 | 343 | 14 | US-10-223-081-12 | Sequence 12, App1 |
| 722 | 39 | 34.8 | 343 | 14 | US-10-223-089-12 | Sequence 12, App1 |
| 723 | 39 | 34.8 | 343 | 14 | US-10-223-081-12 | Sequence 12, App1 |
| 724 | 39 | 34.8 | 343 | 14 | US-10-223-082-12 | Sequence 12, App1 |
| 725 | 39 | 34.8 | 343 | 15 | US-10-305-654-12 | Sequence 12, App1 |
| 726 | 39 | 34.8 | 343 | 15 | US-10-081-055-12 | Sequence 12, App1 |
| 727 | 39 | 34.8 | 348 | 15 | US-10-282-122A-46564 | Sequence 46564, A |
| 728 | 39 | 34.8 | 351 | 15 | US-10-374-780A-2118 | Sequence 2118, App |
| 729 | 39 | 34.8 | 367 | 15 | US-10-369-493-3459 | Sequence 3459, App |
| 730 | 39 | 34.8 | 368 | 14 | US-09-925-700-1356 | Sequence 1356, App |
| 731 | 39 | 34.8 | 369 | 14 | US-10-156-761-11423 | Sequence 11423, A |
| 732 | 39 | 34.8 | 377 | 15 | US-10-240-145-166 | Sequence 1466, App |
| 733 | 39 | 34.8 | 382 | 15 | US-10-424-599-149553 | Sequence 149553, A |
| 734 | 39 | 34.8 | 385 | 14 | US-10-168-274-6 | Sequence 6, App1 |
| 735 | 39 | 34.8 | 385 | 16 | US-10-755-889-512 | Sequence 512, App |
| 736 | 39 | 34.8 | 388 | 15 | US-10-236-392-34 | Sequence 34, App1 |
| 737 | 39 | 34.8 | 393 | 15 | US-10-282-122A-54250 | Sequence 54250, A |
| 738 | 39 | 34.8 | 405 | 9 | US-09-738-626-6717 | Sequence 6717, App |
| 739 | 39 | 34.8 | 408 | 10 | US-09-988-462-21 | Sequence 21, App1 |
| 740 | 39 | 34.8 | 420 | 9 | US-09-946-142-2 | Sequence 2, App1 |
| 741 | 39 | 34.8 | 420 | 16 | US-10-781-014-136 | Sequence 136, App |
| 742 | 39 | 34.8 | 446 | 15 | US-10-282-122A-58019 | Sequence 58019, A |
| 743 | 39 | 34.8 | 446 | 15 | US-10-282-122A-63415 | Sequence 63415, A |
| 744 | 39 | 34.8 | 448 | 15 | US-10-282-122A-76710 | Sequence 76710, A |
| 745 | 39 | 34.8 | 452 | 14 | US-10-148-907A-15 | Sequence 15, App1 |
| 746 | 39 | 34.8 | 455 | 15 | US-10-369-493-13712 | Sequence 13712, A |
| 747 | 39 | 34.8 | 463 | 10 | US-09-988-462-25 | Sequence 25, App1 |
| 748 | 39 | 34.8 | 464 | 10 | US-09-988-462-22 | Sequence 22, App1 |
| 749 | 39 | 34.8 | 465 | 17 | US-10-675-086-23 | Sequence 23, App1 |
| 750 | 39 | 34.8 | 468 | 9 | US-09-875-573-10 | Sequence 10201, A |
| 751 | 39 | 34.8 | 468 | 9 | US-09-875-573-29 | Sequence 29, App1 |
| 752 | 39 | 34.8 | 468 | 9 | US-09-875-573-31 | Sequence 31, App1 |
| 753 | 39 | 34.8 | 468 | 9 | US-09-875-573-37 | Sequence 37, App1 |
| 754 | 39 | 34.8 | 468 | 9 | US-09-875-573-39 | Sequence 39, App1 |
| 755 | 39 | 34.8 | 468 | 9 | US-09-875-573-41 | Sequence 41, App1 |
| 756 | 39 | 34.8 | 468 | 15 | US-10-369-493-866 | Sequence 866, App |
| 757 | 39 | 34.8 | 468 | 15 | US-10-282-122A-56569 | Sequence 56569, A |
| 758 | 39 | 34.8 | 472 | 15 | US-10-282-122A-60359 | Sequence 60359, A |
| 759 | 39 | 34.8 | 473 | 9 | US-09-815-242-5008 | Sequence 5008, App |
| 760 | 39 | 34.8 | 473 | 9 | US-09-815-242-10478 | Sequence 10478, A |
| 761 | 39 | 34.8 | 473 | 15 | US-10-282-122A-42521 | Sequence 42521, A |
| 762 | 39 | 34.8 | 480 | 15 | US-10-282-122A-54024 | Sequence 54024, A |
| 763 | 39 | 34.8 | 485 | 15 | US-10-282-122A-51755 | Sequence 51755, A |
| 764 | 39 | 34.8 | 486 | 16 | US-10-437-963-120442 | Sequence 120442, A |
| 765 | 39 | 34.8 | 508 | 15 | US-10-424-599-242297 | Sequence 242297, A |
| 766 | 39 | 34.8 | 510 | 16 | US-10-437-963-143565 | Sequence 143565, A |
| 767 | 39 | 34.8 | 513 | 9 | US-09-833-745-56 | Sequence 56, App1 |
| 768 | 39 | 34.8 | 517 | 15 | US-10-425-114-65871 | Sequence 65871, A |
| 769 | 39 | 34.8 | 520 | 15 | US-10-369-493-11092 | Sequence 11092, A |
| 770 | 39 | 34.8 | 525 | 15 | US-10-282-122A-62585 | Sequence 62585, A |
| 771 | 39 | 34.8 | 525 | 15 | US-10-282-122A-64802 | Sequence 64802, A |
| 772 | 39 | 34.8 | 527 | 15 | US-10-425-114-51766 | Sequence 51766, A |
| 773 | 39 | 34.8 | 530 | 15 | US-10-282-122A-77659 | Sequence 77659, A |
| 774 | 39 | 34.8 | 536 | 15 | US-10-369-493-1992 | Sequence 1992, App |
| 775 | 39 | 34.8 | 545 | 9 | US-09-995-749A-10 | Sequence 10, App1 |
| 776 | 39 | 34.8 | 546 | 11 | US-09-882-227-418 | Sequence 418, App1 |
| 777 | 39 | 34.8 | 546 | 11 | US-10-282-122A-58603 | Sequence 58603, A |
| 778 | 39 | 34.8 | 546 | 15 | US-10-335-977-7645 | Sequence 7645, App |
| 779 | 39 | 34.8 | 555 | 16 | US-10-767-701-46075 | Sequence 46075, App |
| 780 | 39 | 34.8 | 555 | 16 | US-10-102-622-12 | Sequence 12, App1 |
| 781 | 39 | 34.8 | 561 | 14 | US-10-389-566-753 | Sequence 753, App |
| 782 | 39 | 34.8 | 579 | 15 | US-10-369-493-3206 | Sequence 3206, App |
| 783 | 39 | 34.8 | 588 | 15 | US-10-369-493-135 | Sequence 135, App |
| 784 | 39 | 34.8 | 595 | 15 | US-10-282-122A-63562 | Sequence 63562, A |
| 785 | 39 | 34.8 | 595 | 15 | US-10-282-122A-64190 | Sequence 64190, A |
| 786 | 39 | 34.8 | 623 | 16 | US-10-437-963-123925 | Sequence 123925, A |
| 787 | 39 | 34.8 | 625 | 16 | US-10-437-963-152224 | Sequence 152224, A |
| 788 | 39 | 34.8 | 635 | 9 | US-09-833-745-38 | Sequence 38, App1 |
| 789 | 39 | 34.8 | 647 | 15 | US-10-282-122A-55195 | Sequence 55195, A |
| 790 | 39 | 34.8 | 655 | 15 | US-10-369-493-20066 | Sequence 20066, A |
| 791 | 39 | 34.8 | 653 | 16 | US-10-437-963-133909 | Sequence 133909, A |
| 792 | 39 | 34.8 | 670 | 14 | US-10-106-698-6282 | Sequence 6282, App |
| 793 | 39 | 34.8 | 679 | 15 | US-10-243-552-973 | Sequence 973, App |
| 794 | 39 | 34.8 | 680 | 15 | US-10-243-552-973 | Sequence 973, App |
| 795 | 39 | 34.8 | 694 | 16 | US-10-767-701-46291 | Sequence 46291, A |
| 796 | 39 | 34.8 | 700 | 16 | US-10-408-765A-2425 | Sequence 2425, App |
| 797 | 39 | 34.8 | 717 | 15 | US-10-369-493-17408 | Sequence 17408, A |
| 798 | 39 | 34.8 | 743 | 14 | US-10-171-311-188 | Sequence 188, App |
| 799 | 39 | 34.8 | 744 | 16 | US-10-437-963-122954 | Sequence 122954, A |
| 799 | 39 | 34.8 | 744 | 16 | US-10-437-963-122954 | Sequence 122954, A |
| 800 | 39 | 34.8 | 773 | 16 | US-10-437-963-136533 | Sequence 136533, A |
| 801 | 39 | 34.8 | 790 | 15 | US-10-437-963-199514 | Sequence 199514, A |
| 802 | 39 | 34.8 | 850 | 9 | US-09-808-602-58 | Sequence 58, App1 |
| 803 | 39 | 34.8 | 850 | 10 | US-09-800-198-47 | Sequence 47, App1 |
| 804 | 39 | 34.8 | 851 | 14 | US-10-259-165-260 | Sequence 260, App |
| 805 | 39 | 34.8 | 867 | 15 | US-10-425-114-17669 | Sequence 17669, A |
| 806 | 39 | 34.8 | 886 | 15 | US-10-369-493-18210 | Sequence 18210, A |
| 807 | 39 | 34.8 | 916 | 15 | US-10-210-130-138 | Sequence 138, App |
| 808 | 39 | 34.8 | 932 | 15 | US-10-282-122A-69195 | Sequence 69195, A |
| 809 | 39 | 34.8 | 955 | 15 | US-10-425-114-58617 | Sequence 58617, A |
| 810 | 39 | 34.8 | 968 | 15 | US-10-108-260A-3838 | Sequence 3838, App |
| 811 | 39 | 34.8 | 972 | 14 | US-10-231-354-2 | Sequence 2, App1 |
| 812 | 39 | 34.8 | 983 | 14 | US-09-808-602-73 | Sequence 73, App1 |
| 813 | 39 | 34.8 | 983 | 14 | US-10-013-136-2 | Sequence 2, App1 |
| 814 | 39 | 34.8 | 990 | 16 | US-10-437-963-143591 | Sequence 143591, A |
| 815 | 39 | 34.8 | 1014 | 15 | US-10-398-663-1 | Sequence 1, App1 |
| 816 | 39 | 34.8 | 1018 | 14 | US-10-101-464A-909 | Sequence 909, App |

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| 817 | 39 | 34.8 | 1018 | 17 | US-10-864-252-909 | Sequence 909, App |
| 818 | 39 | 34.8 | 1056 | 14 | US-10-231-354-6 | Sequence 6, Appl |
| 819 | 39 | 34.8 | 1061 | 16 | US-10-437-963-133988 | Sequence 133988, A |
| 820 | 39 | 34.8 | 1076 | 16 | US-10-437-963-201416 | Sequence 201416, A |
| 821 | 39 | 34.8 | 1167 | 16 | US-10-437-963-132719 | Sequence 132719, A |
| 822 | 39 | 34.8 | 1166 | 16 | US-10-282-122A-68505 | Sequence 68505, A |
| 823 | 39 | 34.8 | 1188 | 16 | US-10-437-963-198278 | Sequence 198278, A |
| 824 | 39 | 34.8 | 1250 | 16 | US-10-437-963-151829 | Sequence 151829, A |
| 825 | 39 | 34.8 | 1270 | 14 | US-10-437-963-151829 | Sequence 10, Appl |
| 826 | 39 | 34.8 | 1275 | 16 | US-10-437-963-19835 | Sequence 19835, A |
| 827 | 39 | 34.8 | 1426 | 13 | US-10-024-623-17 | Sequence 17, Appl |
| 828 | 39 | 34.8 | 1426 | 14 | US-10-231-354-14 | Sequence 14, Appl |
| 829 | 39 | 34.8 | 1426 | 14 | US-10-154-419-67 | Sequence 67, Appl |
| 830 | 39 | 34.8 | 1426 | 14 | US-10-146-733-62 | Sequence 62, Appl |
| 831 | 39 | 34.8 | 1426 | 15 | US-10-236-417-140 | Sequence 140, App |
| 832 | 39 | 34.8 | 1430 | 9 | US-09-740-274-6 | Sequence 6, Appl |
| 833 | 39 | 34.8 | 1430 | 16 | US-10-383-930-36 | Sequence 36, Appl |
| 834 | 39 | 34.8 | 1430 | 17 | US-10-797-821-36 | Sequence 36, Appl |
| 835 | 39 | 34.8 | 1520 | 9 | US-09-738-626-4444 | Sequence 4444, App |
| 836 | 39 | 34.8 | 1520 | 17 | US-10-494-541-102 | Sequence 102, App |
| 837 | 39 | 34.8 | 1533 | 15 | US-10-282-122A-46454 | Sequence 46454, A |
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ALIGNMENTS

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US-10-839-729-6
; Sequence 6, Application US/10839729
; Publication No. US20050002953A1
; GENERAL INFORMATION:
; APPLICANT: Jens Herold
; TITLE OF INVENTION: SARS-CORONAVIRUS VIRUS-LIKE PARTICLES
; FILE REFERENCE: BIOBANK.013A
; CURRENT APPLICATION NUMBER: US/10/839,729
; CURRENT FILING DATE: 2004-05-04
; PRIOR APPLICATION NUMBER: 60/468703
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 221
; TYPE: PRT
; ORGANISM: SARS Coronavirus
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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MADNGTIVBELKQLEQNNLV 22
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US-10-839-729-7
; Sequence 7, Application US/10839729
; Publication No. US20050002953A1
; GENERAL INFORMATION:
; APPLICANT: Jens Herold
; TITLE OF INVENTION: SARS-CORONAVIRUS VIRUS-LIKE PARTICLES
; FILE REFERENCE: BIOBANK.013A
; CURRENT APPLICATION NUMBER: US/10/839,729
; CURRENT FILING DATE: 2004-05-04
; PRIOR APPLICATION NUMBER: 60/468703
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 221
; TYPE: PRT
; ORGANISM: SARS Coronavirus
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Best Local Similarity 100.0%; Pred. No. 3.7e-08;
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US-10-839-729-8
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; Publication No. US20050002953A1
; GENERAL INFORMATION:
; APPLICANT: Jens Herold
; TITLE OF INVENTION: SARS-CORONAVIRUS VIRUS-LIKE PARTICLES
; FILE REFERENCE: BIOBANK.013A
; CURRENT APPLICATION NUMBER: US/10/839,729
; CURRENT FILING DATE: 2004-05-04
; PRIOR APPLICATION NUMBER: 60/468703
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 49
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; TYPE: PRT
; ORGANISM: SARS Coronavirus
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RESULT 4
US-10-839-729-9
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; Publication No. US20050002953A1
; GENERAL INFORMATION:
; APPLICANT: Jens Herold
; TITLE OF INVENTION: SARS-CORONAVIRUS VIRUS-LIKE PARTICLES
; FILE REFERENCE: BIOBANK.013A
; CURRENT APPLICATION NUMBER: US/10/839,729
; CURRENT FILING DATE: 2004-05-04
; PRIOR APPLICATION NUMBER: 60/468703
; PRIOR FILING DATE: 2003-05-06
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NUMBER OF SEQ ID NOS: 49
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US-10-839-729-9

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DB 1 MADNGTITVEELKQLLEQNMNV 22

RESULT 5
US-10-699-936-24
Sequence 24, Application US/10699936
Publication No. US20050095582A1
GENERAL INFORMATION:
APPLICANT: Gillim-Ross, Laura
APPLICANT: Taylor, Jill
APPLICANT: Scholl, David R.
APPLICANT: Wentworth, David E.
APPLICANT: Jollick, Joseph D.
TITLE OF INVENTION: Compositions and Methods for Detecting Severe Acute Respiratory
FILE REFERENCE: DHI-07986
CURRENT APPLICATION NUMBER: US/10/699,936
CURRENT FILING DATE: 2003-11-03
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PatentIn version 3.2
SEQ ID NO 24
LENGTH: 221
TYPE: PRT
ORGANISM: SARS-CoV Urban1
US-10-699-936-24

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DB 1 MADNGTITVEELKQLLEQNMNV 22

RESULT 6
US-10-699-936-81
Sequence 81, Application US/10699936
Publication No. US20050095582A1
GENERAL INFORMATION:
APPLICANT: Gillim-Ross, Laura
APPLICANT: Taylor, Jill
APPLICANT: Scholl, David R.
APPLICANT: Wentworth, David E.
APPLICANT: Jollick, Joseph D.
TITLE OF INVENTION: Compositions and Methods for Detecting Severe Acute Respiratory
FILE REFERENCE: DHI-07986
CURRENT APPLICATION NUMBER: US/10/699,936
CURRENT FILING DATE: 2003-11-03
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PatentIn version 3.2
SEQ ID NO 81
LENGTH: 221
TYPE: PRT
ORGANISM: SARS coronavirus Tor2
US-10-699-936-81

Query Match 100.0%; Score 112; DB 17; Length 221;

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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MADNGTITVEELKQLLEQNMNV 22

RESULT 7
US-10-699-936-82
Sequence 82, Application US/10699936
Publication No. US20050095582A1
GENERAL INFORMATION:
APPLICANT: Gillim-Ross, Laura
APPLICANT: Taylor, Jill
APPLICANT: Scholl, David R.
APPLICANT: Wentworth, David E.
APPLICANT: Jollick, Joseph D.
TITLE OF INVENTION: Compositions and Methods for Detecting Severe Acute Respiratory
FILE REFERENCE: DHI-07986
CURRENT APPLICATION NUMBER: US/10/699,936
CURRENT FILING DATE: 2003-11-03
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PatentIn version 3.2
SEQ ID NO 82
LENGTH: 221
TYPE: PRT
ORGANISM: SARS coronavirus Shanghai QXC
US-10-699-936-82

Query Match 100.0%; Score 112; DB 17; Length 221;
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DB 1 MADNGTITVEELKQLLEQNMNV 22

RESULT 8
US-10-699-936-83
Sequence 83, Application US/10699936
Publication No. US20050095582A1
GENERAL INFORMATION:
APPLICANT: Gillim-Ross, Laura
APPLICANT: Taylor, Jill
APPLICANT: Scholl, David R.
APPLICANT: Wentworth, David E.
APPLICANT: Jollick, Joseph D.
TITLE OF INVENTION: Compositions and Methods for Detecting Severe Acute Respiratory
FILE REFERENCE: DHI-07986
CURRENT APPLICATION NUMBER: US/10/699,936
CURRENT FILING DATE: 2003-11-03
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PatentIn version 3.2
SEQ ID NO 83
LENGTH: 221
TYPE: PRT
ORGANISM: SARS coronavirus Shanghai QXC
US-10-699-936-83

Query Match 100.0%; Score 112; DB 17; Length 221;
Best Local Similarity 100.0%; Pred. No. 3.7e-08;
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DB 1 MADNGTITVEELKQLLEQNMNV 22

RESULT 9

US-10-808-187-214
; Sequence 214, Application US/10808187
; Publication No. US2005009009A1
; GENERAL INFORMATION:
; APPLICANT: PEIRIS, JOSEPH S. M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: GUAN, YI
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: NICHOLLS, JOHN
; TITLE OF INVENTION: A DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS CAUSING SEVERE ACUTE
; FILE REFERENCE: V9661.0078
; CURRENT APPLICATION NUMBER: US/10/808,187
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/457,031
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: 60/457,730
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 60/459,931
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/460,357
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; PRIOR APPLICATION NUMBER: 60/461,265
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/462,805
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: 60/468,139
; PRIOR FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: 60/464,886
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 60/471,200
; PRIOR FILING DATE: 2003-05-16
; NUMBER OF SEQ ID NOS: 2476
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 214
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Human severe acute respiratory system virus
US-10-808-187-214

Query Match 100.0%; Score 112; DB 17; Length 242;
Best Local Similarity 100.0%; Pred. No. 4.1e-08;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTIVTEELKQLEOMNLV 22
DB 22 MADNGTIVTEELKQLEOMNLV 43

RESULT 10
US-10-839-729-46
; Sequence 46, Application US/10839729
; Publication No. US2005002953A1
; GENERAL INFORMATION:
; APPLICANT: JENS Herold
; TITLE OF INVENTION: SARS-CORONAVIRUS VIRUS-LIKE PARTICLES
; FILE REFERENCE: BIOBANK 013A
; CURRENT APPLICATION NUMBER: US/10/839,729
; CURRENT FILING DATE: 2004-05-04
; PRIOR APPLICATION NUMBER: 60/468703
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically prepared polypeptide sequence
US-10-839-729-46

Query Match 65.2%; Score 73; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00083;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTIVTEELKQLEOMNLV 15
DB 1 MADNGTIVTEELKQLEOMNLV 15

RESULT 11
US-10-425-114-69487
; Sequence 69487, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabacka, Jack B.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53113)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 69487
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73003G04_FLI.pep
US-10-425-114-69487

Query Match 47.8%; Score 53.5; DB 15; Length 336;
Best Local Similarity 57.1%; Pred. No. 19;
Matches 12; Conservative 3; Mismatches 3; Indels 3; Gaps 1;

QY 4 NGTIVTEELKQLEOMNLV 21
DB 196 NGTIVTEELKQLEOMNLV 216

RESULT 12
US-10-437-963-158994
; Sequence 158994, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Bardazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 158994
; LENGTH: 486
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_58414C.1.pep
US-10-437-963-158994

Query Match 47.8%; Score 53.5; DB 16; Length 486;
Best Local Similarity 57.1%; Pred. No. 29;
Matches 12; Conservative 3; Mismatches 3; Indels 3; Gaps 1;

QY 4 NGTITVEELKQLEQ---WNL 21
||||:||||| | | |
Db 346 NGTISLEELKQALAKDVPWRL 366

RESULT 13

US-10-437-963-158996
; Sequence 158996, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 158996
; LENGTH: 512
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_58416C.1.pcp
US-10-437-963-158996

Query Match 47.8%; Score 53.5; DB 16; Length 512;
Best Local Similarity 57.1%; Pred. No. 30;
Matches 12; Conservative 3; Mismatches 3; Indels 3; Gaps 1;

QY 4 NGTITVEELKQLEQ---WNL 21
||||:||||| | | |
Db 372 NGTISLEELKQALAKDVPWRL 392

RESULT 14

US-10-425-114-57880
; Sequence 57880, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovacic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 57880
; LENGTH: 523
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-2MFLM017084F11_FLI.pep
US-10-425-114-57880

Query Match 47.8%; Score 53.5; DB 15; Length 523;
Best Local Similarity 57.1%; Pred. No. 31;
Matches 12; Conservative 3; Mismatches 3; Indels 3; Gaps 1;

QY 4 NGTITVEELKQLEQ---WNL 21
||||:||||| | | |

Db 383 NGTISLEELKQALAKDVPWRL 403

RESULT 15

US-10-369-294-11
; Sequence 11, Application US/10369294
; Publication No. US20030162170A1
; GENERAL INFORMATION:
; APPLICANT: Hahn, Beatrice H.
; APPLICANT: Gao, Feng
; APPLICANT: Marx, Preston A.
; APPLICANT: Shaw, George M.
; APPLICANT: Smith, Stephen M.
; APPLICANT: Georges-Courbot, Marie Claude
; APPLICANT: Lu, Chang Yong
; TITLE OF INVENTION: Complete Genome Sequences of a Simian
; TITLE OF INVENTION: Immunodeficiency Virus from a Red-Capped
; FILE REFERENCE: D6286D
; CURRENT APPLICATION NUMBER: US/10/369,294
; CURRENT FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 09/206,551
; PRIOR FILING DATE: 1998-12-07
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 11
; LENGTH: 855
; TYPE: PRT
; ORGANISM: Simian immunodeficiency virus
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of homologous region of
; OTHER INFORMATION: A_U455 lentiviral env protein
US-10-369-294-11

Query Match 46.0%; Score 51.5; DB 14; Length 855;
Best Local Similarity 43.5%; Pred. No. 1.le+02;
Matches 10; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

QY 1 MADNGTITVE-ELKQLEQWNL 22
||||:||||| | | |
Db 401 MCPNGTITVEELKQALAKDVPWRL 423

RESULT 16

US-10-369-294-12
; Sequence 12, Application US/10369294
; Publication No. US20030162170A1
; GENERAL INFORMATION:
; APPLICANT: Hahn, Beatrice H.
; APPLICANT: Gao, Feng
; APPLICANT: Marx, Preston A.
; APPLICANT: Shaw, George M.
; APPLICANT: Smith, Stephen M.
; APPLICANT: Georges-Courbot, Marie Claude
; APPLICANT: Lu, Chang Yong
; TITLE OF INVENTION: Complete Genome Sequences of a Simian
; TITLE OF INVENTION: Immunodeficiency Virus from a Red-Capped
; FILE REFERENCE: D6286D
; CURRENT APPLICATION NUMBER: US/10/369,294
; CURRENT FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 09/206,551
; PRIOR FILING DATE: 1998-12-07
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 12
; LENGTH: 855
; TYPE: PRT
; ORGANISM: Simian immunodeficiency virus
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of homologous region of
; OTHER INFORMATION: B_HXB2R lentiviral env protein
US-10-369-294-12

Query Match 46.0%; Score 51.5; DB 14; Length 855;

Best Local Similarity 43.5%; Pred. No. 1.1e+02;
Matches 10; Conservative 5; Mismatches 7; Indels 1; Gaps 1;
Qy 1 MADNGTIVTEELKQLEQNNLV 22
Db 401 MGPNGITTLQCRIRKQITNMQRV 423

RESULT 17
US-09-864-761-39008
; Sequence 39008, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 39008
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC004837.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.9
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.6
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.9
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.9
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.6

; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.6
; OTHER INFORMATION: SWISSPROT HIT: P11233, EVALU 5.00e-25
; OTHER INFORMATION: EST_HUMAN HIT: A1344679.1, EVALU 6.00e-24
US-09-864-761-39008

Query Match 45.5%; Score 51; DB 9; Length 54;
Best Local Similarity 42.9%; Pred. No. 5.5;
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MADNGTIVTEELKQLEQNNLV 21
Db 23 LEDKQVSYVEAKNRARQNNV 43

RESULT 18
US-09-873-546-10
; Sequence 10, Application US/09873546
; Publication No. US20030059771A1
; GENERAL INFORMATION:
; APPLICANT: Clark, Geoff
; APPLICANT: Ellis, Chad
; APPLICANT: Vos, Michelle
; TITLE OF INVENTION: Rtg; No. US20030059771A1el Ras-Related Gene
; FILE REFERENCE: NIH-05080
; CURRENT APPLICATION NUMBER: US/09/873,546
; CURRENT FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-873-546-10

Query Match 45.5%; Score 51; DB 10; Length 206;
Best Local Similarity 42.9%; Pred. No. 25;
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MADNGTIVTEELKQLEQNNLV 21
Db 131 LEDKQVSYVEAKNRARQNNV 151

RESULT 19
US-10-153-668-214
; Sequence 214, Application US/10153668
; Publication No. US20030092616A1
; GENERAL INFORMATION:
; APPLICANT: HONDA, Goichi
; APPLICANT: MATSUDA, Akio
; APPLICANT: MURAMATSU, Shuji
; APPLICANT: ISHIZAWA, Kenya
; TITLE OF INVENTION: STAT6 Activating Gene
; FILE REFERENCE: 1254-0207P
; CURRENT APPLICATION NUMBER: US/10/153,668
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US 60/293,172
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/316,031
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/328,403
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: JP 2001-157043
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: JP 2001-260681
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: JP 2001-313175
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 488
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 214
; LENGTH: 206
; TYPE: PRT

ORGANISM: Homo sapiens
US-10-153-668-214

Query Match 45.5%; Score 51; DB 14; Length 206;
Best Local Similarity 42.9%; Pred. No. 25;
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 MADNGTIVEELKQLEQWNL 21
DB 131 LEDKQVSEAEKRAEQWNV 151

RESULT 20
US-10-021-660-132
Sequence 132, Application US/10021660
Publication No. US20030152926A1

GENERAL INFORMATION:
APPLICANT: Murray, Richard
APPLICANT: Glynn, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: No. US20030152926A1 Methods of Diagnosis of Angiogenesis,
TITLE OF INVENTION: Compositions and Methods of Screening for Angiogenesis
FILE REFERENCE: 018501-000710US
CURRENT APPLICATION NUMBER: US/10/021,660
CURRENT FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: US/09/784,356
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: US 09/637,977
PRIOR FILING DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 135
SOFTWARE: PaetecSeq for Windows Version 3.0
SEQ ID NO 132
LENGTH: 206
TYPE: PRT
ORGANISM: Homo sapiens
US-10-021-660-132

Query Match 45.5%; Score 51; DB 14; Length 206;
Best Local Similarity 42.9%; Pred. No. 25;
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 MADNGTIVEELKQLEQWNL 21
DB 131 LEDKQVSEAEKRAEQWNV 151

RESULT 21
US-10-231-913-64
Sequence 64, Application US/10231913
Publication No. US20040005576A1

GENERAL INFORMATION:
APPLICANT: Guo, Xiaojia S.
APPLICANT: Li, Li
APPLICANT: Patuturajan, Meera
APPLICANT: Shinkets, Richard A.
APPLICANT: Casman, Stacie J.
APPLICANT: Malyankar, Uriel M.
APPLICANT: Tchernov, Velizar T.
APPLICANT: Vernet, Corinne A.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Alsobrook II, John P.
APPLICANT: Edinger, Schlomik
APPLICANT: Peyman, John A.
APPLICANT: Stone, David J.
APPLICANT: Ellerman, Karen
APPLICANT: Gangolli, Esha A.
APPLICANT: Boldog, Ference L.
APPLICANT: Colman, Steven D.
APPLICANT: Eisen, Andrew J.
APPLICANT: Liu, Xiaohong

APPLICANT: Padigaru, Muralidhara
APPLICANT: Spaderina, Steven K.
APPLICANT: Zerhusen, Bryan P.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-216
CURRENT APPLICATION NUMBER: US/10/231,913
CURRENT FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: 60/251,660
PRIOR FILING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: 60/255,029
PRIOR FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: 60/260,326
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/263,800
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: 60/269,942
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/286,183
PRIOR FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: 60/313,627
PRIOR FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: 60/318,712
PRIOR FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 292
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 64
LENGTH: 206
TYPE: PRT
ORGANISM: Homo sapiens
US-10-231-913-64

Query Match 45.5%; Score 51; DB 15; Length 206;
Best Local Similarity 42.9%; Pred. No. 25;
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 MADNGTIVEELKQLEQWNL 21
DB 131 LEDKQVSEAEKRAEQWNV 151

RESULT 22
US-10-211-462-79
Sequence 79, Application US/10211462
Publication No. US20040033495A1

GENERAL INFORMATION:
APPLICANT: Murray, Richard
APPLICANT: Glynn, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Aziz, Natsaba
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis, Compositions and
TITLE OF INVENTION: Methods of Screening for Angiogenesis Modulators
FILE REFERENCE: 018501-006200US
CURRENT APPLICATION NUMBER: US/10/211,462
CURRENT FILING DATE: 2003-02-13
PRIOR APPLICATION NUMBER: US 09/784,356
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: US 09/791,390
PRIOR FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: US 60/310,025
PRIOR FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: US 60/334,244
PRIOR FILING DATE: 2001-11-29
NUMBER OF SEQ ID NOS: 230
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 79
LENGTH: 206
TYPE: PRT
ORGANISM: Homo sapiens
US-10-211-462-79

Query Match 45.5%; Score 51; DB 15; Length 206;
Best Local Similarity 42.9%; Pred. No. 25;


```
APPLICANT: Zykkind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Foreyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITPA.034A
CURRENT APPLICATION NUMBER: US/10/282.122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 51593
LENGTH: 351
TYPE: PRF
ORGANISM: Clostridium acetobutylicum
US-10-282-122A-51593

Query Match 45.5%; Score 51; DB 15; Length 351;
Best Local Similarity 42.1%; Pred. No. 46;
Matches 8; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 4 NGTIVBELKQLEQWNLV 22
DB 132 NGELSTBELKQWMDASNTV 150

RESULT 27
US-10-424-599-219887
Sequence 219887, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J
APPLICANT: Kovalic, David K
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 219887
LENGTH: 92
TYPE: PRF
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_40586C.1.pep
US-10-424-599-219887

Query Match 44.6%; Score 50; DB 15; Length 92;
```

```
Best Local Similarity 47.4%; Pred. No. 14;
Matches 9; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 3 DNGTIVBELKQLEQWNL 21
DB 25 NSGFTTBEELQALREYNM 43

RESULT 28
US-10-437-963-186189
Sequence 186189, Application US/10437963
Publication No. US2004012343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 186189
LENGTH: 174
TYPE: PRF
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_83010C.1.pep
US-10-437-963-186189

Query Match 44.6%; Score 50; DB 16; Length 174;
Best Local Similarity 55.6%; Pred. No. 29;
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 4 NGTIVBELKQLEQWNL 21
DB 119 NGVTIABELRLRLRLNL 136

RESULT 29
US-10-417-700A-49
Sequence 49, Application US/10417700A
Publication No. US2004003581A1
GENERAL INFORMATION:
APPLICANT: ECOPIA BIOSCIENCES INC.
APPLICANT: ZAZOROUOS, Emmanuel
APPLICANT: STAFPA, Alfredo
APPLICANT: FARNET, Chris
TITLE OF INVENTION: Specialized dual condensation/epimerization domain in non-ribosom
FILE REFERENCE: 3002-14US
CURRENT APPLICATION NUMBER: US/10/417,700A
CURRENT FILING DATE: 2003-04-17
NUMBER OF SEQ ID NOS: 139
SOFTWARE: PatentIn version 3.0
SEQ ID NO 49
LENGTH: 469
TYPE: PRF
ORGANISM: Pseudomonas syringae pv. syringae strain B301D
US-10-417-700A-49

Query Match 44.6%; Score 50; DB 15; Length 469;
Best Local Similarity 64.3%; Pred. No. 89;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 7 ITVEELKQLEQWNL 20
DB 432 LPLNERKQLEQWNL 445
```

```
RESULT 30
US-10-424-599-203557
; Sequence 203557, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 203557
; LENGTH: 546
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_25838C.1.pep
US-10-424-599-203557

Query Match          44.6%; Score 50; DB 15; Length 546;
Best Local Similarity 47.4%; Pred. No. 1.1e+02;
Matches 9; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY      3 DNGTIVEELKQLEQWNL 21
Db      477 NSGFITTELEQLREYNM 495

RESULT 31
US-10-425-114-54704
; Sequence 54704, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 54704
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: JC-GWFL0222063C09_FTLI.pep
US-10-425-114-54704

Query Match          44.6%; Score 50; DB 15; Length 549;
Best Local Similarity 47.4%; Pred. No. 1.1e+02;
Matches 9; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY      3 DNGTIVEELKQLEQWNL 21
Db      480 NSGFITTELEQLREYNM 498

RESULT 32
US-10-282-122A-76721
; Sequence 76721, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zykkind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT FILING DATE: 2003-02-20
; PRIOR FILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-05-23
; PRIOR FILING DATE: 2000-05-23
; PRIOR FILING DATE: 2000-05-26
; PRIOR FILING DATE: 2000-05-26
; PRIOR FILING DATE: 2000-09-06
; PRIOR FILING DATE: 2000-09-06
; PRIOR FILING DATE: 2000-09-09
; PRIOR FILING DATE: 2000-10-23
; PRIOR FILING DATE: 2000-10-23
; PRIOR FILING DATE: 2000-11-27
; PRIOR FILING DATE: 2000-11-27
; PRIOR FILING DATE: 2000-12-22
; PRIOR FILING DATE: 2000-12-22
; PRIOR FILING DATE: 2001-02-09
; PRIOR FILING DATE: 2001-02-09
; PRIOR FILING DATE: 2001-02-16
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 76721
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Ureaplasma urealyticum
US-10-282-122A-76721

Query Match          44.6%; Score 50; DB 15; Length 673;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      9 VEELKQLEQWNL 20
Db      8 IDELKQKLDQWNL 19

RESULT 33
US-09-953-348-132
; Sequence 132, Application US/09953348
; Publication No. US20030134398A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, David. H
; APPLICANT: Mao, Yingding
; APPLICANT: Varoglu, Mustafa
; APPLICANT: He, Min
; APPLICANT: Sheldon, Paul
; TITLE OF INVENTION: MITOMYCIN BIOSYNTHETIC GENE CLUSTER
; FILE REFERENCE: 600.5300S1
; CURRENT FILING DATE: 2001-09-12
; PRIOR FILING DATE: 2000-03-10
; PRIOR FILING DATE: 2000-03-10
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 153
```

```

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 132
; LENGTH: 123
; TYPE: PRF
; ORGANISM: Streptomyces lavendulae
US-09-953-348-132

```

```

Query Match      43.8%; Score 49; DB 10; Length 123;
Best Local Similarity 57.1%; Pred. No. 27;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      4 NGTIVTEELKQLE 17
      |||:|||||:|
DB      86 NGTVPVEELREWE 99

```

```

RESULT 34
US-10-267-255-132
; Sequence 132, Application US/10267255
; Publication No. US20030124689A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, D
; APPLICANT: Mao, Y
; APPLICANT: Varoglu, M
; APPLICANT: He, M
; APPLICANT: Sheldon, P
; TITLE OF INVENTION: Mitomycin biosynthetic gene cluster
; FILE REFERENCE: 600,436US1
; CURRENT APPLICATION NUMBER: US/10/267,255
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 09/266,965
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: US 08/624,447
; PRIOR FILING DATE: 1996-08-19
; PRIOR APPLICATION NUMBER: PCT/US94/11279
; PRIOR FILING DATE: 1994-10-06
; PRIOR APPLICATION NUMBER: US 08/133,963
; PRIOR FILING DATE: 1993-10-07
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 132
; LENGTH: 123
; TYPE: PRF
; ORGANISM: Streptomyces lavendulae
US-10-267-255-132

```

```

Query Match      43.8%; Score 49; DB 14; Length 123;
Best Local Similarity 57.1%; Pred. No. 27;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      4 NGTIVTEELKQLE 17
      |||:|||||:|
DB      86 NGTVPVEELREWE 99

```

```

RESULT 35
US-10-231-913-63
; Sequence 63, Application US/10231913
; Publication No. US20040005576A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Xiaojia S.
; APPLICANT: Li, Li
; APPLICANT: Patursajan, Meera
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Vernet, Corine A.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Edinger, Schlomit
; APPLICANT: Peyman, John A.

```

```

; APPLICANT: Stone, David J.
; APPLICANT: Ellerman, Karen
; APPLICANT: Gangoli, Baha A.
; APPLICANT: Boldog, Ference L.
; APPLICANT: Colman, Steven D.
; APPLICANT: Eissen, Andrew J.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Spaderma, Steven K.
; APPLICANT: Zernusen, Bryan D.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-216
; CURRENT APPLICATION NUMBER: US/10/231,913
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 60/251,660
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: 60/255,029
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/260,326
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/263,800
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/269,942
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/286,183
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 60/313,627
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/318,712
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 206
; TYPE: PRF
; ORGANISM: Mus musculus
US-10-231-913-63

```

```

Query Match      42.9%; Score 48; DB 15; Length 206;
Best Local Similarity 38.1%; Pred. No. 69;
Matches 8; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

```

```

QY      1 MADNGTIVTEELKQLEORNNL 21
      :|:|||||:|
DB      131 LEDKQGVSEAKNRADQNNV 151

```

```

RESULT 36
US-10-231-913-65
; Sequence 65, Application US/10231913
; Publication No. US20040005576A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Xiaojia S.
; APPLICANT: Li, Li
; APPLICANT: Patursajan, Meera
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Vernet, Corine A.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Edinger, Schlomit
; APPLICANT: Peyman, John A.
; APPLICANT: Stone, David J.
; APPLICANT: Ellerman, Karen
; APPLICANT: Gangoli, Baha A.
; APPLICANT: Boldog, Ference L.
; APPLICANT: Colman, Steven D.
; APPLICANT: Eissen, Andrew J.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Padigar, Muralidhara

```

```

; APPLICANT: Spaderna, Steven K.
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-216
; CURRENT APPLICATION NUMBER: US/10/231,913
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 60/251,660
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: 60/255,029
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/260,326
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/263,800
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/269,942
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/286,183
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 60/313,627
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/318,712
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-231-913-65
```

```

Query Match          42.9%; Score 48; DB 15; Length 206;
Best Local Similarity 38.1%; Pred. No. 69;
Matches      8; Conservative      5; Mismatches      8; Indels      0; Gaps      0;
```

```

QY      1  MADNGTIVTEELKQLEQWNL 21
DB      131 LEDKQGVSEAKSRADQWNV 151
```

```

RESULT 37
US-10-231-913-67
; Sequence 67, Application US/10231913
; Publication No. US20040005576A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Xiaojia S.
; APPLICANT: Li, Li
; APPLICANT: Patuturajan, Meera
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyanekar, Uriel M.
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Vernet, Corine A.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Edinger, Schlomlt
; APPLICANT: Peyman, John A.
; APPLICANT: Stone, David J.
; APPLICANT: Ellerman, Karen
; APPLICANT: Ganggilli, Esha A.
; APPLICANT: Boldog, Ference L.
; APPLICANT: Colman, Steven D.
; APPLICANT: Eisen, Andrew J.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-216
; CURRENT APPLICATION NUMBER: US/10/231,913
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 60/251,660
; PRIOR FILING DATE: 2000-12-06
```

```

; PRIOR APPLICATION NUMBER: 60/255,029
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/260,326
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/263,800
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/269,942
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/286,183
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 60/313,627
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/318,712
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Xenopus laevis
US-10-231-913-67
```

```

Query Match          42.9%; Score 48; DB 15; Length 206;
Best Local Similarity 38.1%; Pred. No. 69;
Matches      8; Conservative      5; Mismatches      8; Indels      0; Gaps      0;
```

```

QY      1  MADNGTIVTEELKQLEQWNL 21
DB      131 LEDKQGVSEAKSRADQWNV 151
```

```

RESULT 38
US-10-437-963-124248
; Sequence 124248, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Boukharov, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 124248
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_27005C.1.pep
US-10-437-963-124248
```

```

Query Match          42.9%; Score 48; DB 16; Length 299;
Best Local Similarity 58.8%; Pred. No. 16+02;
Matches     10; Conservative      3; Mismatches      4; Indels      0; Gaps      0;
```

```

QY      3  DNGTIVTEELKQLEQWNL 19
DB      281 DSGTIVEDLIQWLYQY 297
```

```

RESULT 39
US-10-369-493-10440
; Sequence 10440, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
```

```

; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 10440
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Cytophaga hutchinsonii
US-10-369-493-10440
```

```

Query Match          42.9%; Score 48; DB 15; Length 401;
Best Local Similarity 46.7%; Pred. No. 1.5e+02;
Matches 7; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      5 GTTVEELKQLLEQW 19
DB      184 GNVTLQVKLSSEKW 198
```

```

RESULT 40
US-10-314-657-45
; Sequence 45; Application US/10314657
; Publication No. US20030175888A1
; GENERAL INFORMATION:
; APPLICANT: SHEN, Ben
; APPLICANT: CHENG, Yi-Qiang
; APPLICANT: TANG, Gong-Li
; TITLE OF INVENTION: Discrete Acyltransferases Associated with Type I Polyketide
; FILE REFERENCE: 054030-0021
; CURRENT APPLICATION NUMBER: US/10/314,657
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: PCT/US02/08937
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US 60/278,935
; PRIOR FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 214
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
; LENGTH: 4437
; TYPE: PRT
; ORGANISM: Streptomyces atroolivaceus
US-10-314-657-45
```

```

Query Match          42.9%; Score 48; DB 14; Length 4437;
Best Local Similarity 42.1%; Pred. No. 2.2e+03;
Matches 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
```

```
QY      2 ADNGTTVEELKQLLEQW 20
DB      949 ADDEVRGAEHLKILHEWN 967
```

```

RESULT 41
US-10-473-193-45
; Sequence 45; Application US/10473193
; Publication No. US20050080247A1
; GENERAL INFORMATION:
; APPLICANT: SHEN, BEN
; APPLICANT: TANG, Gong-Li
; APPLICANT: CHEN, Xianfeng
; TITLE OF INVENTION: LEUAMCIN BIOSYNTHESIS GENE CLUSTER AND ITS COMPONENTS AND THEIR
; FILE REFERENCE: 309T-000110US
; CURRENT APPLICATION NUMBER: US/10/473,193
```

```

; CURRENT FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/278,935
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: PCT/US02/08937
; PRIOR FILING DATE: 2002-03-22
; NUMBER OF SEQ ID NOS: 222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
; LENGTH: 4437
; TYPE: PRT
; ORGANISM: Streptomyces atroolivaceus
US-10-473-193-45
```

```

Query Match          42.9%; Score 48; DB 17; Length 4437;
Best Local Similarity 42.1%; Pred. No. 2.2e+03;
Matches 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
```

```
QY      2 ADNGTTVEELKQLLEQW 20
DB      949 ADDEVRGAEHLKILHEWN 967
```

```

RESULT 42
US-10-429-812-4
; Sequence 4; Application US/10429812
; Publication No. US20040003432A1
; GENERAL INFORMATION:
; APPLICANT: Obukowicz, Mark
; TITLE OF INVENTION: THE PRODUCTION OF HEXOSAMINES AND USES THEREFORE
; FILE REFERENCE: 18438/09004
; CURRENT APPLICATION NUMBER: US/10/429,812
; CURRENT FILING DATE: 2003-05-05
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-429-812-4
```

```

Query Match          42.0%; Score 47; DB 15; Length 159;
Best Local Similarity 50.0%; Pred. No. 71;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
```

```
QY      5 GTTVEELKQLLEQW 20
DB      31 GTTPESFSLIKIKWN 46
```

```

RESULT 43
US-10-612-779-30
; Sequence 30; Application US/10612779
; Publication No. US20040091976A1
; GENERAL INFORMATION:
; APPLICANT: Deng, Ming-De
; APPLICANT: Angerer, J. David
; APPLICANT: Cyron, Don
; APPLICANT: Grund, Alan
; APPLICANT: Jerrell Jr., Thomas
; APPLICANT: Leanna, Candice
; APPLICANT: Mathre, Owen
; APPLICANT: Rosson, Reinhardt
; APPLICANT: Running, Jeff
; APPLICANT: Severson, Dave
; APPLICANT: Song, Linsheng
; TITLE OF INVENTION: Process and Materials for Production of Glucosamine and N-Acetylc
; FILE REFERENCE: 3161-18-2
; CURRENT APPLICATION NUMBER: US/10/612,779
; CURRENT FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: 60/393,348
; PRIOR FILING DATE: 2002-07-01
```

NUMBER OF SEQ ID NOS: 137
SOFTWARE: Patent version 3.1
SEQ ID NO 30
LENGTH: 159
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-10-612-779-30

Query Match 42.0%; Score 47; DB 15; Length 159;
Best Local Similarity 50.0%; Pred. No. 71;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 5 GTTVEELKQLEQWN 20
Db 31 GTTPESFKLRKWN 46

RESULT 44
US-10-823-397-33

Sequence 33, Application US/10823397
Publication No. US20050042735A1
GENERAL INFORMATION:

APPLICANT: McMullin, Thomas
APPLICANT: Ding, Ming-De
APPLICANT: Grund, Alan

TITLE OF INVENTION: Metabolic Engineering for Enhanced Production of Chitin and
FILE REFERENCE: 3161-18-3

CURRENT APPLICATION NUMBER: US/10/823,397

CURRENT FILING DATE: 2004-04-12

PRIOR APPLICATION NUMBER: 60/462,087

PRIOR FILING DATE: 2003-04-11

NUMBER OF SEQ ID NOS: 59

SOFTWARE: Patent version 3.2

SEQ ID NO 33

LENGTH: 159

TYPE: PRT

ORGANISM: Saccharomyces cerevisiae

US-10-823-397-33

Query Match 42.0%; Score 47; DB 17; Length 159;
Best Local Similarity 50.0%; Pred. No. 71;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 5 GTTVEELKQLEQWN 20
Db 31 GTTPESFKLRKWN 46

RESULT 45
US-10-686-947-238

Sequence 238, Application US/10686947
Publication No. US20040162420A1
GENERAL INFORMATION:

APPLICANT: Profigen Inc.

TITLE OF INVENTION: Cloning of Cytochrome P450 Genes from Tobacco
FILE REFERENCE: 79601

CURRENT APPLICATION NUMBER: US/10/686,947

CURRENT FILING DATE: 2003-10-16

PRIOR APPLICATION NUMBER: US 10/387346

PRIOR FILING DATE: 2003-03-12

NUMBER OF SEQ ID NOS: 298

SOFTWARE: Patent version 3.2

SEQ ID NO 238

LENGTH: 508

TYPE: PRT

ORGANISM: NICOTIANATABACUM

US-10-686-947-238

Query Match 42.0%; Score 47; DB 16; Length 508;
Best Local Similarity 47.1%; Pred. No. 2.7e+02;
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 6 TTTVEELKQLEQWNLY 22
Db 196 TVRVEDLYLVDPWFLL 212

RESULT 46
US-10-686-947-266

Sequence 266, Application US/10686947
Publication No. US20040162420A1
GENERAL INFORMATION:

APPLICANT: Profigen Inc.

TITLE OF INVENTION: Cloning of Cytochrome P450 Genes from Tobacco

FILE REFERENCE: 79601

CURRENT APPLICATION NUMBER: US/10/686,947

CURRENT FILING DATE: 2003-10-16

PRIOR APPLICATION NUMBER: US 10/387346

PRIOR FILING DATE: 2003-03-12

NUMBER OF SEQ ID NOS: 298

SOFTWARE: Patent version 3.2

SEQ ID NO 266

LENGTH: 508

TYPE: PRT

ORGANISM: NICOTIANATABACUM

US-10-686-947-266

Query Match 42.0%; Score 47; DB 16; Length 508;
Best Local Similarity 47.1%; Pred. No. 2.7e+02;
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 6 TTTVEELKQLEQWNLY 22
Db 196 TVRVEDLYLVDPWFLL 212

RESULT 47
US-10-686-947-240

Sequence 240, Application US/10686947
Publication No. US20040162420A1
GENERAL INFORMATION:

APPLICANT: Profigen Inc.

TITLE OF INVENTION: Cloning of Cytochrome P450 Genes from Tobacco

FILE REFERENCE: 79601

CURRENT APPLICATION NUMBER: US/10/686,947

CURRENT FILING DATE: 2003-10-16

PRIOR APPLICATION NUMBER: US 10/387346

PRIOR FILING DATE: 2003-03-12

NUMBER OF SEQ ID NOS: 298

SOFTWARE: Patent version 3.2

SEQ ID NO 240

LENGTH: 509

TYPE: PRT

ORGANISM: NICOTIANATABACUM

US-10-686-947-240

Query Match 42.0%; Score 47; DB 16; Length 509;
Best Local Similarity 47.1%; Pred. No. 2.7e+02;
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

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RESULT 48
US-10-369-493-2600

Sequence 2600, Application US/10369493
Publication No. US2003023675A1
GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

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; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 2600
; LENGTH: 659
; TYPE: PRT
; ORGANISM: Synechocystis sp.
US-10-369-493-2600

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Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY      4 NGTITVEELKQLEOW 19
DB      633 NGQITLESRRLEDDY 648

RESULT 49
US-10-156-761-14515
; Sequence 14515, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 14515
; LENGTH: 987
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-14515

Query Match      42.0%; Score 47; DB 14; Length 987;
Best Local Similarity 50.0%; Pred. NO. 5.6e+02;
Matches 9; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

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DB      652 ADGDEIDVEDLRKRIEY 669

RESULT 50
US-10-282-122A-77230
; Sequence 77230, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haeselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zybkind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
```

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; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77230
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Vibrio cholerae
US-10-282-122A-77230
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Best Local Similarity 42.9%; Pred. NO. 2.6e+02;
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DB      107 LADSGSVAVESLKMALQYWH 127
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Search completed: May 11, 2005, 21:43:28
Job time : 100.66 secs

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GenCore version 5.1.6
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OM protein - protein search, using bw model

Run on: May 11, 2005, 21:05:14 / Search time 133.511 Seconds

(without alignments)
72.421 Million cell updates/sec

Title: US-10-712-812-6

Perfect score: 127
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 1000 summaries

Database : A.Geneseq_16Dec04:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| 28 | 51 | 40.2 | 224 | 6 | ABU00236 | ABU00236 Human nov |
| 29 | 51 | 40.2 | 572 | 2 | AAW68488 | AAW68488 Mouse Utl |
| 30 | 51 | 40.2 | 626 | 5 | ABR49107 | ABR49107 Listeria |
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| 37 | 50 | 39.4 | 534 | 8 | ABW83406 | ABW83406 Human dia |
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| 50 | 50 | 39.4 | 2000 | 8 | ADAE4333 | ADAE4333 Antipept |
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| 264 | 45 | 35.4 | 535 | 2 | AA086825 | AA086825 | 337 | 45 | 35.4 | 882 | 4 | AAE07889 | AAE07889 | Modified |
| 265 | 45 | 35.4 | 535 | 2 | AA086826 | AA086826 | 338 | 45 | 35.4 | 887 | 4 | AAE07892 | AAE07892 | Modified |
| 266 | 45 | 35.4 | 535 | 2 | AA024876 | AA024876 | 339 | 45 | 35.4 | 895 | 5 | AA075369 | AA075369 | AA075369 |
| 267 | 45 | 35.4 | 535 | 2 | AA046448 | AA046448 | 340 | 45 | 35.4 | 895 | 5 | AA075368 | AA075368 | AA075368 |
| 268 | 45 | 35.4 | 535 | 2 | AA068090 | AA068090 | 341 | 45 | 35.4 | 896 | 5 | AA075367 | AA075367 | AA075367 |
| 269 | 45 | 35.4 | 535 | 3 | AA096456 | AA096456 | 342 | 45 | 35.4 | 896 | 5 | AA075366 | AA075366 | AA075366 |
| 270 | 45 | 35.4 | 535 | 3 | AA097280 | AA097280 | 343 | 45 | 35.4 | 896 | 6 | AA029672 | AA029672 | AA029672 |
| 271 | 45 | 35.4 | 535 | 6 | AB097867 | AB097867 | 344 | 45 | 35.4 | 896 | 6 | AA029671 | AA029671 | AA029671 |
| 272 | 45 | 35.4 | 545 | 2 | AA074339 | AA074339 | 345 | 45 | 35.4 | 907 | 4 | AAE07891 | AAE07891 | Modified |
| 273 | 45 | 35.4 | 545 | 2 | AA067374 | AA067374 | 346 | 45 | 35.4 | 907 | 6 | AAE35713 | AAE35713 | AAE35713 |
| 274 | 45 | 35.4 | 545 | 2 | AA067372 | AA067372 | 347 | 45 | 35.4 | 999 | 6 | AAE35712 | AAE35712 | AAE35712 |
| 275 | 45 | 35.4 | 546 | 2 | AA041200 | AA041200 | 348 | 45 | 35.4 | 1052 | 3 | AA066336 | AA066336 | Mouse sub |
| 276 | 45 | 35.4 | 546 | 2 | AA041661 | AA041661 | 349 | 45 | 35.4 | 1052 | 3 | AA066334 | AA066334 | Human sub |
| 277 | 45 | 35.4 | 546 | 2 | AA098776 | AA098776 | 350 | 45 | 35.4 | 1052 | 3 | AA054619 | AA054619 | Human sub |
| 278 | 45 | 35.4 | 546 | 6 | AB030679 | AB030679 | 351 | 45 | 35.4 | 1052 | 3 | AA066982 | AA066982 | Human sub |
| 279 | 45 | 35.4 | 546 | 7 | AD035415 | AD035415 | 352 | 45 | 35.4 | 1052 | 3 | AA048227 | AA048227 | AA048227 |
| 280 | 45 | 35.4 | 546 | 7 | AD035417 | AD035417 | 353 | 45 | 35.4 | 1052 | 3 | AA048228 | AA048228 | AA048228 |
| 281 | 45 | 35.4 | 548 | 6 | AB062383 | AB062383 | 354 | 45 | 35.4 | 1052 | 3 | AA085820 | AA085820 | Human sub |
| 282 | 45 | 35.4 | 548 | 6 | AB097863 | AB097863 | 355 | 45 | 35.4 | 1052 | 5 | AA045427 | AA045427 | Human sit |
| 283 | 45 | 35.4 | 560 | 1 | AA060516 | AA060516 | 356 | 45 | 35.4 | 1052 | 5 | AA045428 | AA045428 | Human sit |
| 284 | 45 | 35.4 | 560 | 1 | AA070597 | AA070597 | 357 | 45 | 35.4 | 1052 | 5 | AB091096 | AB091096 | Human sub |
| 285 | 45 | 35.4 | 560 | 6 | AB096305 | AB096305 | 358 | 45 | 35.4 | 1192 | 6 | AAE35711 | AAE35711 | AAE35711 |
| 286 | 45 | 35.4 | 560 | 8 | ADP44536 | ADP44536 | 359 | 45 | 35.4 | 1192 | 6 | AAE35710 | AAE35710 | AAE35710 |
| 287 | 45 | 35.4 | 560 | 8 | ADP44538 | ADP44538 | 360 | 45 | 35.4 | 1212 | 6 | AAE35709 | AAE35709 | AAE35709 |
| 288 | 45 | 35.4 | 567 | 2 | AA066607 | AA066607 | 361 | 45 | 35.4 | 1212 | 6 | AAE35708 | AAE35708 | TEMT-Hc-D |
| 289 | 45 | 35.4 | 567 | 4 | AA000220 | AA000220 | 362 | 45 | 35.4 | 1256 | 4 | AB064133 | AB064133 | AB064133 |
| 290 | 45 | 35.4 | 568 | 4 | AA073924 | AA073924 | 363 | 45 | 35.4 | 1537 | 4 | AA083971 | AA083971 | AA083971 |
| 291 | 45 | 35.4 | 605 | 2 | AA073924 | AA073924 | 364 | 45 | 35.4 | 1549 | 8 | ADN23049 | ADN23049 | ADN23049 |
| 292 | 45 | 35.4 | 615 | 2 | AA095056 | AA095056 | 365 | 45 | 35.4 | 1577 | 4 | ABG10016 | ABG10016 | Novel hum |
| 293 | 45 | 35.4 | 617 | 2 | AA095057 | AA095057 | 366 | 45 | 35.4 | 1596 | 7 | ADJ69016 | ADJ69016 | Human hea |
| 294 | 45 | 35.4 | 619 | 2 | AA026486 | AA026486 | 367 | 45 | 35.4 | 1720 | 6 | AA078886 | AA078886 | Human pro |
| 295 | 45 | 35.4 | 629 | 6 | AB025441 | AB025441 | 368 | 45 | 35.4 | 1720 | 6 | AB007115 | AB007115 | Novel hum |
| 296 | 45 | 35.4 | 637 | 5 | AA075365 | AA075365 | 369 | 45 | 35.4 | 1721 | 4 | AA079870 | AA079870 | Human pro |
| 297 | 45 | 35.4 | 638 | 5 | AA075370 | AA075370 | 370 | 45 | 35.4 | 3432 | 6 | ABU41925 | ABU41925 | Protein e |
| 298 | 45 | 35.4 | 641 | 2 | AA099383 | AA099383 | 371 | 44.5 | 35.0 | 280 | 5 | AB055405 | AB055405 | Lactococc |
| 299 | 45 | 35.4 | 642 | 5 | AA075382 | AA075382 | 372 | 44.5 | 35.0 | 368 | 2 | AA084128 | AA084128 | AA084128 |
| 300 | 45 | 35.4 | 642 | 5 | AA029675 | AA029675 | 373 | 44.5 | 35.0 | 368 | 2 | AAE29785 | AAE29785 | AAE29785 |
| 301 | 45 | 35.4 | 643 | 5 | AA075390 | AA075390 | 374 | 44.5 | 35.0 | 368 | 8 | ADK39716 | ADK39716 | Paity fan |
| 302 | 45 | 35.4 | 643 | 6 | AA029670 | AA029670 | 375 | 44.5 | 35.0 | 417 | 8 | AD042706 | AD042706 | Bacterial |
| 303 | 45 | 35.4 | 645 | 4 | AA070894 | AA070894 | 376 | 44.5 | 35.0 | 424 | 6 | AB067843 | AB067843 | Phototrab |
| 304 | 45 | 35.4 | 645 | 5 | AAE35692 | AAE35692 | 377 | 44.5 | 35.0 | 499 | 8 | AD026143 | AD026143 | HIV gp120 |
| 305 | 45 | 35.4 | 646 | 5 | AA075383 | AA075383 | 378 | 44.5 | 35.0 | 545 | 8 | ADP04793 | ADP04793 | Sea equit |
| 306 | 45 | 35.4 | 657 | 5 | AA075389 | AA075389 | 379 | 44.5 | 35.0 | 549 | 5 | AA052842 | AA052842 | Physcomit |
| 307 | 45 | 35.4 | 657 | 5 | AA075389 | AA075389 | 379 | 44.5 | 35.0 | 549 | 5 | AB060235 | AB060235 | AB060235 |
| 308 | 45 | 35.4 | 657 | 6 | AA035693 | AA035693 | 380 | 44.5 | 35.0 | 571 | 4 | AA075156 | AA075156 | AA075156 |
| 309 | 45 | 35.4 | 660 | 4 | AA070898 | AA070898 | 381 | 44.5 | 35.0 | 619 | 5 | AA075155 | AA075155 | N-termina |
| 310 | 45 | 35.4 | 665 | 4 | AA070895 | AA070895 | 382 | 44.5 | 35.0 | 646 | 5 | AB066211 | AB066211 | HIV Env 1 |
| 311 | 45 | 35.4 | 665 | 6 | AA035689 | AA035689 | 383 | 44.5 | 35.0 | 842 | 5 | AB066565 | AB066565 | Human imm |
| 312 | 45 | 35.4 | 666 | 5 | AB090255 | AB090255 | 384 | 44.5 | 35.0 | 842 | 6 | AB055684 | AB055684 | HIV Ibo1a |
| 313 | 45 | 35.4 | 669 | 2 | AB044499 | AB044499 | 385 | 44.5 | 35.0 | 842 | 7 | AD013218 | AD013218 | Protein o |
| 314 | 45 | 35.4 | 671 | 6 | AA068500 | AA068500 | 386 | 44.5 | 35.0 | 842 | 8 | AD073868 | AD073868 | HIV-1 pol |
| 315 | 45 | 35.4 | 676 | 1 | AA093172 | AA093172 | 387 | 44.5 | 35.0 | 847 | 3 | AA097073 | AA097073 | Variant H |
| 316 | 45 | 35.4 | 676 | 3 | AA090706 | AA090706 | 388 | 44.5 | 35.0 | 847 | 8 | AD0005103 | AD0005103 | Human imm |
| 317 | 45 | 35.4 | 676 | 4 | AA070526 | AA070526 | 390 | 44 | 34.6 | 151 | 5 | AB055486 | AB055486 | Lactococc |

| | | | | | | | | | | | | | | |
|-----|----|------|------|---|-----------|------------|-----|------|------|------|---|-----------|-----------|------------|
| 391 | 44 | 34.6 | 157 | 8 | ADN17554 | Bacterial | 464 | 43.5 | 34.3 | 495 | 5 | AAH48000 | Aam48000 | Arabidops |
| 392 | 44 | 34.6 | 172 | 4 | ABG09791 | Novel hum | 465 | 43.5 | 34.3 | 501 | 3 | AAG35776 | Aag35776 | Arabidops |
| 393 | 44 | 34.6 | 176 | 3 | AAAG54430 | Zea mays | 466 | 43.5 | 34.3 | 501 | 5 | AAH48001 | Aam48001 | Arabidops |
| 394 | 44 | 34.6 | 215 | 3 | AAAG54429 | Zea mays | 467 | 43.5 | 34.3 | 523 | 3 | AAH48010 | Aag48010 | Arabidops |
| 395 | 44 | 34.6 | 282 | 5 | ABP27289 | Streptoco | 468 | 43.5 | 34.3 | 523 | 8 | ADN73153 | Adn73153 | Thale cre |
| 396 | 44 | 34.6 | 302 | 3 | AAAG54428 | Zea mays | 469 | 43.5 | 34.3 | 540 | 7 | ADP05702 | Adp05702 | Bacterial |
| 397 | 44 | 34.6 | 308 | 8 | ADSA44636 | Bacterial | 470 | 43.5 | 34.3 | 555 | 2 | AAH43340 | Adh43340 | Alpha-glu |
| 398 | 44 | 34.6 | 322 | 6 | ABU79113 | Staphyloc | 471 | 43.5 | 34.3 | 619 | 8 | ADSA30170 | Adsa30170 | Bacterial |
| 399 | 44 | 34.6 | 322 | 7 | ADFA3360 | Bacterial | 472 | 43.5 | 34.3 | 1551 | 4 | AAAG85026 | Aag85026 | Shirine wh |
| 400 | 44 | 34.6 | 328 | 3 | AAAG65657 | Arabidops | 473 | 43.5 | 34.3 | 2402 | 4 | AAU07131 | Aau07131 | Porcine r |
| 401 | 44 | 34.6 | 404 | 3 | AAAG65656 | Arabidops | 474 | 43.5 | 34.3 | 42 | 8 | ABO58010 | Abos8010 | Human gen |
| 402 | 44 | 34.6 | 420 | 3 | AAAG20726 | Arabidops | 475 | 43.5 | 34.3 | 71 | 6 | ABU01950 | Abu01950 | S. pneumo |
| 403 | 44 | 34.6 | 429 | 6 | ABM15850 | Mycobacte | 476 | 43.5 | 34.3 | 126 | 4 | ABH62908 | Abh62908 | Drosophil |
| 404 | 44 | 34.6 | 443 | 4 | AAAB96153 | Putative | 477 | 43.5 | 34.3 | 148 | 5 | ABU051032 | Abu051032 | Helicobac |
| 405 | 44 | 34.6 | 463 | 3 | AAAG65655 | Arabidops | 478 | 43.5 | 34.3 | 162 | 7 | ADP06342 | Adp06342 | Bacterial |
| 406 | 44 | 34.6 | 480 | 6 | ADAA48242 | Rice prot | 479 | 43.5 | 34.3 | 172 | 6 | ABU40649 | Abu40649 | Protein e |
| 407 | 44 | 34.6 | 484 | 6 | ABU24912 | Protein e | 480 | 43.5 | 34.3 | 172 | 8 | ADSA42775 | Adsa42775 | Bacterial |
| 408 | 44 | 34.6 | 491 | 4 | AAU34175 | Staphyloc | 481 | 43.5 | 34.3 | 184 | 6 | ABU62866 | Abu62866 | Ras-fam1 |
| 409 | 44 | 34.6 | 504 | 4 | AAU37099 | Staphyloc | 482 | 43.5 | 34.3 | 184 | 7 | ADBS9010 | Adbs9010 | Rat Prote |
| 410 | 44 | 34.6 | 504 | 6 | ABM72813 | Staphyloc | 483 | 43.5 | 34.3 | 184 | 7 | ADBS9012 | Adbs9012 | Human Pro |
| 411 | 44 | 34.6 | 511 | 6 | ABU16504 | Protein e | 484 | 43.5 | 34.3 | 184 | 7 | ADG31704 | Adg31704 | Human Ras |
| 412 | 44 | 34.6 | 523 | 3 | AAAG20725 | Arabidops | 485 | 43.5 | 34.3 | 184 | 8 | ADOS5215 | Ados5215 | Human pro |
| 413 | 44 | 34.6 | 530 | 6 | ABU49735 | Protein e | 486 | 43.5 | 34.3 | 184 | 8 | ABM80954 | Abm80954 | Tumour-as |
| 414 | 44 | 34.6 | 534 | 4 | ABH6941 | Drosophil | 487 | 43.5 | 34.3 | 184 | 8 | ADP23197 | Adp23197 | PRO polyP |
| 415 | 44 | 34.6 | 540 | 3 | AAAY75735 | Neisseria | 488 | 43.5 | 34.3 | 186 | 6 | ABH72361 | Abh72361 | Staphyloc |
| 416 | 44 | 34.6 | 547 | 4 | AAAG2001 | C. glutami | 489 | 43.5 | 34.3 | 196 | 4 | ABH03883 | Abh03883 | Human mus |
| 417 | 44 | 34.6 | 547 | 7 | ADDI3276 | C. glutami | 490 | 43.5 | 34.3 | 196 | 6 | ABU13177 | Abu13177 | Novel hum |
| 418 | 44 | 34.6 | 553 | 8 | ADSA28434 | Bacterial | 491 | 43.5 | 34.3 | 196 | 8 | ADJ29203 | Adj29203 | Human mus |
| 419 | 44 | 34.6 | 555 | 2 | AAH49098 | Amino aci | 492 | 43.5 | 34.3 | 256 | 3 | AAH82452 | Aah82452 | Spinach c |
| 420 | 44 | 34.6 | 555 | 8 | ADGA6834 | Bacterial | 493 | 43.5 | 34.3 | 276 | 7 | ADH86761 | Adh86761 | Enterococ |
| 421 | 44 | 34.6 | 555 | 8 | ADGA6831 | Bacterial | 494 | 43.5 | 34.3 | 311 | 6 | ADHP96401 | Adhp96401 | Prochlotro |
| 422 | 44 | 34.6 | 555 | 8 | ADGA6816 | Bacterial | 495 | 43.5 | 34.3 | 332 | 8 | ADH56074 | Adh56074 | Debaromy |
| 423 | 44 | 34.6 | 555 | 8 | ADGA6832 | Bacterial | 496 | 43.5 | 34.3 | 352 | 4 | AAU23088 | Aau23088 | Novel hum |
| 424 | 44 | 34.6 | 555 | 8 | ADGA6833 | Bacterial | 497 | 43.5 | 34.3 | 352 | 5 | ABBS3959 | Abbs3959 | Lactococc |
| 425 | 44 | 34.6 | 555 | 8 | ADGA6833 | Bacterial | 498 | 43.5 | 34.3 | 399 | 7 | ADH88134 | Adh88134 | Enterococ |
| 426 | 44 | 34.6 | 556 | 5 | AAE27868 | Mutant Tn | 499 | 43.5 | 34.3 | 407 | 7 | ADM05407 | Adm05407 | Human pro |
| 427 | 44 | 34.6 | 556 | 5 | AAE27867 | Mutant Tn | 500 | 43.5 | 34.3 | 436 | 8 | ADM26344 | Adm26344 | Chromobac |
| 428 | 44 | 34.6 | 556 | 5 | AAE27863 | Wild-type | 501 | 43.5 | 34.3 | 455 | 8 | ADS29127 | Ads29127 | Bacterial |
| 429 | 44 | 34.6 | 556 | 5 | AAE27866 | Mutant Tn | 502 | 43.5 | 34.3 | 467 | 3 | AAAY9855 | Aay9855 | Escherich |
| 430 | 44 | 34.6 | 556 | 5 | AAE27870 | Mutant Tn | 503 | 43.5 | 34.3 | 467 | 3 | AAAY9854 | Aay9854 | Escherich |
| 431 | 44 | 34.6 | 556 | 5 | AAE27869 | Mutant Tn | 504 | 43.5 | 34.3 | 467 | 3 | AAAY9853 | Aay9853 | Escherich |
| 432 | 44 | 34.6 | 560 | 6 | ABM68550 | Photochab | 505 | 43.5 | 34.3 | 467 | 7 | ADG33780 | Adg33780 | Actinomyc |
| 433 | 44 | 34.6 | 571 | 8 | ADN17386 | Bacterial | 506 | 43.5 | 34.3 | 468 | 3 | AAAY9857 | Aay9857 | Escherich |
| 434 | 44 | 34.6 | 580 | 4 | ABG20724 | Arabidops | 507 | 43.5 | 34.3 | 468 | 3 | AAAY9856 | Aay9856 | Escherich |
| 435 | 44 | 34.6 | 584 | 4 | ABG26094 | Novel hum | 508 | 43.5 | 34.3 | 468 | 3 | AAAY9858 | Aay9858 | Escherich |
| 436 | 44 | 34.6 | 586 | 4 | ABBS58288 | Drosophil | 509 | 43.5 | 34.3 | 469 | 8 | ADN20290 | Adn20290 | Bacterial |
| 437 | 44 | 34.6 | 726 | 6 | ABP96033 | Human sur | 510 | 43.5 | 34.3 | 477 | 6 | ABO07142 | Ab007142 | Novel hum |
| 438 | 44 | 34.6 | 748 | 6 | ABU20785 | Protein e | 511 | 43.5 | 34.3 | 481 | 8 | ADN01952 | Adn01952 | Staphyloc |
| 439 | 44 | 34.6 | 765 | 7 | ADP74168 | Human nov | 512 | 43.5 | 34.3 | 481 | 8 | ADN01939 | Adn01939 | Staphyloc |
| 440 | 44 | 34.6 | 814 | 6 | ABU24538 | Protein e | 513 | 43.5 | 34.3 | 481 | 8 | ADN01953 | Adn01953 | Staphyloc |
| 441 | 44 | 34.6 | 904 | 8 | ADOC67715 | Novel hum | 514 | 43.5 | 34.3 | 481 | 8 | ADN01955 | Adn01955 | Staphyloc |
| 442 | 44 | 34.6 | 952 | 7 | ABO68769 | Pseudomon | 515 | 43.5 | 34.3 | 486 | 6 | ADN01946 | Adn01946 | Staphyloc |
| 443 | 44 | 34.6 | 1577 | 2 | AAH91047 | Alpha-D-g | 516 | 43.5 | 34.3 | 486 | 6 | ABH71573 | Abh71573 | Staphyloc |
| 444 | 44 | 34.6 | 2349 | 6 | AAOI6359 | Human tra | 517 | 43.5 | 34.3 | 486 | 7 | ABO70890 | Ab070890 | Pseudomon |
| 445 | 44 | 34.6 | 2400 | 4 | ABG20278 | Novel hum | 518 | 43.5 | 34.3 | 490 | 2 | AAH89764 | Aah89764 | Staphyloc |
| 446 | 44 | 34.6 | 2415 | 4 | ABG20279 | Novel hum | 519 | 43.5 | 34.3 | 490 | 2 | ADN01954 | Adn01954 | Staphyloc |
| 447 | 44 | 34.6 | 3196 | 6 | ABU41611 | Protein e | 520 | 43.5 | 34.3 | 495 | 7 | ABO74573 | Ab074573 | Pseudomon |
| 448 | 44 | 34.6 | 3196 | 6 | ABU41611 | Protein e | 521 | 43.5 | 34.3 | 510 | 8 | ADN17403 | Adn17403 | Bacterial |
| 449 | 44 | 34.6 | 3196 | 6 | ABU41611 | Protein e | 522 | 43.5 | 34.3 | 521 | 7 | ABO23592 | Ab023592 | Rickettsi |
| 450 | 44 | 34.6 | 3196 | 6 | ABU41611 | Protein e | 523 | 43.5 | 34.3 | 539 | 2 | AAH23306 | Aah23306 | Amino aci |
| 451 | 44 | 34.6 | 3196 | 6 | ABU41611 | Protein e | 524 | 43.5 | 34.3 | 539 | 2 | AAH23306 | Aah23306 | Amino aci |
| 452 | 44 | 34.6 | 3196 | 6 | ABU41611 | Protein e | 525 | 43.5 | 34.3 | 540 | 6 | ABU20002 | Abu20002 | Protein e |
| 453 | 44 | 34.6 | 3196 | 6 | ABU41611 | Protein e | 526 | 43.5 | 34.3 | 542 | 4 | ABG64458 | Abg64458 | S. putref |
| 454 | 44 | 34.6 | 3196 | 6 | ABU41611 | Protein e | 527 | 43.5 | 34.3 | 543 | 2 | AAH42456 | Aah42456 | Enzyme in |
| 455 | 44 | 34.6 | 3196 | 6 | ABU41611 | Protein e | 528 | 43.5 | 34.3 | 543 | 2 | AAH42456 | Aah42456 | Enzyme in |
| 456 | 44 | 34.6 | 3196 | 6 | ABU41611 | Protein e | 529 | 43.5 | 34.3 | 543 | 2 | AAH42456 | Aah42456 | Enzyme in |
| 457 | 44 | 34.6 | 3196 | 6 | ABU41611 | Protein e | 530 | 43.5 | 34.3 | 543 | 2 | AAH42456 | Aah42456 | Enzyme in |
| 458 | 44 | 34.6 | 3196 | 6 | ABU41611 | Protein e | 531 | 43.5 | 34.3 | 543 | 2 | AAH42456 | Aah42456 | Enzyme in |
| 459 | 44 | 34.6 | 3196 | 6 | ABU41611 | Protein e | 532 | 43.5 | 34.3 | 543 | 2 | AAH42456 | Aah42456 | Enzyme in |
| 460 | 44 | 34.6 | 3196 | 6 | ABU41611 | Protein e | 533 | 43.5 | 34.3 | 543 | 2 | AAH42456 | Aah42456 | Enzyme in |
| 461 | 44 | 34.6 | 3196 | 6 | ABU41611 | Protein e | 534 | 43.5 | 34.3 | 543 | 2 | AAH42456 | Aah42456 | Enzyme in |
| 462 | 44 | 34.6 | 3196 | 6 | ABU41611 | Protein e | 535 | 43.5 | 34.3 | 543 | 2 | AAH42456 | Aah42456 | Enzyme in |
| 463 | 44 | 34.6 | 3196 | 6 | ABU41611 | Protein e | 536 | 43.5 | 34.3 | 543 | 2 | AAH42456 | Aah42456 | Enzyme in |

| | | | | | | | | | | | | | |
|-----|------|------|------|---|-----------|---------------------|-----|------|------|-----|---|-----------|---------------------|
| 537 | 43 | 33.9 | 555 | 6 | ABU39997 | Abu39997 Protein e | 610 | 42.5 | 33.5 | 278 | 6 | ADA87267 | Ada87267 Novel hum |
| 538 | 43 | 33.9 | 555 | 8 | ADM57219 | Adm57219 A thalian | 611 | 42.5 | 33.5 | 278 | 6 | ADA81649 | Ada81649 Human PRO |
| 539 | 43 | 33.9 | 575 | 4 | AA679220 | Aa679220 Amino aci | 612 | 42.5 | 33.5 | 278 | 6 | ADA91561 | Ada91561 Novel hum |
| 540 | 43 | 33.9 | 579 | 8 | ADJ48749 | Adj48749 Oll-aseoc | 613 | 42.5 | 33.5 | 278 | 6 | ADBI4624 | Adbi4624 Human PRO |
| 541 | 43 | 33.9 | 580 | 6 | ABM69228 | Abm69228 Phototrab | 614 | 42.5 | 33.5 | 278 | 6 | ADBI8585 | Adbi8585 Novel hum |
| 542 | 43 | 33.9 | 587 | 6 | ABU29807 | Abu29807 Protein e | 615 | 42.5 | 33.5 | 278 | 6 | ADA93800 | Ada93800 Human PRO |
| 543 | 43 | 33.9 | 594 | 8 | ADN20584 | Adn20584 Bacterial | 616 | 42.5 | 33.5 | 278 | 6 | ADBI1966 | Adbi1966 Novel hum |
| 544 | 43 | 33.9 | 597 | 8 | ADC97426 | E. faeciu | 617 | 42.5 | 33.5 | 278 | 6 | ADBI3008 | Adbi3008 Human PRO |
| 545 | 43 | 33.9 | 608 | 6 | ABU43518 | Abu43518 Protein e | 618 | 42.5 | 33.5 | 278 | 6 | ABO43216 | AbO43216 Novel hum |
| 546 | 43 | 33.9 | 684 | 6 | ABU19991 | Abu19991 Protein e | 619 | 42.5 | 33.5 | 278 | 6 | ADA74262 | Ada74262 Human PRO |
| 547 | 43 | 33.9 | 774 | 8 | ABM63465 | Abm63465 Human dia | 620 | 42.5 | 33.5 | 278 | 6 | ADB24495 | Adb24495 Human PRO |
| 548 | 43 | 33.9 | 786 | 4 | AAV70243 | Aay70243 Human RNA | 621 | 42.5 | 33.5 | 278 | 6 | ADA82019 | Ada82019 Human PRO |
| 549 | 43 | 33.9 | 798 | 4 | ABB61410 | Abb61410 Drosophil | 622 | 42.5 | 33.5 | 278 | 6 | ADA74982 | Ada74982 Human PRO |
| 550 | 43 | 33.9 | 815 | 7 | AD62881 | Ad62881 Rat Prote | 623 | 42.5 | 33.5 | 278 | 6 | ADA85060 | Ada85060 Novel hum |
| 551 | 43 | 33.9 | 821 | 8 | ADN20138 | Adn20138 Bacterial | 624 | 42.5 | 33.5 | 278 | 6 | ADA84508 | Ada84508 Human PRO |
| 552 | 43 | 33.9 | 887 | 4 | AAU37586 | Aau37586 Streptoco | 625 | 42.5 | 33.5 | 278 | 6 | ADB29764 | Adb29764 Human PRO |
| 553 | 43 | 33.9 | 890 | 6 | ABP81476 | Abp81476 Streptoco | 626 | 42.5 | 33.5 | 278 | 6 | ADA80292 | Ada80292 Human PRO |
| 554 | 43 | 33.9 | 890 | 6 | ABU46263 | Abu46263 Protein e | 627 | 42.5 | 33.5 | 278 | 6 | ADA75534 | Ada75534 Human PRO |
| 555 | 43 | 33.9 | 890 | 6 | ADK48224 | Adk48224 Streptoco | 628 | 42.5 | 33.5 | 278 | 6 | ADA46759 | Ada46759 Human PRO |
| 556 | 43 | 33.9 | 1086 | 7 | ADP07411 | Adp07411 Bacterial | 629 | 42.5 | 33.5 | 278 | 6 | ADB25055 | Adb25055 Human PRO |
| 557 | 43 | 33.9 | 1133 | 3 | AA638914 | Aa638914 Arabidops | 630 | 42.5 | 33.5 | 278 | 6 | ADA93231 | Ada93231 Human PRO |
| 558 | 43 | 33.9 | 1186 | 3 | AA841528 | Aa841528 Human ORF | 631 | 42.5 | 33.5 | 278 | 6 | ADB26581 | Adb26581 Human PRO |
| 559 | 43 | 33.9 | 1188 | 8 | ADO80423 | Ado80423 Zebrafish | 632 | 42.5 | 33.5 | 278 | 6 | ADB30868 | Adb30868 Human PRO |
| 560 | 43 | 33.9 | 1192 | 7 | AD62883 | Ad62883 Human PRO | 633 | 42.5 | 33.5 | 278 | 6 | ADA60796 | Ada60796 Homo sapl |
| 561 | 43 | 33.9 | 1193 | 3 | AA638913 | Aa638913 Arabidops | 634 | 42.5 | 33.5 | 278 | 6 | ADB23943 | Adb23943 Human PRO |
| 562 | 43 | 33.9 | 1214 | 4 | ABG22123 | Abg22123 Novel hum | 635 | 42.5 | 33.5 | 278 | 6 | ADA96272 | Ada96272 Human PRO |
| 563 | 43 | 33.9 | 1363 | 6 | ABU08100 | Abu08100 Human kin | 636 | 42.5 | 33.5 | 278 | 6 | ADA80844 | Ada80844 Human PRO |
| 564 | 43 | 33.9 | 1467 | 5 | ABB97605 | Abb97605 Novel hum | 637 | 42.5 | 33.5 | 278 | 6 | ADA95720 | Ada95720 Human PRO |
| 565 | 43 | 33.9 | 1673 | 5 | ABP69698 | Abp69698 Human pol | 638 | 42.5 | 33.5 | 278 | 6 | ADB26029 | Adb26029 Human PRO |
| 566 | 43 | 33.9 | 1683 | 5 | AAV71160 | Aay71160 Rat phosph | 639 | 42.5 | 33.5 | 278 | 6 | ADB21514 | Adb21514 Human PRO |
| 567 | 43 | 33.9 | 1690 | 5 | ABP69699 | Abp69699 Human pol | 640 | 42.5 | 33.5 | 278 | 7 | ADA77293 | Ada77293 Human PRO |
| 568 | 43 | 33.9 | 1893 | 5 | AAU84593 | Aau84593 HIV Casse | 641 | 42.5 | 33.5 | 278 | 7 | ADBI18033 | Adbi18033 Human PRO |
| 569 | 43 | 33.9 | 1896 | 5 | AAU84590 | Aau84590 HIV Casse | 642 | 42.5 | 33.5 | 278 | 7 | ADA86716 | Ada86716 Novel hum |
| 570 | 43 | 33.9 | 2188 | 6 | ADA36476 | Ada36476 Actinocoba | 643 | 42.5 | 33.5 | 278 | 7 | ADA87819 | Ada87819 Novel hum |
| 571 | 43 | 33.9 | 3290 | 6 | ADA34199 | Ada34199 Actinocoba | 644 | 42.5 | 33.5 | 278 | 7 | ADA46207 | Ada46207 Novel hum |
| 572 | 43 | 33.9 | 5245 | 7 | AD123931 | Ad123931 Streptomy | 645 | 42.5 | 33.5 | 278 | 7 | ADB28237 | Adb28237 Human PRO |
| 573 | 43 | 33.9 | 5245 | 7 | AD123931 | Ad123931 Streptomy | 646 | 42.5 | 33.5 | 278 | 7 | ADB28789 | Adb28789 Human PRO |
| 574 | 43 | 33.9 | 5746 | 8 | AAU84596 | Aau84596 HIV compl | 647 | 42.5 | 33.5 | 278 | 7 | ADA76741 | Ada76741 Human PRO |
| 575 | 43 | 33.5 | 147 | 8 | ADRA9441 | Adra9441 Mouse sma | 648 | 42.5 | 33.5 | 278 | 7 | ADA88371 | Ada88371 Novel hum |
| 576 | 42.5 | 33.5 | 210 | 3 | AA807846 | Aa807846 Amino aci | 649 | 42.5 | 33.5 | 278 | 7 | ADA87376 | Ada87376 Human PRO |
| 577 | 42.5 | 33.5 | 226 | 6 | ABP40649 | Abp40649 Staphyloc | 650 | 42.5 | 33.5 | 278 | 7 | ADB27133 | Adb27133 Human PRO |
| 578 | 42.5 | 33.5 | 226 | 8 | ADO807889 | Ado807889 Staphyloc | 651 | 42.5 | 33.5 | 278 | 7 | ADB22066 | Adb22066 Novel hum |
| 579 | 42.5 | 33.5 | 227 | 6 | ABM72833 | Abm72833 Staphyloc | 652 | 42.5 | 33.5 | 278 | 7 | ADA66757 | Ada66757 Human PRO |
| 580 | 42.5 | 33.5 | 240 | 6 | ABU57647 | Abu57647 Different | 653 | 42.5 | 33.5 | 278 | 7 | ADB22618 | Adb22618 Human PRO |
| 581 | 42.5 | 33.5 | 266 | 7 | ADC25187 | Adc25187 A. altern | 654 | 42.5 | 33.5 | 278 | 7 | ADB23391 | Adb23391 Human PRO |
| 582 | 42.5 | 33.5 | 276 | 4 | AAU02498 | Aau02498 Murine tr | 655 | 42.5 | 33.5 | 278 | 7 | ADA82113 | Ada82113 Novel hum |
| 583 | 42.5 | 33.5 | 276 | 8 | ADRA9483 | Adra9483 Mouse sma | 656 | 42.5 | 33.5 | 278 | 7 | ADB15176 | Adb15176 Human PRO |
| 584 | 42.5 | 33.5 | 277 | 2 | AAW78312 | Aaw78312 Fragment | 657 | 42.5 | 33.5 | 278 | 7 | ADB38428 | Adb38428 Novel hum |
| 585 | 42.5 | 33.5 | 277 | 2 | AAW78312 | Aaw78312 Fragment | 658 | 42.5 | 33.5 | 278 | 7 | ADB37876 | Adb37876 Novel hum |
| 586 | 42.5 | 33.5 | 278 | 4 | AAU02499 | Aau02499 Human PRO | 659 | 42.5 | 33.5 | 278 | 7 | ADB66348 | Adb66348 Novel hum |
| 587 | 42.5 | 33.5 | 278 | 4 | AAU02499 | Aau02499 Human PRO | 660 | 42.5 | 33.5 | 278 | 7 | ADB69428 | Adb69428 Human PRO |
| 588 | 42.5 | 33.5 | 278 | 6 | ABU69616 | Abu69616 Human trl | 661 | 42.5 | 33.5 | 278 | 7 | ADB80160 | Adb80160 Human PRO |
| 589 | 42.5 | 33.5 | 278 | 6 | ABO17683 | AbO17683 Novel hum | 662 | 42.5 | 33.5 | 278 | 7 | ADB39261 | Adb39261 Novel hum |
| 590 | 42.5 | 33.5 | 278 | 6 | ABU80937 | Abu80937 Human PRO | 663 | 42.5 | 33.5 | 278 | 7 | ADB46884 | Adb46884 Novel hum |
| 591 | 42.5 | 33.5 | 278 | 6 | ABU66637 | Abu66637 Human PRO | 664 | 42.5 | 33.5 | 278 | 7 | ADB86491 | Adb86491 Human PRO |
| 592 | 42.5 | 33.5 | 278 | 6 | ABU59718 | Abu59718 Novel sec | 665 | 42.5 | 33.5 | 278 | 7 | ADB77096 | Adb77096 Novel hum |
| 593 | 42.5 | 33.5 | 278 | 6 | ABO24908 | AbO24908 Human sec | 666 | 42.5 | 33.5 | 278 | 7 | ADB34253 | Adb34253 Human PRO |
| 594 | 42.5 | 33.5 | 278 | 6 | ABU66913 | Abu66913 Human sec | 667 | 42.5 | 33.5 | 278 | 7 | ADB35357 | Adb35357 Human PRO |
| 595 | 42.5 | 33.5 | 278 | 6 | ABR58397 | AbR58397 Human NOV | 668 | 42.5 | 33.5 | 278 | 7 | ADB33701 | Adb33701 Human PRO |
| 596 | 42.5 | 33.5 | 278 | 6 | ADA45655 | Ada45655 Novel hum | 669 | 42.5 | 33.5 | 278 | 7 | ADB34805 | Adb34805 Human PRO |
| 597 | 42.5 | 33.5 | 278 | 6 | ADA76086 | Ada76086 Human PRO | 670 | 42.5 | 33.5 | 278 | 7 | ADB35909 | Adb35909 Human PRO |
| 598 | 42.5 | 33.5 | 278 | 6 | ADA18736 | Ada18736 Human PRO | 671 | 42.5 | 33.5 | 278 | 7 | ADB46304 | Adb46304 Novel hum |
| 599 | 42.5 | 33.5 | 278 | 6 | ADA61359 | Ada61359 Homo sapl | 672 | 42.5 | 33.5 | 278 | 7 | ADC50177 | Adc50177 Novel hum |
| 600 | 42.5 | 33.5 | 278 | 6 | ADB19144 | Adb19144 Novel hum | 673 | 42.5 | 33.5 | 278 | 7 | ADC71724 | Adc71724 Novel hum |
| 601 | 42.5 | 33.5 | 278 | 6 | ADB27685 | Adb27685 Human PRO | 674 | 42.5 | 33.5 | 278 | 7 | ADC59703 | Adc59703 Novel hum |
| 602 | 42.5 | 33.5 | 278 | 6 | ADA86164 | Ada86164 Novel hum | 675 | 42.5 | 33.5 | 278 | 7 | ADC52710 | Adc52710 Novel hum |
| 603 | 42.5 | 33.5 | 278 | 6 | ADBI5728 | Adbi5728 Human PRO | 676 | 42.5 | 33.5 | 278 | 7 | ADC57064 | Adc57064 Novel hum |
| 604 | 42.5 | 33.5 | 278 | 6 | ADA47514 | Ada47514 Human PRO | 677 | 42.5 | 33.5 | 278 | 7 | ADC60255 | Adc60255 Novel hum |
| 605 | 42.5 | 33.5 | 278 | 6 | ADA67309 | Ada67309 Human PRO | 678 | 42.5 | 33.5 | 278 | 7 | ADC50730 | Adc50730 Novel hum |
| 606 | 42.5 | 33.5 | 278 | 6 | ADB30316 | Adb30316 Human PRO | 679 | 42.5 | 33.5 | 278 | 7 | ADC65257 | Adc65257 Human PRO |
| 607 | 42.5 | 33.5 | 278 | 6 | ADA85612 | Ada85612 Novel hum | 680 | 42.5 | 33.5 | 278 | 7 | ADC43355 | Adc43355 Novel hum |
| 608 | 42.5 | 33.5 | 278 | 6 | ADA96824 | Ada96824 Human PRO | 681 | 42.5 | 33.5 | 278 | 7 | ADC53316 | Adc53316 Novel hum |
| 609 | 42.5 | 33.5 | 278 | 6 | ADA79128 | Ada79128 Human PRO | 682 | 42.5 | 33.5 | 278 | 7 | ADC58839 | Adc58839 Novel hum |

| | | | | | | | | | | | | | | | | |
|-----|------|------|-----|---|-----------|-------|-----|-----|------|------|-----|---|-----------|-----------|-----|-----------|
| 683 | 42.5 | 33.5 | 278 | 7 | ADCS5717 | Novel | hum | 756 | 42.5 | 33.5 | 278 | 8 | ADBS8999 | Human | PRO | Adc88999 |
| 684 | 42.5 | 33.5 | 278 | 7 | ADCS8287 | Novel | hum | 757 | 42.5 | 33.5 | 278 | 8 | ADBS1838 | Human | PRO | Adc18138 |
| 685 | 42.5 | 33.5 | 278 | 7 | ADDO2961 | Novel | hum | 758 | 42.5 | 33.5 | 278 | 8 | ADBS8447 | Human | PRO | Adc88447 |
| 686 | 42.5 | 33.5 | 278 | 7 | ADCS9953 | Novel | hum | 759 | 42.5 | 33.5 | 278 | 8 | ADBS9467 | Human | PRO | Adc94467 |
| 687 | 42.5 | 33.5 | 278 | 7 | ADCS69372 | Human | PRO | 760 | 42.5 | 33.5 | 278 | 8 | ADBS0878 | Human | PRO | Adc90878 |
| 688 | 42.5 | 33.5 | 278 | 7 | ADCA8261 | Human | PRO | 761 | 42.5 | 33.5 | 278 | 8 | ADBS5019 | Human | PRO | Adc95019 |
| 689 | 42.5 | 33.5 | 278 | 7 | ADDO9790 | Human | PRO | 762 | 42.5 | 33.5 | 278 | 8 | ADBS3129 | Human | PRO | Adc93129 |
| 690 | 42.5 | 33.5 | 278 | 7 | ADDO4365 | Novel | hum | 763 | 42.5 | 33.5 | 278 | 8 | ADFS34710 | Human | PRO | Adf34710 |
| 691 | 42.5 | 33.5 | 278 | 7 | ADCS80321 | Novel | hum | 764 | 42.5 | 33.5 | 278 | 8 | ADBS2025 | Novel | hum | Adc92025 |
| 692 | 42.5 | 33.5 | 278 | 7 | ADDI10828 | Human | PRO | 765 | 42.5 | 33.5 | 278 | 8 | ADBS0326 | Human | PRO | Adc90326 |
| 693 | 42.5 | 33.5 | 278 | 7 | ADCA7709 | Human | PRO | 766 | 42.5 | 33.5 | 278 | 8 | ADBS1473 | Novel | hum | Adc91473 |
| 694 | 42.5 | 33.5 | 278 | 7 | ADCS9769 | Human | PRO | 767 | 42.5 | 33.5 | 278 | 8 | ADGO2052 | Human | PRO | Adg02052 |
| 695 | 42.5 | 33.5 | 278 | 7 | ADDO9238 | Novel | hum | 768 | 42.5 | 33.5 | 278 | 8 | ADG21838 | Novel | hum | Adg21838 |
| 696 | 42.5 | 33.5 | 278 | 7 | ADDO40951 | Novel | hum | 769 | 42.5 | 33.5 | 278 | 8 | ADFI19908 | Human | PRO | Adfi19908 |
| 697 | 42.5 | 33.5 | 278 | 7 | ADDO52090 | Human | PRO | 770 | 42.5 | 33.5 | 278 | 8 | ADFI97814 | Human | PRO | Adfi97814 |
| 698 | 42.5 | 33.5 | 278 | 7 | ADDS2830 | Human | PRO | 771 | 42.5 | 33.5 | 278 | 8 | ADG24031 | Novel | hum | Adg24031 |
| 699 | 42.5 | 33.5 | 278 | 7 | ADDS3382 | Novel | hum | 772 | 42.5 | 33.5 | 278 | 8 | ADFS98385 | Human | PRO | Adf98385 |
| 700 | 42.5 | 33.5 | 278 | 7 | ADDS1538 | Human | PRO | 773 | 42.5 | 33.5 | 278 | 8 | ADGO3216 | Novel | hum | Adg03216 |
| 701 | 42.5 | 33.5 | 278 | 7 | ADDO2337 | Human | PRO | 774 | 42.5 | 33.5 | 278 | 8 | ADFI98937 | Human | PRO | Adfi98937 |
| 702 | 42.5 | 33.5 | 278 | 7 | ADDO1771 | Human | PRO | 775 | 42.5 | 33.5 | 278 | 8 | ADFI6522 | Human | PRO | Adfi6522 |
| 703 | 42.5 | 33.5 | 278 | 7 | ADDS5953 | Novel | hum | 776 | 42.5 | 33.5 | 278 | 8 | ADGO4981 | Human | PRO | Adg04981 |
| 704 | 42.5 | 33.5 | 278 | 7 | ADDO92270 | Human | PRO | 777 | 42.5 | 33.5 | 278 | 8 | ADGI19248 | Human | PRO | Adgi19248 |
| 705 | 42.5 | 33.5 | 278 | 7 | ADDO91166 | Human | PRO | 778 | 42.5 | 33.5 | 278 | 8 | ADGI3085 | Novel | hum | Adgi3085 |
| 706 | 42.5 | 33.5 | 278 | 7 | ADBO3780 | Human | PRO | 779 | 42.5 | 33.5 | 278 | 8 | ADGO8142 | Novel | hum | Adg08142 |
| 707 | 42.5 | 33.5 | 278 | 7 | ADBS2077 | Novel | hum | 780 | 42.5 | 33.5 | 278 | 8 | ADGI5312 | Human | PRO | Adgi5312 |
| 708 | 42.5 | 33.5 | 278 | 7 | ADBE22009 | Human | PRO | 781 | 42.5 | 33.5 | 278 | 8 | ADFI96710 | Human | PRO | Adfi96710 |
| 709 | 42.5 | 33.5 | 278 | 7 | ADDD79233 | Human | PRO | 782 | 42.5 | 33.5 | 278 | 8 | ADGO5895 | Human | PRO | Adg05895 |
| 710 | 42.5 | 33.5 | 278 | 7 | ADBE1769 | Human | PRO | 783 | 42.5 | 33.5 | 278 | 8 | ADG23479 | Novel | hum | Adg23479 |
| 711 | 42.5 | 33.5 | 278 | 7 | ADBE17586 | Human | PRO | 784 | 42.5 | 33.5 | 278 | 8 | ADGO3768 | Human | PRO | Adg03768 |
| 712 | 42.5 | 33.5 | 278 | 7 | ADDP91738 | Novel | hum | 785 | 42.5 | 33.5 | 278 | 8 | ADG24669 | Novel | hum | Adg24669 |
| 713 | 42.5 | 33.5 | 278 | 7 | ADBS3181 | Novel | hum | 786 | 42.5 | 33.5 | 278 | 8 | ADGO6966 | Novel | hum | Adg06966 |
| 714 | 42.5 | 33.5 | 278 | 7 | ADBS3733 | Novel | hum | 787 | 42.5 | 33.5 | 278 | 8 | ADGO7518 | Novel | hum | Adg07518 |
| 715 | 42.5 | 33.5 | 278 | 7 | ADDD79785 | Human | PRO | 788 | 42.5 | 33.5 | 278 | 8 | ADGS5013 | Novel | hum | Adg55013 |
| 716 | 42.5 | 33.5 | 278 | 7 | ADDD92822 | Human | PRO | 789 | 42.5 | 33.5 | 278 | 8 | ADGO6067 | Novel | hum | Adg6067 |
| 717 | 42.5 | 33.5 | 278 | 7 | ADBE19242 | Human | PRO | 790 | 42.5 | 33.5 | 278 | 8 | ADGI61781 | Novel | hum | Adgi61781 |
| 718 | 42.5 | 33.5 | 278 | 7 | ADBE18680 | Human | PRO | 791 | 42.5 | 33.5 | 278 | 8 | ADGB1982 | Human | PRO | Adgb1982 |
| 719 | 42.5 | 33.5 | 278 | 7 | ADBE2886 | Human | PRO | 792 | 42.5 | 33.5 | 278 | 8 | ADGS7221 | Novel | hum | Adgs7221 |
| 720 | 42.5 | 33.5 | 278 | 7 | ADDO95675 | Human | PRO | 793 | 42.5 | 33.5 | 278 | 8 | ADGS6669 | Novel | hum | Adgs6669 |
| 721 | 42.5 | 33.5 | 278 | 7 | ADBE22561 | Human | PRO | 794 | 42.5 | 33.5 | 278 | 8 | ADGS5565 | Novel | hum | Adgs5565 |
| 722 | 42.5 | 33.5 | 278 | 7 | ADDD78679 | Human | PRO | 795 | 42.5 | 33.5 | 278 | 8 | ADGS8325 | Novel | hum | Adgs8325 |
| 723 | 42.5 | 33.5 | 278 | 7 | ADBS32629 | Novel | hum | 796 | 42.5 | 33.5 | 278 | 8 | ADGO70691 | Novel | hum | Adg70691 |
| 724 | 42.5 | 33.5 | 278 | 7 | ADBE42321 | Human | PRO | 797 | 42.5 | 33.5 | 278 | 8 | ADGS7773 | Novel | hum | Adgs7773 |
| 725 | 42.5 | 33.5 | 278 | 7 | ADDO80337 | Human | PRO | 798 | 42.5 | 33.5 | 278 | 8 | ADGS3357 | Novel | hum | Adgs3357 |
| 726 | 42.5 | 33.5 | 278 | 7 | ADDO89365 | Human | PRO | 799 | 42.5 | 33.5 | 278 | 8 | ADGI1243 | Novel | hum | Adgi1243 |
| 727 | 42.5 | 33.5 | 278 | 7 | ADBE40649 | Human | PRO | 800 | 42.5 | 33.5 | 278 | 8 | ADGB1430 | Novel | hum | Adgb1430 |
| 728 | 42.5 | 33.5 | 278 | 7 | ADBE04448 | Human | PRO | 801 | 42.5 | 33.5 | 278 | 8 | ADGO3392 | Human | PRO | Adgo3392 |
| 729 | 42.5 | 33.5 | 278 | 7 | ADBE92577 | Human | PRO | 802 | 42.5 | 33.5 | 278 | 8 | ADHI11759 | Novel | hum | Adhi11759 |
| 730 | 42.5 | 33.5 | 278 | 7 | ADGB21286 | Novel | hum | 803 | 42.5 | 33.5 | 278 | 8 | ADGS2181 | Novel | hum | Adgs2181 |
| 731 | 42.5 | 33.5 | 278 | 7 | ADG22927 | Novel | hum | 804 | 42.5 | 33.5 | 278 | 8 | ADGS3909 | Novel | hum | Adgs3909 |
| 732 | 42.5 | 33.5 | 278 | 7 | ADFP97262 | Human | PRO | 805 | 42.5 | 33.5 | 278 | 8 | ADGB0878 | Human | PRO | Adgb0878 |
| 733 | 42.5 | 33.5 | 278 | 7 | ADGO80326 | Human | PRO | 806 | 42.5 | 33.5 | 278 | 8 | ADGS6117 | Novel | hum | Adgs6117 |
| 734 | 42.5 | 33.5 | 278 | 7 | ADG79774 | Human | PRO | 807 | 42.5 | 33.5 | 278 | 8 | ADHI2383 | Novel | hum | Adhi2383 |
| 735 | 42.5 | 33.5 | 278 | 7 | ADHS5066 | Novel | hum | 808 | 42.5 | 33.5 | 278 | 8 | ADGI61229 | Novel | hum | Adgi61229 |
| 736 | 42.5 | 33.5 | 278 | 7 | ADHS5618 | Novel | hum | 809 | 42.5 | 33.5 | 278 | 8 | ADH28316 | Novel | hum | Adh28316 |
| 737 | 42.5 | 33.5 | 278 | 7 | ADFI63837 | Novel | hum | 810 | 42.5 | 33.5 | 278 | 8 | ADGS4461 | Novel | hum | Adgs4461 |
| 738 | 42.5 | 33.5 | 278 | 7 | ADFI64786 | Novel | hum | 811 | 42.5 | 33.5 | 278 | 8 | ADGS9501 | Novel | hum | Adgs9501 |
| 739 | 42.5 | 33.5 | 278 | 7 | ADHB1699 | Novel | hum | 812 | 42.5 | 33.5 | 278 | 8 | ADLI80925 | Human | PRO | Adli80925 |
| 740 | 42.5 | 33.5 | 278 | 7 | ADHB1147 | Novel | hum | 813 | 42.5 | 33.5 | 278 | 8 | ADGO9668 | Novel | hum | Adgo9668 |
| 741 | 42.5 | 33.5 | 278 | 7 | ADMB2316 | Novel | hum | 814 | 42.5 | 33.5 | 278 | 8 | ADLI15139 | Novel | hum | Adli15139 |
| 742 | 42.5 | 33.5 | 278 | 7 | ADNI5715 | Novel | hum | 815 | 42.5 | 33.5 | 278 | 8 | ADGO9016 | Novel | hum | Adgo9016 |
| 743 | 42.5 | 33.5 | 278 | 7 | ADNI6344 | Novel | hum | 816 | 42.5 | 33.5 | 278 | 8 | ADLI4471 | Novel | hum | Adli4471 |
| 744 | 42.5 | 33.5 | 278 | 7 | ADNI15153 | Novel | hum | 817 | 42.5 | 33.5 | 278 | 8 | ADLI18066 | Novel | hum | Adli18066 |
| 745 | 42.5 | 33.5 | 278 | 7 | ADNI4611 | Novel | hum | 818 | 42.5 | 33.5 | 278 | 8 | ADFI63347 | Novel | hum | Adfi63347 |
| 746 | 42.5 | 33.5 | 278 | 7 | ADFI63285 | Novel | hum | 819 | 42.5 | 33.5 | 278 | 8 | ADJ77242 | Human | PRO | Adj77242 |
| 747 | 42.5 | 33.5 | 278 | 8 | ADCO80873 | Novel | hum | 820 | 42.5 | 33.5 | 278 | 8 | ADFI65364 | Novel | hum | Adfi65364 |
| 748 | 42.5 | 33.5 | 278 | 8 | ADDT6321 | Human | PRO | 821 | 42.5 | 33.5 | 278 | 8 | ADMI27500 | Human | PRO | Admi27500 |
| 749 | 42.5 | 33.5 | 278 | 8 | ADDB7685 | Human | PRO | 822 | 42.5 | 33.5 | 278 | 8 | ADMI42224 | Human | PRO | Admi42224 |
| 750 | 42.5 | 33.5 | 278 | 8 | ADDB6089 | Human | PRO | 823 | 42.5 | 33.5 | 278 | 8 | ADMI28086 | Human | PRO | Admi28086 |
| 751 | 42.5 | 33.5 | 278 | 8 | ADERT5537 | Human | PRO | 824 | 42.5 | 33.5 | 278 | 8 | ADDI17575 | Human | BOF | Adi17575 |
| 752 | 42.5 | 33.5 | 278 | 8 | ADERT3113 | Human | PRO | 825 | 42.5 | 33.5 | 278 | 8 | ADFI95568 | Human | PRO | Adfi95568 |
| 753 | 42.5 | 33.5 | 278 | 8 | ADERT3665 | Human | PRO | 826 | 42.5 | 33.5 | 278 | 8 | ADFI96120 | Novel | hum | Adfi96120 |
| 754 | 42.5 | 33.5 | 278 | 8 | ADERT4308 | Human | PRO | 827 | 42.5 | 33.5 | 278 | 8 | ADRI9444 | Human | ema | Adri9444 |
| 755 | 42.5 | 33.5 | 278 | 8 | ADDB7133 | Human | PRO | 828 | 42.5 | 33.5 | 279 | 4 | AAU02500 | Expressio | | Aau02500 |

| | | | | | | | | | | | | | | | |
|-----|------|------|------|---|-----------|-----------|------------|-----|----|------|-----|---|----------|----------|------------|
| 829 | 42.5 | 33.5 | 291 | 7 | ADC96763 | Adc96763 | E. faeciu | 902 | 42 | 33.1 | 278 | 8 | AD004614 | Ad004614 | Human lys |
| 830 | 42.5 | 33.5 | 351 | 6 | ABB82606 | Abb82606 | Maize X-r | 903 | 42 | 33.1 | 278 | 8 | ADQ19763 | Adq19763 | Human sof |
| 831 | 42.5 | 33.5 | 353 | 5 | ABP41913 | Abp41913 | Human ova | 904 | 42 | 33.1 | 278 | 8 | ABM81103 | Abm81103 | Tumour-as |
| 832 | 42.5 | 33.5 | 424 | 8 | ADN17579 | Adn17579 | Bacterial | 905 | 42 | 33.1 | 282 | 6 | ABU36887 | Abu36887 | Protein e |
| 833 | 42.5 | 33.5 | 429 | 1 | AA91958 | Aap91958 | Peptide e | 906 | 42 | 33.1 | 282 | 6 | ABU34865 | Abu34865 | Protein e |
| 834 | 42.5 | 33.5 | 429 | 2 | AA91587 | Aars1587 | DNA Bynt | 907 | 42 | 33.1 | 284 | 6 | ADN22257 | Adn22257 | Bacterial |
| 835 | 42.5 | 33.5 | 429 | 1 | AAU34505 | Aau34505 | E. coli c | 908 | 42 | 33.1 | 292 | 5 | AD664666 | Ad664666 | Sacharom |
| 836 | 42.5 | 33.5 | 429 | 6 | ABU28561 | Abu28561 | Protein e | 909 | 42 | 33.1 | 302 | 5 | ABG70074 | Abg70074 | Human pre |
| 837 | 42.5 | 33.5 | 429 | 6 | ADP04948 | Adp04948 | Bacterial | 910 | 42 | 33.1 | 306 | 6 | ABM69568 | Abm69568 | Photocarb |
| 838 | 42.5 | 33.5 | 429 | 8 | ADN18117 | Adn18117 | Bacterial | 911 | 42 | 33.1 | 307 | 2 | AAW93255 | Aaw93255 | Tobacco C |
| 839 | 42.5 | 33.5 | 429 | 8 | AAW73903 | Aaw73903 | E. coli D | 912 | 42 | 33.1 | 311 | 7 | ADP59532 | Adp59532 | Human pol |
| 840 | 42.5 | 33.5 | 435 | 6 | ABU31641 | Abu31641 | Protein e | 913 | 42 | 33.1 | 321 | 8 | ADN18479 | Adn18479 | Bacterial |
| 841 | 42.5 | 33.5 | 447 | 7 | ABO67770 | Abob67770 | Klebsiell | 914 | 42 | 33.1 | 324 | 6 | ABU29166 | Abu29166 | Protein e |
| 842 | 42.5 | 33.5 | 513 | 7 | ADP63833 | Adp63833 | Rat Prote | 915 | 42 | 33.1 | 324 | 7 | ADM25910 | Adm25910 | Hyperther |
| 843 | 42.5 | 33.5 | 546 | 4 | AAU23561 | Aau23561 | Novel hum | 916 | 42 | 33.1 | 326 | 2 | AAV20119 | Aav20119 | B. burgdo |
| 844 | 42.5 | 33.5 | 546 | 4 | AAU87604 | Aau87604 | Novel cen | 917 | 42 | 33.1 | 328 | 7 | ADH86358 | Adh86358 | Enterococ |
| 845 | 42.5 | 33.5 | 546 | 8 | AD154919 | Ad154919 | Novel hum | 918 | 42 | 33.1 | 328 | 7 | ADP58887 | Adp58887 | E. faeciu |
| 846 | 42.5 | 33.5 | 568 | 8 | ADU87314 | Aau87314 | Novel cen | 919 | 42 | 33.1 | 331 | 8 | ADN47212 | Adn47212 | Thermococ |
| 847 | 42.5 | 33.5 | 568 | 8 | AD154629 | Ad154629 | Novel hum | 920 | 42 | 33.1 | 349 | 5 | ADP73534 | Adp73534 | Candida a |
| 848 | 42.5 | 33.5 | 586 | 2 | AA949855 | Aar49855 | Sequence | 921 | 42 | 33.1 | 351 | 5 | ABP73057 | Abp73057 | E. faeciu |
| 849 | 42.5 | 33.5 | 624 | 3 | AAU22925 | Aau22925 | Novel hum | 922 | 42 | 33.1 | 357 | 6 | ABU24898 | Abu24898 | Protein e |
| 850 | 42.5 | 33.5 | 866 | 4 | AA869345 | Aab69345 | HIV-1 non | 923 | 42 | 33.1 | 358 | 8 | ADP30357 | Adp30357 | Human sec |
| 851 | 42.5 | 33.5 | 883 | 4 | AA882761 | Aab82761 | Ancestral | 924 | 42 | 33.1 | 359 | 2 | AA120118 | Aa120118 | B. burgdo |
| 852 | 42.5 | 33.5 | 1300 | 7 | ADP63060 | Adp63060 | Rat Prote | 925 | 42 | 33.1 | 366 | 5 | ABP29871 | Abp29871 | Streptoco |
| 853 | 42.5 | 33.5 | 1809 | 7 | ADP55015 | Adp55015 | Rat Prote | 926 | 42 | 33.1 | 370 | 7 | ADP31201 | Adp31201 | Human dia |
| 854 | 42.5 | 33.5 | 1809 | 7 | ADP55009 | Adp55009 | Rat Prote | 927 | 42 | 33.1 | 372 | 4 | AA681063 | Aa681063 | HIV prote |
| 855 | 42.5 | 33.5 | 1809 | 7 | ADP55006 | Adp55006 | Rat Prote | 928 | 42 | 33.1 | 374 | 8 | AD142450 | Ad142450 | Plant tra |
| 856 | 42.5 | 33.5 | 1809 | 7 | ADP55012 | Adp55012 | Rat Prote | 929 | 42 | 33.1 | 376 | 8 | AD142449 | Ad142449 | Plant tra |
| 857 | 42 | 33.1 | 55 | 8 | ADP508183 | Aay91084 | Staphyloc | 930 | 42 | 33.1 | 395 | 4 | AAU03633 | Aau03633 | Group B S |
| 858 | 42 | 33.1 | 60 | 4 | AA830625 | Aay91084 | Human LPA | 931 | 42 | 33.1 | 395 | 5 | ABP28295 | Abp28295 | Streptoco |
| 859 | 42 | 33.1 | 60 | 5 | AAE15301 | Aae15301 | Fragment | 932 | 42 | 33.1 | 396 | 4 | ABG04922 | Abg04922 | Novel hum |
| 860 | 42 | 33.1 | 60 | 6 | ABG74257 | Abg74257 | Human LPA | 933 | 42 | 33.1 | 410 | 4 | ABG63528 | Abg63528 | Amino aci |
| 861 | 42 | 33.1 | 60 | 6 | ADU93807 | Adu93807 | Human Lys | 934 | 42 | 33.1 | 415 | 4 | AA862035 | Aa862035 | P. furios |
| 862 | 42 | 33.1 | 60 | 8 | ADN49491 | Adn49491 | Human Lys | 936 | 42 | 33.1 | 420 | 4 | ADP54467 | Adp54467 | Bacterial |
| 863 | 42 | 33.1 | 60 | 8 | ADN49491 | Adn49491 | Human Lys | 937 | 42 | 33.1 | 431 | 8 | ADP54467 | Adp54467 | Bacterial |
| 864 | 42 | 33.1 | 70 | 8 | ADP04630 | Adp04630 | Human Lys | 938 | 42 | 33.1 | 435 | 3 | AA83780 | Aa83780 | Human ATI |
| 865 | 42 | 33.1 | 70 | 3 | AA612432 | Aag12432 | Zea maye | 939 | 42 | 33.1 | 436 | 5 | AAU74345 | Aau74345 | Human cye |
| 866 | 42 | 33.1 | 78 | 8 | ADP41591 | Adp41591 | Bacterial | 940 | 42 | 33.1 | 436 | 7 | ADP39836 | Adp39836 | Protein e |
| 867 | 42 | 33.1 | 82 | 7 | ADP00634 | Adp00634 | Enterococ | 941 | 42 | 33.1 | 436 | 8 | ADP66697 | Adp66697 | Human pro |
| 868 | 42 | 33.1 | 95 | 8 | ADN46185 | Adn46185 | Thermococ | 942 | 42 | 33.1 | 436 | 8 | ADP66355 | Adp66355 | Human pro |
| 869 | 42 | 33.1 | 115 | 6 | ADP434222 | Adp434222 | Actinocoba | 943 | 42 | 33.1 | 440 | 3 | AA83777 | Aa83777 | Mouss ATI |
| 870 | 42 | 33.1 | 117 | 3 | AA612617 | Aag12617 | Zea maye | 944 | 42 | 33.1 | 450 | 6 | ABU41584 | Abu41584 | Protein e |
| 871 | 42 | 33.1 | 120 | 8 | ADP065051 | Adp065051 | Novel hum | 945 | 42 | 33.1 | 451 | 6 | ABU39727 | Abu39727 | Protein e |
| 872 | 42 | 33.1 | 127 | 3 | AA612616 | Aag12616 | Zea maye | 946 | 42 | 33.1 | 451 | 8 | ADN46347 | Adn46347 | Thermococ |
| 873 | 42 | 33.1 | 129 | 7 | ADH86956 | Adh86956 | Enterococ | 947 | 42 | 33.1 | 451 | 8 | ADP29591 | Adp29591 | Arabidops |
| 874 | 42 | 33.1 | 156 | 3 | AA612615 | Aag12615 | Zea maye | 948 | 42 | 33.1 | 459 | 5 | ABP53427 | Abp53427 | Lactococ |
| 875 | 42 | 33.1 | 178 | 6 | ABM71384 | Abm71384 | Staphyloc | 949 | 42 | 33.1 | 459 | 8 | ADP52629 | Adp52629 | Bacterial |
| 876 | 42 | 33.1 | 185 | 8 | ADH72789 | Adh72789 | B. subcili | 950 | 42 | 33.1 | 460 | 7 | ADG33874 | Adg33874 | Actinomyc |
| 877 | 42 | 33.1 | 206 | 5 | ABP51289 | Abp51289 | Human MDD | 951 | 42 | 33.1 | 462 | 6 | ABU25489 | Abu25489 | Protein e |
| 878 | 42 | 33.1 | 211 | 6 | ABM67384 | Abm67384 | Photocarb | 952 | 42 | 33.1 | 464 | 8 | ADN24352 | Adn24352 | Bacterial |
| 879 | 42 | 33.1 | 218 | 4 | AAW5257 | Aam25257 | Human pro | 953 | 42 | 33.1 | 470 | 5 | ABR52410 | AbR52410 | Protein e |
| 880 | 42 | 33.1 | 222 | 5 | ABP39419 | Abp39419 | Staphyloc | 954 | 42 | 33.1 | 474 | 4 | AAU46847 | Aau46847 | Proplionib |
| 881 | 42 | 33.1 | 222 | 8 | ADP04520 | Adp04520 | Staphyloc | 955 | 42 | 33.1 | 474 | 6 | ABM43366 | Abm43366 | Proplionib |
| 882 | 42 | 33.1 | 225 | 6 | ABU50105 | Abu50105 | Protein e | 956 | 42 | 33.1 | 485 | 4 | AA663531 | Aa663531 | Amino aci |
| 883 | 42 | 33.1 | 240 | 4 | AA895831 | Aab95831 | Human pro | 957 | 42 | 33.1 | 490 | 8 | ADP57426 | Adp57426 | Bacterial |
| 884 | 42 | 33.1 | 240 | 7 | ADP39837 | Adp39837 | Protein e | 958 | 42 | 33.1 | 509 | 5 | ABP49686 | Abp49686 | Lactococ |
| 885 | 42 | 33.1 | 244 | 7 | ADP10006 | Adp10006 | Human NOV | 959 | 42 | 33.1 | 517 | 8 | ADP65825 | Adp65825 | Novel hum |
| 886 | 42 | 33.1 | 244 | 8 | ADN20298 | Adn20298 | Bacterial | 960 | 42 | 33.1 | 518 | 4 | ABG16535 | Abg16535 | Novel hum |
| 887 | 42 | 33.1 | 247 | 5 | ABP28843 | Abp28843 | Streptoco | 961 | 42 | 33.1 | 529 | 3 | AA629590 | Aa629590 | Arabidops |
| 888 | 42 | 33.1 | 250 | 4 | ABP64023 | Abp64023 | Drosophili | 962 | 42 | 33.1 | 541 | 6 | ABU29251 | Abu29251 | Protein e |
| 889 | 42 | 33.1 | 252 | 7 | ADP64936 | Adp64936 | Human pro | 963 | 42 | 33.1 | 541 | 6 | ABU29521 | Abu29521 | Protein e |
| 890 | 42 | 33.1 | 258 | 6 | ADP36831 | Adp36831 | Actinocoba | 964 | 42 | 33.1 | 542 | 3 | AA629559 | Aa629559 | Arabidops |
| 891 | 42 | 33.1 | 274 | 2 | AAW88117 | Aaw88117 | Human Lys | 965 | 42 | 33.1 | 545 | 7 | ADH86674 | Adh86674 | Enterococ |
| 892 | 42 | 33.1 | 275 | 8 | ADN25015 | Adn25015 | Bacterial | 966 | 42 | 33.1 | 546 | 6 | ABU22008 | Abu22008 | Protein e |
| 893 | 42 | 33.1 | 278 | 2 | AAW29875 | Aaw29875 | Lyophosp | 967 | 42 | 33.1 | 550 | 2 | AA623923 | Aa623923 | Amino aci |
| 894 | 42 | 33.1 | 278 | 3 | AAW6302 | Aaw6302 | Human Lys | 968 | 42 | 33.1 | 559 | 5 | ADJ33778 | Adj33778 | Protein o |
| 895 | 42 | 33.1 | 278 | 3 | AAW96589 | Aay96589 | Human Lys | 969 | 42 | 33.1 | 560 | 4 | AAU31067 | Aau31067 | Novel hum |
| 896 | 42 | 33.1 | 278 | 4 | AAW91082 | Aay91082 | Human Lys | 970 | 42 | 33.1 | 564 | 8 | ABP66319 | Abp66319 | Drosophili |
| 897 | 42 | 33.1 | 278 | 4 | AAW30623 | Aab30623 | Amino aci | 971 | 42 | 33.1 | 564 | 4 | ADP89714 | Adp89714 | Antagonis |
| 898 | 42 | 33.1 | 278 | 6 | AAE15289 | Abg74252 | Human LPA | 972 | 42 | 33.1 | 574 | 8 | ADK70709 | Adk70709 | Coliapsin |
| 899 | 42 | 33.1 | 278 | 6 | ABG74252 | Abg74252 | Human Lys | 973 | 42 | 33.1 | 576 | 2 | AA666929 | Aa666929 | AMWL chro |
| 900 | 42 | 33.1 | 278 | 8 | ADJ93791 | Adj93791 | Human Lys | 974 | 42 | 33.1 | 585 | 4 | AA663530 | Aa663530 | Amino aci |
| 901 | 42 | 33.1 | 278 | 8 | ADN49475 | Adn49475 | Human Lys | 974 | 42 | 33.1 | 585 | 4 | AA663530 | Aa663530 | Amino aci |


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975 42 33.1 585 6 ABU43406 Abu43406 Protein e
976 42 33.1 596 4 AAU33748 Aau33748 Staphyloc
977 42 33.1 603 6 AAE37962 Aae37962 Human kin
978 42 33.1 604 4 AAU36932 Aau36932 Staphyloc
979 42 33.1 604 6 ABU6053 Abui6053 Protein e
980 42 33.1 604 6 ABM73224 Abm73224 Staphyloc
981 42 33.1 611 8 ABN22551 Abn22551 Bacterial
982 42 33.1 618 5 ABP38324 Abp38324 Staphyloc
983 42 33.1 618 8 ADS04832 Adso4832 Staphyloc
984 42 33.1 621 7 ADP30481 Adp30481 Rat angio
985 42 33.1 650 8 ADK70696 Adk70696 Chicken C
986 42 33.1 659 5 ABB93561 Abb93561 Herbicida
987 42 33.1 658 8 ADS24539 Ads24539 Bacterial
988 42 33.1 698 8 ADS29165 Ads29165 Bacterial
989 42 33.1 747 6 ADR86215 Ader86215 Aspergill
990 42 33.1 769 6 ABU20332 Abu20332 Protein e
991 42 33.1 816 2 AAR66931 Aar66931 AMWL chro
992 42 33.1 835 3 AAB01470 Aab01470 Human CAR
993 42 33.1 835 4 AAB65674 Aab65674 Novel pro
994 42 33.1 835 6 ABR41886 Abr41886 Human car
995 42 33.1 835 8 ADI29282 Adi29282 Human MAR
996 42 33.1 835 8 ADOS7048 Ados7048 Human car
997 42 33.1 885 2 AAR66930 Aar66930 AMWL chro
998 42 33.1 889 4 AAU33860 Aau33860 Staphyloc
999 42 33.1 902 7 ABR62799 Abr62799 VISA Scap
1000 42 33.1 910 7 ABR62791 Abr62791 MESA 2-Xe

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ALIGNMENTS

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RESULT 1
AD195325 standard; protein; 221 AA.
XX AD195325;
AC AD195325;
XX
DT 04-NOV-2004 (first entry)
XX
DE OSPF-related SARS coronavirus matrix protein.
XX
KW immune response; overlapping synthetic peptide formulation; OSPF;
KW immunostimulant; virucide; antibacterial; antiparasitic; cytostatic;
KW vaccine; viral; bacterial; parasitic infection; prion disease;
KW neoplastic; toxin; matrix.
XX
OS SARS coronavirus.
XX
PN MO2004002415-A2.
XX
PD 08-JAN-2004.
XX
PF 27-JUN-2003; 2003WO-US020322.
XX
PR 27-JUN-2002; 2002US-0392718P.
XX
PA (DAND ) DANA FARBER CANCER INST INC.
XX
PI Ruprecht RM, Jiang S;
XX
PI WPI; 2004-082868/08.
XX
DR
XX
XX Modulating an immune response, useful for treating immune disorders, e.g.
XX PT viral, bacterial and parasitic infections, prion diseases, or neoplastic
XX PT diseases, administering to a subject an overlapping synthetic peptide
XX PT formulation.
XX
XX Claim 13; SEQ ID NO 233; 175bp; English.
XX
XX The invention relates to a novel method for modulating an immune response
XX CC comprising administering to a subject an overlapping synthetic peptide
XX CC formulation (OSPF) which comprises a combination of single chain peptides
XX CC corresponding to the amino acid sequence of a protein of interest. The

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CC method of the invention has immunostimulant, virucide, antibacterial,
CC antiparasitic and cytostatic applications and may be useful during
CC vaccine production and for treating immune disorders including viral,
CC bacterial and parasitic infections, prion diseases, neoplastic diseases,
CC as well as providing protection against toxins. The current sequence is
CC that of the OSPF-related SARS coronavirus matrix protein of the
CC invention.
XX
SQ Sequence 221 AA;

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Query Match 88.2%; Score 112; DB 8; Length 221;
Best Local Similarity 100.0%; Pred. No. 5.8e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 4 MADNGTITVEELKQLLEQNNLV 25
Db 1 MADNGTITVEELKQLLEQNNLV 22

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RESULT 2
AAM19303 standard; protein; 54 AA.
XX AAM19303;
AC AAM19303;
XX
DT 12-OCT-2001 (first entry)
XX
DE Peptide #5737 encoded by probe for measuring cervical gene expression.
XX
XX Probe; human; microarray; gene expression; cervical epithelial cell;
XX KW cervical cancer.
XX
XX Homo sapiens.
XX
OS
XX
PN MO200157278-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000670.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn Sq, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488901/53.
XX
DR
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX PT gene expression in human cervical epithelial cells.
XX
XX Claim 27; SEQ ID NO 24129; 487bp; English.
XX
XX
XX The present invention relates to human single exon nucleic acid probes
XX CC (SENP; see AAT110068-AAT18459). The present sequence is a peptide encoded
XX CC by one such probe. The SENPs are derived from human HeLa cells. The SENPs
XX CC can be used to produce a single exon microarray, which can be used for
XX CC measuring human gene expression in a sample derived from human cervical
XX CC epithelial cells. By measuring gene expression, the probes are therefore
XX CC useful in grading and/or staging of diseases of the cervix, notably
XX CC cervical cancer. Note: The sequence data for this patent did not form
XX CC part of the printed specification, but was obtained in electronic format
XX CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 54 AA;

```

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Query Match 43.3%; Score 55; DB 4; Length 54;

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Best Local Similarity 41.7%; Pred. No. 6.1;
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
QY 1 KKKMADNGTITVEELKQLEQWNL 24
DB 20 KSDLEDKQVSVVEAKNRABQWNV 43

RESULT 3

ABB38595
ID ABB38595 standard; peptide, 54 AA.

AC ABB38595;

DT 04-FEB-2002 (first entry)

XX Peptide #6101 encoded by human foetal liver single exon probe.

XX Human; foetal liver; gene expression; single exon nucleic acid probe.

OS Homo sapiens.

PN WO200157277-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US000669.

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-483447/52.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

XX gene expression in human fetal liver.

XX Claim 27; SEQ ID NO 31230; 639pp + Sequence Listing; English.

XX The invention relates to a single exon nucleic acid probe for measuring

XX human gene expression in a sample derived from human foetal liver. The

XX single exon nucleic acid probes may be used for predicting, measuring and

XX displaying gene expression in samples derived from human fetal liver. The

XX present sequence is a peptide encoded by a single exon nucleic acid probe

XX of the invention. Note: The sequence data for this patent did not form

XX part of the printed specification, but was obtained in electronic format

XX directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 54 AA;

XX Query Match 43.3%; Score 55; DB 4; Length 54;

XX Best Local Similarity 41.7%; Pred. No. 6.1;

XX Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

DT 17-OCT-2001 (first entry)
XX Peptide #6086 encoded by probe for measuring placental gene expression.
DE Probe; microarray; human; placenta; antenatal diagnosis;
XX genetic disorder.
KW Homo sapiens.

OS Homo sapiens.

PN WO200157272-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US000663.

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488897/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

XX gene expression in human placenta.

XX Claim 27; SEQ ID NO 32318; 654pp; English.

XX The present invention relates to single exon nucleic acid probes (SNP:

XX see AAI31315-AA157546). The present sequence is a peptide encoded by one

XX such probe. The probes are useful for producing a microarray for

XX predicting, measuring and displaying gene expression in samples derived

XX from human placenta. The probes are useful for antenatal diagnosis of

XX human genetic disorders

XX Sequence 54 AA;

XX Query Match 43.3%; Score 55; DB 4; Length 54;

XX Best Local Similarity 41.7%; Pred. No. 6.1;

XX Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

XX 1 KKKMADNGTITVEELKQLEQWNL 24

XX 20 KSDLEDKQVSVVEAKNRABQWNV 43

XX RESULT 5

XX ABB23710

XX ID ABB23710 standard; protein; 54 AA.

XX ABB23710;

XX 23-JAN-2002 (first entry)

XX Protein #5709 encoded by probe for measuring heart cell gene expression.

XX Human; gene expression; heart; microarray; vascular system;

XX cardiovascular disease; hypertension; cardiac arrhythmia;

XX congenital heart disease.

XX Homo sapiens.

XX WO200157274-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000666.

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XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207455P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488899/53.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT hearts.
PS
PS Claim 15; SEQ ID NO 25480; 530bp; English.
XX
XX The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart (see
CC AB#21555-ABA1305). The present sequence is a protein encoded by one such
CC probe. The probes may be used for predicting, measuring and displaying
CC gene expression in samples derived from the human heart via microarrays.
CC By measuring gene expression, the probes are useful for predicting,
CC diagnosing, grading, staging, monitoring and prognosing diseases of the
CC human heart and vascular system e.g. cardiovascular disease,
CC hypertension, cardiac arrhythmias and congenital heart disease.
CC Sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/Published_pct_sequences
XX
SQ Sequence 54 AA;
XX
Query Match      43.3%; Score 55; DB 4; Length 54;
Best Local Similarity 41.7%; Pred. No. 6.1; Mismatches 10; Gaps 0;
Matches 10; Conservative 4; Indels 0;
QY      1 KKKMADNGTIVTEELKQLLEQWNTL 24
Db       | : | | | | | | | | | |
        20 KSLEDKRQVSVEAKNRABEQMNV 43
XX
RESULT 6
AAM71757
ID AAM71757 standard; protein; 54 AA.
XX
AC AAM71757;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 32063.
XX
KW Human; bone marrow expressed exon; Gene expression analysis; probe;
XX microarray; cancer; leukemia; lymphoma; myeloma.
XX
OS Homo sapiens.
XX
XX WO200157276-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000668.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
```

PA (MOLE-) MOLECULAR DYNAMICS INC.

Pt Penn SG, Hanzel DK, Chen W, Rank DR;

XX MPI; 2001-488900/53.

DR Human genome-derived single exon nucleic acid probes useful for analyzing

Pt gene expression in human bone marrow.

XX Example 4; SEQ ID NO 32063; 658bp + Sequence Listing; English.

XX The present invention provides a number of single exon nucleic acid

CC probes which are derived from genomic sequences expressed in the human

CC bone marrow. They can be used to measure gene expression in bone marrow

CC samples, which may enable the improved diagnosis and treatment of cancers

CC such as lymphoma, leukemia and myeloma. The present sequence is a

CC protein encoded by one of the probes of the invention

XX

SQ Sequence 54 AA;

Query Match 43.3%; Score 55; DB 4; Length 54;
Best Local Similarity 41.7%; Pred.No. 6.1;
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0,

Oy 1 KKKRADNGTIVEELKQLLEQNTL 24
: : ::||| | ||||:
20 KSDLEDKROVSVEEAKRNAEQMNV 43

Db

RESULT 7
AAMS9222
ID AAMS9222 standard; protein; 54 AA.
XX
AC AAMS9222;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 31327.
XX
KW Human; brain expressed exon; gene expression analysis; probe; microarray;
KV Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
XX
OS Homo sapiens.
XX
FN WO200157275-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000667.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX MPI; 2001-483446/52.
XX
DR Single exon nucleic acid probes for analyzing gene expression in human
Pt brains.
XX
PS Example 4; SEQ ID NO 31327; 650pp + Sequence Listing; English.
XX

The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system

CC schizoprenia, Niemann-Pick's disease. This sequence corresponds to a
 CC protein of the invention.

XX
 CC Sequence 206 AA;

Query Match 43.3%; Score 55; DB 8; Length 206;

Best Local Similarity 41.7%; Pred. No. 26;

Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy 1 KKKMADNGTITVEELKQLEQNL 24

Db 128 KSDLEDKQVSVSEAKNRAEQMNV 151

RESULT 16

ADD14139

ID ADD14139 standard; protein; 209 AA.

XX ADD14139;

XX 01-JAN-2004 (first entry)

DE Human src biomarker polypeptide SEQ ID NO:328.

XX predictor set; protein tyrosine kinase activity modulator;

KM protein tyrosine kinase pathway; protein tyrosine kinase; cytosolic;

XX gene therapy; drug sensitivity; genetic profile; cancer; human.

OS Homo sapiens.

XX MO2003062395-A2.

XX 31-JUL-2003.

XX 17-JAN-2003; 2003WO-US001981.

XX 18-JAN-2002; 2002US-0350061P.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

XX Huang F, Fairchild CR, Lee FY, Shaw P;

XX WPI; 2003-636735/60.

XX N-PSDB; ADD14741.

XX New polynucleotides and polypeptides for predicting the activity of
 XX compounds that interact with protein tyrosine kinases and/or protein
 XX tyrosine kinase pathways.

XX Claim 10; SEQ ID NO 328; 139pp; English.

CC The present invention describes a predictor set comprising a plurality of
 CC polynucleotides or polypeptides whose expression pattern is predictive of
 CC the response of cells to treatment with a compound that modulates protein
 CC tyrosine kinase activity or members of the protein tyrosine kinase
 CC pathway. Also described: (1) predicting whether a compound is capable of
 CC modulating the activity of cells, comprising obtaining a sample of cells,
 CC determining whether the cells express a plurality of markers, and
 CC correlating the expression of the markers to the compound's ability to
 CC modulate the activity of the cells; (2) a plurality of cell lines for
 CC identifying polynucleotides and polypeptides whose expression levels
 CC correlate with compound sensitivity or resistance of cells associated
 CC with a disease state; and (3) identifying polynucleotides and
 CC polypeptides that predict compound sensitivity or resistance of cells
 CC associated with a disease state, comprising subjecting the plurality of
 CC cell lines to one or more compounds, analysing the expression pattern of
 CC a microarray of polynucleotides or polypeptides, and selecting
 CC polynucleotides or polypeptides that predict the sensitivity or
 CC resistance of cells associated with a disease state by using the
 CC expression pattern of the microarray. The polynucleotides and
 CC polypeptides have cytosolic activities, and can be used in gene therapy.
 CC The polynucleotides and polypeptides are useful in predicting the
 CC activity of compounds that interact with protein tyrosine kinases and/or

CC protein tyrosine kinase pathways. These may be used in determining drug
 CC sensitivity in patients to allow the development of individualized
 CC genetic profiles which aid in treating diseases and disorders (e.g.
 CC cancer) based on patient response at a molecular level. The present
 CC sequence is used in the exemplification of the present invention.

XX Sequence 209 AA;

Query Match 43.3%; Score 55; DB 7; Length 209;

Best Local Similarity 41.7%; Pred. No. 26;

Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy 1 KKKMADNGTITVEELKQLEQNL 24

Db 131 KSDLEDKQVSVSEAKNRAEQMNV 154

RESULT 17

ADP24705

XX ADP24705 standard; protein; 209 AA.

XX ADP24705;

XX 18-NOV-2004 (first entry)

DE PRO polypeptide SEQ ID NO:1883.

XX PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;

XX osteopathic; antidiabetic; dermatological; antiporiatic; antiallergic;

XX antidiabetic; hepatotropic; reepiratory; gene therapy; immune system.

XX Unidentified.

XX WO2004041170-A2.

XX 21-MAY-2004.

XX 30-OCT-2003; 2003WO-US034312.

XX 01-NOV-2002; 2002US-0423394P.

XX (GETH) GENENTECH INC.

XX Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;

XX WPI; 2004-419628/39.

XX N-PSDB; ADP24704.

XX New PRO polypeptides and polynucleotides, useful for treating e.g.
 XX erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
 XX nervous system.

XX Claim 7; SEQ ID NO 1883; 2940pp; English.

CC The invention relates to a novel isolated nucleic acid and the PRO
 CC polypeptide encoded by it. A protein of the invention has
 CC antiinflammatory, antirheumatic, antirheumatic, immunosuppressive,
 CC osteopathic, antidiabetic, dermatological, antiporiatic, antiallergic,
 CC antidiabetic, hepatotropic, and respiratory activity. A polynucleotide
 CC of the invention may have a use in gene therapy. The PRO polypeptide, its
 CC agonist, antagonist, or antibody that specifically binds to the
 CC polypeptide is useful for treating an immune related disorder such as
 CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
 CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
 CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
 CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
 CC disease, a demyelinating disease of the central or peripheral nervous
 CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
 CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
 CC disease, infectious or autoimmune chronic active hepatitis, primary

CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
 CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
 CC disease, an autoimmune or immune-mediated skin disease, a bulloous skin
 CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
 CC disease, asthma, allergic rhinitis, atopic dermatitis, food
 CC hypersensitivity, urticaria, an immunologic disease of the lung,
 CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
 CC pneumonitis, a transplantation associated disease, graft rejection or
 CC graft-versus-host disease. The present sequence represents a PRO protein
 CC of the invention.
 XX
 SQ Sequence 209 AA;
 Query Match 43.3%; Score 55; DB 8; Length 209;
 Best Local Similarity 41.7%; Pred. No. 26;
 Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
 QY 1 KKKMADNGITTYEELKQLEQNTL 24
 DB 131 KSDLEDKQVSEAKNRAEQNNV 154
 RESULT 18
 ADS34490 standard; protein; 209 AA.
 XX
 AC ADS34490;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE POSH protein associated protein #54.
 XX
 KW cytosolic; neurotropic; neuroprotective; antiparkinsonian; anticonvulsant;
 KW antiviral; neurotropic; central nervous system; POSH polypeptide;
 KW POSH-associated protein; POSH-AP; HERPUDI; Ubiquitin ligase;
 KW antiviral agent; anti-apoptotic agent; anti-cancer agent;
 KW secretory pathway trafficking inhibitor;
 KW neurological disorder progression disorder; Alzheimer's disease;
 KW Parkinson's disease; Huntington's disease; schizophrenia;
 KW Niemann-Pick's disease.
 XX
 OS Homo sapiens.
 XX
 PN WO2004078130-A2.
 PD 16-SEP-2004.
 XX
 PF 02-MAR-2004; 2004WO-US006308.
 XX
 PR 03-MAR-2003; 2003US-0451437P.
 PR 05-MAR-2003; 2003US-0452284P.
 PR 19-MAR-2003; 2003US-0455760P.
 PR 20-MAR-2003; 2003US-0456640P.
 PR 03-APR-2003; 2003US-0460526P.
 PR 04-APR-2003; 2003US-0460792P.
 PR 21-APR-2003; 2003US-0464285P.
 PR 09-MAY-2003; 2003US-0469462P.
 PR 15-MAY-2003; 2003US-0471378P.
 PR 20-MAY-2003; 2003US-0472327P.
 PR 30-MAY-2003; 2003US-0474706P.
 PR 03-JUN-2003; 2003US-0475825P.
 PR 17-JUN-2003; 2003US-0479317P.
 PR 19-JUN-2003; 2003US-0480215P.
 PR 19-JUN-2003; 2003US-0480376P.
 PR 08-AUG-2003; 2003US-0493860P.
 PR 28-AUG-2003; 2003US-049834P.
 PR 16-SEP-2003; 2003US-0503931P.
 PR 10-NOV-2003; 2003WO-US035712.
 PR 05-FEB-2004; 2004WO-US003600.
 PR 02-MAR-2004; 2004US-0549896P.
 XX
 PA (PROT-) PROTEOLOGICS INC.
 XX

PI Taglicht DN, Alroy I, Reiss Y, Yaar L, Ben-Avraham D, Tuvia S;
 PI Greener T;
 XX
 DR WPI; 2004-662346/64.
 XX
 PT Isolated, purified or recombinant complex, useful for identifying an
 PT antiviral, anti-apoptotic or anti-cancer, comprising POSH polypeptide and
 PT POSH-associated protein (POSH-AP).
 PS
 XS Disclosure; SEQ ID NO 254; 374pp; English.
 XX
 CC The invention relates to an isolated, purified or recombinant complex (I)
 CC comprising a POSH polypeptide and a POSH-associated protein (POSH-AP) (a)
 CC or HERPUDI and a Ubiquitin ligase (b). Methods using (I), (a) or (b) are
 CC useful for identifying an agent that modulates an activity of a POSH
 CC polypeptide or POSH-AP, for identifying an antiviral agent, an anti-
 CC apoptotic agent, an anti-cancer agent, an agent that inhibits trafficking
 CC of a protein through the secretory pathway, an agent that inhibits the
 CC progression of a neurological disorder, an agent that modulates a POSH
 CC function, an agent that modulates a HERPUDI function. The methods can be
 CC used for treating a viral infection, for inhibiting an activity of a POSH
 CC -AP in a cell, for treating a POSH-associated disease in a subject. The
 CC POSH-associated disease is viral infection, POSH-associated cancer or
 CC POSH-associated neurological disorder. The methods are useful for
 CC treating or preventing POSH-associated neurological disorder in a subject
 CC e.g. Alzheimer's disease, Parkinson's disease, Huntington's disease,
 CC schizophrenia, Niemann-Pick's disease. This sequence corresponds to a
 CC protein of the invention.
 XX
 SQ Sequence 209 AA;
 Query Match 43.3%; Score 55; DB 8; Length 209;
 Best Local Similarity 41.7%; Pred. No. 26;
 Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
 QY 1 KKKMADNGITTYEELKQLEQNTL 24
 DB 131 KSDLEDKQVSEAKNRAEQNNV 154
 RESULT 19
 AAU31548
 ID AAU31548 standard; protein; 246 AA.
 XX
 AC AAU31548;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Novel human secreted protein #2039.
 XX
 KW Human; vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200179449-A2.
 PD 25-OCT-2001.
 XX
 PF 16-APR-2001; 2001WO-US008656.
 XX
 PR 18-APR-2000; 2000US-00552929.
 PR 26-JAN-2001; 2001US-00770160.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YF, Liu C, Drmanac RT;
 XX
 DR WPI; 2001-611725/70.
 XX
 PT Nucleic acids encoding a range of human polypeptides, useful in genetic
 PT vaccination, testing and therapy.

XX Claim 20; Page 457; 765pp; English.

XX The invention relates to novel human secreted polypeptides. The
CC polypeptides and antibodies to the polypeptides are useful for
CC determining the presence of or predisposition to a disease associated
CC with altered levels of polypeptide. The polypeptides are also useful for
CC identifying agents (agonists and antagonists) that bind to them. Cells
CC expressing the proteins are useful for identifying a therapeutic agent
CC for use in treatment of a pathology related to aberrant expression or
CC physiological interactions of the polypeptide. Vectors comprising the
CC nucleic acids encoding the polypeptides and cells genetically engineered
CC to express them are also useful for producing the proteins. The proteins
CC are useful in genetic vaccination, testing and therapy, and can be used
CC as nutritional supplements. They may be used to increase stem cell
CC proliferation, to regulate haematopoiesis; and in bone, cartilage, tendon
CC and/or nerve tissue growth or regeneration; immune suppression and/or
CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
CC AAU29510-AAU33304 represent the amino acid sequences of novel human
CC secreted proteins of the invention

XX Sequence 246 AA;

XX

XX Query Match 43.3%; Score 55; DB 4; Length 246;
Best Local Similarity 41.7%; Pred. NO. 31;
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0.

QY 1 KKKMADNGTIVEELKQLLEQMNL 24
| : | : | : | : | : | :
Db 133 KSULEDKRQVSEVEAKRNRAEQMN 156

RESULT 20

ADP07641
ID ADF07641 standard; protein; 300 AA.
XX
AC ADF07641;
XX
DT 12-FEB-2004 (first entry)
XX
DE Bacterial polypeptide #3754.
XX
KW Proteus mirabilis infection; bacterial infection; antibacterial;
KM Immunostimulant.
XX
OS Proteus mirabilis.
XX
PN US6605709-B1.
XX
PD 12-AUG-2003.
XX
PF 05-APR-2000; 2000US-00543681.
XX
PR 09-APR-1999; 99US-0128706P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Breton GL;
XX
DR WPI; 2003-895291/82.
XX
N-PSDB; ADF03469.

PT New Proteus mirabilis polypeptides and polynucleotides, useful as
PT reagents for diagnosis of bacterial disease, as components of
PT antibacterial vaccines, as targets for antibacterial drugs, or as
PT biocontrol agents for plants.

PS Disclosure; SEQ ID NO 7926; 870pp; English.

XX The invention relates to new Proteus mirabilis polypeptides and
CC polynucleotides. The invention also relates to antibodies against the
CC polypeptides, methods for producing the polypeptides, a method of
CC generating vaccines for immunising an individual against P. mirabilis, a

| Query March | 41.7%; | Score 53; | DB 7; | Length 300; |
|-----------------------|---|----------------------------|-----------|-------------|
| Best Local Similarity | 47.6%; | Pred. No. 72; | | |
| Matches 10; | Conservative 4; | Mismatches 7; | Indels 0; | Gaps 0; |
| Qy | 3 | KMADNGTITVEELKQLEQNN 23 | | |
| | : : : : : : : | | | |
| Db | 59 | KLTDGALVHEAKQILAQFN 79 | | |
| RESULT 21 | | | | |
| ABU23669 | ABU23669 | standard; protein; 351 AA. | | |
| AC | ABU23669; | | | |
| DT | 19-JUN-2003 | (first entry) | | |
| DE | Protein encoded by Prokaryotic essential gene #9196. | | | |
| XX | Antisense; prokaryotic essential gene; cell proliferation; drug design. | | | |
| XX | Clostridium acetobutylicum. | | | |
| OS | WO200277183-A2. | | | |
| XX | 03-OCT-2002. | | | |
| PD | 21-MAR-2002; 2002WO-US009107. | | | |
| PF | 21-MAR-2001; 2001US-00815242. | | | |
| PR | 06-SEP-2001; 2001US-00948993. | | | |
| PR | 25-OCT-2001; 2001US-0342923P. | | | |
| PR | 08-FEB-2002; 2002US-00072851. | | | |
| PR | 06-MAR-2002; 2002US-0362659P. | | | |
| XX | (ELIT-) ELITRA PHARM INC. | | | |
| XX | Wang L, Zamudio C, Malone C, Hasebeck R, Ohlsen KL, Zykkind JW; | | | |
| F1 | Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH; | | | |
| F1 | WPI; 2003-029926/02. | | | |
| DR | N-PSDB; ACA27539. | | | |
| XX | New antisense nucleic acids, useful for identifying proteins or screening | | | |
| FT | for homologous nucleic acids required for cellular proliferation to | | | |
| FT | isolate candidate molecules for rational drug discovery programs. | | | |
| PS | Claim 25; SEQ ID NO 51593; 1766pp; English. | | | |
| XX | The invention relates to an isolated nucleic acid comprising any one of | | | |
| CC | the 6213 antisense sequences given in the specification where expression | | | |
| CC | of the nucleic acid inhibits proliferation of a cell. Also included are: | | | |
| CC | (1) a vector comprising a promoter operably linked to the nucleic acid | | | |
| CC | encoding a polypeptide whose expression is inhibited by the antisense | | | |
| CC | nucleic acid; (2) a host cell containing the vector; (3) an isolated | | | |
| CC | polypeptide or its fragment whose expression is inhibited by the | | | |
| CC | antisense nucleic acid; (4) an antibody capable of specifically binding | | | |
| CC | the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular | | | |
| CC | proliferation or the activity of a gene in an operon required for | | | |
| CC | proliferation; (7) identifying a compound that influences the activity of | | | |
| CC | the gene product or that has an activity against a biological pathway | | | |
| CC | required for proliferation, or that inhibits cellular proliferation; (8) | | | |

PT Genomic sequence of Photobacterium luminescens and encoded polypeptides,
 useful e.g. as therapeutic antimicrobials and agricultural pesticides.
 XX
 PS Claim 2; SEQ ID NO 266; 1205bp; French.
 XX
 CC The invention relates to the isolation of genes and their encoded
 CC proteins from Photobacterium luminescens. The isolated sequences are
 CC sources of probes and primers for detecting the genome of P. luminescens
 CC and related species; to study polymorphisms; for gene analysis and for
 CC detection/amplification of the genes. Antibodies (Ab) raised against the
 CC polypeptides encoded by the genes are used for detection/identification
 CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that
 CC carry a gene-containing vector are used to select compounds that
 CC modulate, regulate, induce or inhibit expression of the genes in plants,
 CC animals or microorganisms other than P. luminescens and are able to alter
 CC response or sensitivity to toxins and antibiotics produced by P.
 CC luminescens. Cells transformed to express the genes are useful for
 CC recombinant production of the proteins, particularly toxins and
 CC antibacterials useful as insecticides, bactericides and fungicides. The
 CC genes, proteins, vectors containing the genes and Ab are also useful
 CC therapeutically (to treat microbial infection by bacteria or fungi that
 CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as
 CC biopesticides. Other uses of the genes and the proteins are as virulence
 CC factors and for identifying targets of human diseases for which P.
 CC luminescens is a model (particularly plague and whooping cough). This
 CC sequence represents one of the isolated P. luminescens proteins
 XX
 SQ Sequence 16368 AA;
 XX
 Query Match 40.9%; Score 52; DB 6; Length 16368;
 Best Local Similarity 71.4%; Pred. No. 7.1e+03;
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 10 ITVEELKQLLEQWN 23
 Db 14404 LTVEERKLLLESWN 14417
 XX
 RESULT 24
 AAB43377
 ID AAB43377 standard; protein; 162 AA.
 XX
 AC AAB43377;
 XX
 DT 08-FEB-2001 (first entry)
 XX
 DE Human ORFX ORF141 polypeptide sequence SEQ ID NO:6282.
 XX
 KW Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
 KW vulnery; antiparasitic; antiparkinsonian; nootropic; neuroprotective;
 KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
 KW immunostimulant; chondrolytic; coagulant; vasotropic; antidiabetic;
 KW hypotensive; dermatological; immunosuppressive; antiinflammatory;
 KW antiviral; antibacterial; antifungal; antirheumatic; antihypertid;
 KW antianemic; gene therapy; cancer; proliferative disorder; hypertension;
 KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
 KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
 KW cholesterol ester storage; systemic lupus erythematosus; infection;
 KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
 KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 KW bone damage; cartilage damage; antinflammatory disease; coagulation;
 KW thrombosis; contraceptive.
 XX
 OS Homo sapiens.
 XX
 PN WO200058473-A2.
 XX
 PD 05-OCT-2000.
 XX
 PF 31-MAR-2000; 2000WO-US008621.
 XX
 PR 31-MAR-1999; 99US-0127607P.
 PR 02-APR-1999; 99US-0127636P.

PR 05-APR-1999; 99US-0127728P.
 PR 30-MAR-2000; 2000US-00540763.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shimkete RA, Leach M;
 XX
 DR WPI/ 2000-602362/57.
 DR N-PSDB; AAC7586.
 XX
 PT Novel nucleic acids and peptides derived from open reading frame X,
 PT useful for treating e.g. cancers, proliferative disorders,
 PT neurodegenerative disorders and cardiovascular disease.
 XX
 PS Claim 11; Page 5469; 5507bp; English.
 XX
 CC AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
 CC sequences have activities such as: cytostatic; hepatotropic; vulnery;
 CC antiparasitic; antiparkinsonian; nootropic; neuroprotective; osteopathic;
 CC anticonvulsant; antirheumatic; immunosuppressant; immunostimulant;
 CC cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
 CC dermatological; immunosuppressive; antirheumatic; antibacterial;
 CC antiviral; antifungal; antirheumatic; antihypertid; and antianemic. The
 CC sequences can be used for determining the presence of or predisposition
 CC to, or preventing or treating pathological conditions associated with an
 CC ORFX-associated disorder. The nucleic acids can be used to express ORFX
 CC proteins in gene therapy vectors. The proteins and nucleic acids may be
 CC used to treat cancers, proliferative disorders, neurodegenerative
 CC disorders, osteoarthritis, graft vs host disease, cardiovascular disease,
 CC diabetes mellitus, hypertension, hypothyroidism, cholesterol ester
 CC storage, systemic lupus erythematosus, severe combined immunodeficiency
 CC (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
 CC disorders, asthma, allergy, aplastic anaemia, burns, wounds, bone and
 CC cartilage damage, nocturnal haemoglobinuria, antinflammatory disease; to
 CC enhance coagulation; to inhibit thrombosis; and as a contraceptive
 XX
 SQ Sequence 162 AA;
 XX
 Query Match 40.2%; Score 51; DB 3; Length 162;
 Best Local Similarity 50.0%; Pred. No. 69;
 Matches 12; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
 QY 1 KKKMANGTITVEELKQLLEQWN 24
 Db 34 KKKQVANVEKQLEAKELQMDL 57
 XX
 RESULT 25
 ABG99957
 ID ABG99957 standard; protein; 162 AA.
 XX
 AC ABG99957;
 XX
 DT 17-JAN-2003 (first entry)
 XX
 DE Human novel polypeptide #70.
 XX
 KW Human; genetic disorder; gene mapping; medical imaging; cancer;
 KW neurodegenerative disorder; lymphoid cell disorder; osteoporosis;
 KW Parkinson's disease; Alzheimer's disease; bone degenerative disorder;
 KW osteoarthritis; periodontal disease; liver fibrosis; viral infection;
 KW fungal infection; bacterial infection; autoimmune disease; diabetes;
 KW atopic dermatitis.
 XX
 OS Homo sapiens.
 XX
 PN WO200274961-A1.
 XX
 PD 26-SEP-2002.
 XX
 PF 14-MAR-2002; 2002WO-US005109.

PR 15-MAR-2001; 2001US-00810173.
 XX (HYSE-) HYSEO INC.
 XX
 XX
 PI Tang YT, Zhou P, Goodrich R, Asundi V, Zhang J, Zhao QA, Ren F;
 PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
 PI Wehrman T, Wang J, Wang D, Dimaac RT;
 XX
 DR MPI; 2003-040556/03.
 DR N-PSDB; ABX05055.
 XX
 PT New isolated polypeptides and polynucleotides, useful for preventing,
 PT treating or ameliorating medical conditions, such as cancer,
 PT neurodegenerative disorders, lymphoid cell disorders, bone degenerative
 PT disorders, and infections.
 XX
 PS Claim 9; SEQ ID NO 596; 235pp; English.
 XX
 CC The invention relates to human polynucleotides and the polypeptides they
 CC encode. The polynucleotides and polypeptides are useful in diagnostics,
 CC forensics, gene mapping, medical imaging, identification of mutations,
 CC responsible for genetic disorders or other traits, assessing biodiversity
 CC and producing many other types of data and products dependent on DNA and
 CC amino acid sequences. They are also useful for preventing, treating or
 CC ameliorating medical conditions, such as cancer, neurodegenerative
 CC disorders (e.g. Parkinson's disease, Alzheimer's disease), lymphoid cell
 CC disorders, osteoporosis, osteoarthritis, bone degenerative disorders,
 CC periodontal disease, liver fibrosis, infections (e.g. viral, fungal or
 CC bacterial) or autoimmune diseases (e.g. diabetes, atopic dermatitis).
 CC Sequences ABG9888-ABG9989 and ABU0010-ABU0043 represent human
 CC polypeptides of the invention. Note: The sequence data for this patent is
 CC not represented in the printed specification but is based on sequence
 CC information supplied by the European Patent Office
 XX
 SQ Sequence 162 AA;
 QY
 Db 1 KKKMADNGITVEELKLEQNL 24
 34 KKMVAVNEKQLEAKELLEDL 57
 RESULT 26
 AAE34443
 ID AAE34443 standard; protein; 217 AA.
 XX
 AC AAE34443;
 XX
 DT 14-MAY-2003 (first entry)
 XX
 DE Human lipid-associated molecule (LIPAM)-4 protein.
 XX
 KW Human; lipid-associated molecule; LIPAM; cardiovascular disorder; stroke;
 KW arteriovenous fistula; atherosclerosis; hypertension; Raynaud's disease;
 KW aneurysm; congestive heart failure; thrombophlebitis; angina pectoris;
 KW ischaemic heart disease; rheumatic heart disease; peptic oesophagitis;
 KW gastrointestinal disorder; lipid metabolism disorder; Crohn's disease;
 KW nausea; peptic ulcer; fatty liver; Fabry's disease; Gaucher's disease;
 KW diabetes mellitus; hyperlipidaemia; hypercholesterolaemia; epilepsy;
 KW autoimmune disorder; inflammatory disorder; neurological disorder; kuru;
 KW acquired immunodeficiency syndrome; anaemia; Alzheimer's disease; asthma;
 KW dementia; prion disease; Creutzfeldt-Jakob disease; leukaemia; cancer;
 KW adenocarcinoma; lymphoma; melanoma; myeloma; sarcoma; gene therapy;
 KW protein replacement therapy.
 XX
 OS Homo sapiens.
 XX
 AC Key Location/Qualifiers
 PH 185..213
 FT Domain /note="Transmembrane domain"

XX
 PN WO200294988-A2.
 XX
 PD 28-NOV-2002.
 XX
 PF 17-MAY-2002; 2002WO-US015688.
 XX
 XX
 XX 18-MAY-2001; 2001US-0292242P.
 PR 25-MAY-2001; 2001US-0293726P.
 PR 01-JUN-2001; 2001US-0295346P.
 PR 06-JUL-2001; 2001US-0303404P.
 PR 24-AUG-2001; 2001US-0314754P.
 PR 22-JUN-2002; 2002US-0351262P.
 PR 29-MAR-2002; 2002US-0368799P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Tang YT, Yue H, Azimzai Y, Baughn MR, Burford N, Reddy R;
 PI Walla NK, Das D, Nguyen DB, Yao WG, Arvizu CS, Lu Y, Gandhi AR;
 PI Griffin JA, Elliott VS, Ramkumar J, Lal PG, Lu DM, Lee EA, Lee SY;
 PI Yue H, Yang J, Tribouley CM, Kable AE, Swarnakar A;
 XX
 DR MPI; 2003-120797/11.
 DR N-PSDB; AAD52629.
 XX
 PS Claim 59; Page 144-145; 171pp; English.
 XX
 CC The present invention relates to novel human lipid-associated molecules
 CC (LIPAM) and polynucleotides encoding such proteins. Sequences of the
 CC invention are useful for treating diseases or conditions associated with
 CC decreased expression of functional LIPAM. The antagonist is useful for
 CC treating a disease or condition associated with the overexpression of
 CC functional LIPAM. They are useful for diagnosing, treating or preventing
 CC cardiovascular disorders (e.g. arteriovenous fistula, atherosclerosis,
 CC hypertension, Raynaud's disease, aneurysms, varicose veins, congestive
 CC heart failure, thrombophlebitis, angina pectoris, ischaemic heart disease
 CC or rheumatic heart disease), gastrointestinal disorders (e.g. peptic
 CC oesophagitis, nausea, peptic ulcer or Crohn's disease), lipid metabolism
 CC disorders (e.g. fatty liver, Fabry's disease, Gaucher's disease, diabetes
 CC mellitus, hyperlipidaemia, hypercholesterolaemia), autoimmune disorders
 CC or inflammatory disorders (e.g. acquired immunodeficiency syndrome,
 CC anaemia, asthma or Crohn's disease), neurological disorders (e.g. stroke,
 CC epilepsy, dementia, Alzheimer's disease, or prion diseases such as kuru
 CC or Creutzfeldt-Jakob disease) or cancers (e.g. adenocarcinoma, leukaemia,
 CC lymphoma, melanoma, myeloma or sarcoma). They are also used in gene
 CC therapy and protein replacement therapy. The present sequence is human
 CC LIPAM-4 protein
 XX
 SQ Sequence 217 AA;
 QY
 Db 1 KKKMADNGITVEELKLEQNL 24
 34 KKMVAVNEKQLEAKELLEDL 57
 RESULT 27
 AAG62621
 ID AAG62621 standard; protein; 224 AA.
 XX
 AC AAG62621;
 XX
 DT 07-SEP-2001 (first entry)
 XX
 DE Human SNARE protein 25.

XX Human: SNARE protein 25; cancer; blood disease; HIV infection;
 KM Immunological disease; inflammation; gene therapy.
 XX Homo sapiens.
 OS
 PN WO200138390-A1.
 XX
 PD 31-MAY-2001.
 XX
 PF 20-NOV-2000; 2000MO-CN000477.
 XX
 PR 26-NOV-1999; 99CN-00124120.
 XX
 PA (BIO-R) BIOROAD GENE DEV LTD SHANGHAI.
 XX
 PI Mao Y, Xie Y;
 XX
 PT WPI; 2001-355907/37.
 DR N-PSDB; AAH45791.
 XX
 PT Human SNARE protein 25 and encoded polynucleotide, used in diagnosis and
 PT treatment of malignant tumors, hemopathy, human immunodeficiency virus
 PT infection, immunological diseases and inflammation.
 XX
 PS Claim 1; Page 23-24; 33pp; Chinese.
 XX
 CC The present invention provides the protein and coding sequences of the
 CC human SNARE protein 25. The sequences can be used in the treatment of
 CC blood diseases, cancer, HIV infection, immunological diseases and
 CC inflammation. The present sequence is the protein of the invention
 XX
 SQ Sequence 224 AA;
 XX
 Query Match 40.2%; Score 51; DB 4; Length 224;
 Best Local Similarity 50.0%; Pred. No. 97;
 Matches 12; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
 QY 1 KKKQADNGITTVBELKQLLEQMDL 24
 Db 34 KKKQVANVEKQLEAKELLEQMDL 57
 XX
 RESULT 28
 ABU00236
 ID ABU00236 standard; protein; 224 AA.
 XX
 AC ABU00236;
 XX
 DT 17-JAN-2003 (first entry)
 XX
 DE Human novel polypeptide #329.
 XX
 KW Human; genetic disorder; gene mapping; medical imaging; cancer;
 KW neurodegenerative disorder; lymphoid cell disorder; osteoporosis;
 KW Parkinson's disease; Alzheimer's disease; bone degenerative disorder;
 KW osteoarthritis; periodontal disease; liver fibrosis; viral infection;
 KW fungal infection; bacterial infection; autoimmune disease; diabetes;
 KW atopic dermatitis.
 XX
 OS Homo sapiens.
 XX
 PN WO200274961-A1.
 XX
 PD 26-SEP-2002.
 XX
 PF 14-MAR-2002; 2002MO-US005109.
 XX
 PR 15-MAR-2001; 2001US-00810173.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PT Tang YT, Zhou P, Goodrich R, Asundi V, Zhang J, Zhao QA, Ren F;

PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
 PI Wehrman T, Wang J, Wang D, Dirmann RT;
 XX
 DR WPI; 2003-040556/03.
 XX
 DR N-PSDB; ABX05314.
 XX
 PT New isolated polypeptides and polynucleotides, useful for preventing,
 PT treating or ameliorating medical conditions, such as cancer,
 PT neurodegenerative disorders, lymphoid cell disorders, bone degenerative
 PT disorders, and infections.
 XX
 PS Claim 9; SEQ ID NO 855; 235pp; English.
 XX
 CC The invention relates to human polynucleotides and the polypeptides they
 CC encode. The polynucleotides and polypeptides are useful in diagnostics,
 CC forensics, gene mapping, medical imaging, identification of mutations,
 CC responsible for genetic disorders or other traits, assessing biodiversity
 CC and producing many other types of data and products dependent on DNA and
 CC amino acid sequences. They are also useful for preventing, treating or
 CC ameliorating medical conditions, such as cancer, neurodegenerative
 CC disorders (e.g. Parkinson's disease, Alzheimer's disease), lymphoid cell
 CC disorders, osteoporosis, osteoarthritis, bone degenerative disorders,
 CC periodontal disease, liver fibrosis, infections (e.g. viral, fungal or
 CC bacterial) or autoimmune diseases (e.g. diabetes, atopic dermatitis).
 CC Sequences ABG9888-ABG9989 and ABU0010-ABU0433 represent human
 CC polypeptides of the invention. Note: The sequence data for this patent is
 CC not represented in the printed specification but is based on sequence
 CC information supplied by the European Patent Office
 XX
 SQ Sequence 224 AA;
 XX
 Query Match 40.2%; Score 51; DB 6; Length 224;
 Best Local Similarity 50.0%; Pred. No. 97;
 Matches 12; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
 QY 1 KKKQADNGITTVBELKQLLEQMDL 24
 Db 34 KKKQVANVEKQLEAKELLEQMDL 57
 XX
 RESULT 29
 AAM68488
 ID AAM68488 standard; protein; 572 AA.
 XX
 AC AAM68488;
 XX
 DT 08-DEC-1998 (first entry)
 XX
 DE Mouse ULIP-4 protein.
 XX
 KW Mouse; Unc-33-like phospho-protein; ULIP; rat; neoplasia; tumorigenesis;
 KW neurodegenerative disorder; diagnosis.
 XX
 OS Mus musculus.
 XX
 PN FR2759701-A1.
 XX
 PD 21-AUG-1998.
 XX
 PF 19-FEB-1997; 97FR-00001961.
 XX
 PR 19-FEB-1997; 97FR-00001961.
 XX
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 XX
 PI Aguera M, Belin MF, Homorac J, Kolatukudy P, Quach TT, Byk T;
 PI Sobel A;
 XX
 DR WPI; 1998-449610/39.
 DR N-PSDB; AAV60817.
 XX
 PT Mouse and human ULIP polypeptide(s) - useful in detection of para-
 PT neoplastic neurological syndromes.

XX Claim 1; Fig 11; 90pp; French.
PS
XX
CC This sequence represents the mouse Unc-53-like phospho-protein (ULIP)-4.
CC The coding sequence was isolated based on similarity to the rat ULIP
CC sequence. Proteins of the ULIP family or their corresponding nucleic
CC acids can be used in compositions for treating neurodegenerative
CC disorders and neoplasms, especially for para-neoplastic neurological
CC syndromes and/or for the early diagnosis of tumorigenesis
XX
SQ Sequence 572 AA;
Query Match 40.2%; Score 51; DB 2; Length 572;
Best Local Similarity 64.7%; Pred. No. 2.7e+02;
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 5 ADNGTIVEELKQLLEQ 21
DB 199 AENGDIVBQKRLLEQ 215
RESULT 30
ID ABB49107 standard; protein; 626 AA.
XX
AC ABB49107;
XX
DT 05-FEB-2002 (first entry)
XX
DE Listeria monocytogenes protein #1811.
XX
KW Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
KW Vitamin B12; bacterial infection; disease.
XX
OS Listeria monocytogenes.
XX
PN WO200177335-A2.
XX
PD 18-OCT-2001.
XX
PF 11-APR-2001; 2001WO-FR001118.
XX
PR 11-APR-2000; 2000FR-00004629.
XX
PA (INSP) INST PASTEUR.
XX
PI Buchrieser C, Frangoul L, Couve E, Ruenick C, Feibi H, Dehoux P;
PI Duseurget O, Chetouani F, Nedjari H, Glaeser P, Kunst F, Cosserat P;
PI Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA;
PI Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;
PI Chakraborty T, Demann E, Hain T, Berche P, Charbit A, Durant L;
PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
PI Madueno E, De Pablos B, Weiland J, Kaerst U, Entian K, Hauf J;
PI Rose M, Voss H;
XX
DR WPI; 2002-010914/01.
XX
PT Genomic sequence for Listeria monocytogenes, useful e.g. for treatment
PT and prevention of Listeria and related bacterial infections, and related
PT polypeptides.
XX
PS Claim 6; SEQ ID NO 1812; 192pp; French.
XX
CC The present invention relates to the genome sequence of Listeria
CC monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of
CC it are useful for selecting probes and primers for detecting genes in L.
CC monocytogenes and related organisms, and for studying genetic
CC polymorphisms and other genomes. The present sequence is a protein
CC encoded by the genome sequence of the present invention. Proteins
CC expressed from the genome sequence are useful for raising specific
CC antibodies, identification of L. monocytogenes and related organisms, and
CC for biosynthesis and biodegradation, especially biosynthesis of Vitamin
CC B12. The genome sequence and proteins encoded by it are also useful for

CC selecting compounds that regulate gene expression and cell replication
CC and modulate L. monocytogenes-related diseases. In addition, the genome
CC sequence and proteins encoded by it are useful in pharmaceutical and
CC vaccines compositions for the treatment or prevention of infections by L.
CC monocytogenes and related organisms. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 626 AA;
Query Match 40.2%; Score 51; DB 5; Length 626;
Best Local Similarity 50.0%; Pred. No. 2.9e+02;
Matches 10; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
QY 2 KXADNGTIVEELKQLLEQ 21
DB 417 KQLADEFLTITELKQLDQ 436
RESULT 31
ID ABU32651 standard; protein; 626 AA.
XX
AC ABU32651;
XX
DT 19-JUN-2003 (first entry)
XX
DE Protein encoded by prokaryotic essential gene #18176.
XX
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
OS Listeria monocytogenes.
XX
PN WO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
XX
PR 06-SEP-2001; 2001US-00948993.
XX
PR 25-OCT-2001; 2001US-0345923P.
XX
PR 08-FEB-2002; 2002US-00072851.
XX
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zykkind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
XX
DR N-PSDB; ACA36521.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 25; SEQ ID NO 60575; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 623 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway;
CC required for proliferation, or that inhibits cellular proliferation; (8)

CC Identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-regulated gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPD at
 CC ftp.wipo.int/pub/published_pct_sequences

SO Sequence 626 AA;

Query Match 40.2%; Score 51; DB 6; Length 626;
 Best Local Similarity 50.0%; Pred. No. 2.9e+02;
 Matches 10; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 KXWADNGTITVEELKOLLEQ 21
 DB 417 KOLADEPELITLTKOOLQ 436

RESULT 32

AAAG02044
 ID AAG02044 standard; protein; 100 AA.

XX AAG02044;

DT 06-OCT-2000 (first entry)

DE Human secreted protein, SEQ ID NO: 6125.

XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KM gene therapy; chromosome mapping.

XX Homo sapiens.

PN EP1033401-A2.

PD 06-SEP-2000.

PF 21-FEB-2000; 2000EB-00200610.

PR 26-FEB-1999; 99US-0122487P.

PA (GEST) GENSET.

PI Dumas Malne Edwards J, Duclert A, Giordano J;

DR WPI; 2000-500381/45.

DR N-PSDB; AAC02050.

PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures.

PS Claim 13; SEQ ID NO 6125; 71bp + Sequence Listing; English.

CC The present sequence is a polypeptide encoded by one of a large number of
 CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
 CC prepared from total human RNAs or polyA+ RNAs derived from 30 different
 CC tissues. EST sequences usually correspond mainly to the 3' untranslated
 CC region (UTR) of the mRNA because they are often obtained from oligo-dT
 CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
 CC sequences derived from the 5' ends of mRNAs and even in those cases where

CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
 CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
 CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
 CC are also used in diagnostic, forensic, gene therapy and chromosome
 CC mapping procedures. They are used to obtain upstream regulatory sequences
 CC and to design expression and secretion vectors

SO Sequence 100 AA;

Query Match 39.4%; Score 50; DB 3; Length 100;
 Best Local Similarity 55.6%; Pred. No. 56;
 Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXWADNGTITVEELKOLLE 20
 DB 44 KOLENGSINIBELKMLE 61

RESULT 33

ADA12194
 ID ADA12194 standard; protein; 300 AA.

XX ADA12194;

DT 06-NOV-2003 (first entry)

DE Acinetobacter sp. hydrolase.

XX adipic acid synthetase; cyclohexanone monooxygenase;
 KM 6-aldehyde hexanoic dehydrogenase; cyclohexanol dehydrogenase;
 KM cyclohexanol; adipic acid; hydrolase; enzyme.

XX Acinetobacter sp.

PN US6498242-B1.

PD 24-DEC-2002.

PF 14-UTL-1999; 99US-00648004.

PR 19-FEB-1999; 99US-00252553.

PA (DUPO) DU PONT DE NEMOURS & CO E. I.

PI Cheng Q, Nagarajan V, Thomas SM;

DR WPI; 2003-605313/57.

DR N-PSDB; ADA12193.

PT New nucleic acid fragment isolated from Acinetobacter for converting
 PT cyclohexanol to adipic acid, encodes adipic acid synthesizing enzymes
 PT e.g. cyclohexanone monooxygenase and caprolactone hydrolase.

PS Example 2; Col 57-58; 43bp; English.

CC The invention relates to an isolated nucleic acid fragment from
 CC Acinetobacter sp. encoding adipic acid synthesizing enzymes where the
 CC nucleic acid comprises open reading frames encoding e.g. cyclohexanone
 CC monooxygenase, 6-aldehyde hexanoic dehydrogenase and cyclohexanol
 CC dehydrogenase. The nucleic acid fragment is useful for isolating cDNAs
 CC and genes encoding homologous enzymes from the same or other bacterial
 CC species, and for the conversion of cyclohexanol to adipic acid. The
 CC nucleic acid fragment is also useful in immunological screening cDNA
 CC expression libraries, and as probes for genetically and physically
 CC mapping the genes that they are a part of, and as markers for traits
 CC linked to expression of the enzymes. The nucleic acid fragment is useful
 CC to design and produce primer pairs for use in the amplification reaction
 CC or in primer extension reactions, and for the creation of recombinant
 CC organisms that have the ability to produce adipic acid while growing on
 CC cyclohexanol. The present sequence represents the amino acid sequence of
 CC the Acinetobacter sp. hydrolase.

SO Sequence 300 AA;

Query Match 39.4%; Score 50; DB 6; Length 300;
Best Local Similarity 22.7%; Pred. No. 1.8e+02;
Matches 5; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY 2 KKMADNGTIVBELKQLEQWN 23
DB 20 RRMQENPNMTIEDFRSMFDEWH 41

RESULT 34
AAE39415
ID AAE39415 standard; protein; 300 AA.
AC AAE39415;
DT 18-DEC-2003 (first entry)
DE Acinetobacter sp. caprolactone hydrolase.
KW Adipic acid; nylon-6,6; lubricant; plasticiser; food acidulant; enzyme;
KM caprolactone hydrolase.
XX Acinetobacter sp.
XX US2003087403-A1.
XX 08-MAY-2003.
XX 16-OCT-2002; 2002US-00272419.
XX 19-FEB-1999; 99US-00252553.
XX 14-JUL-1999; 99US-00648004.
XX (CHEN/) CHENG Q.
XX (NAGA/) NAGARAJAN V.
XX (THOM/) THOMAS S M.
XX Cheng Q, Nagarajan V, Thomas SM;
XX WPI; 2003-755145/71.
XX N-PSDB; AAD59830.
XX New nucleic acid fragment encoding an adipic acid synthesizing enzyme,
XX PT useful for producing nylon-6,6, lubricants and plasticizers, or as food
XX PT acidulant.
XX Claim 4; Page 31-32; 45pp; English.
XX The present invention provides novel nucleic acid molecules derived from
XX CC Acinetobacter sp. encoding adipic acid synthesizing enzymes, useful for
XX CC producing nylon-6,6, lubricants and plasticizers. The invention is also
XX CC useful as food acidulant. The present sequence is Acinetobacter sp.
XX CC caprolactone hydrolase enzyme. This enzyme is involved in the synthesis
XX CC of adipic acid
XX SQ Sequence 300 AA;

Query Match 39.4%; Score 50; DB 7; Length 300;
Best Local Similarity 22.7%; Pred. No. 1.8e+02;
Matches 5; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY 2 KKMADNGTIVBELKQLEQWN 23
DB 20 RRMQENPNMTIEDFRSMFDEWH 41

RESULT 35
ADG33790
ID ADG33790 standard; protein; 469 AA.
AC ADG33790;
XX

DT 26-FEB-2004 (first entry)
XX Actinomycetes dual condensation/epimerisation NRPS domain protein ID 49.
DE non-ribosomal peptide synthetase; NRPS; dual condensation; epimerisation;
XX ramoplanin; complestatin; actinomycetes taxon.
XX Pseudomonas syringae pv. syringae.
XX WO2003089641-A2.
XX 30-OCT-2003.
XX 17-APR-2003; 2003WO-CA000575.
XX 17-APR-2002; 2002US-0372790P.
XX (ECOP-) ECOPIA BIOSCIENCES INC.
XX Farnet CM, Staiffa A;
XX WPI; 2003-854123/79.
XX N-PSDB; ADG33791.
XX New dual condensation/epimerization non-ribosomal peptide synthetase
XX PT domain and encoding polynucleotide, useful for modifying the
XX PT stereochemistry of synthesized peptides (e.g. ramoplanin or complestatin)
XX PT in vitro or in vivo.
XX Claim 9; SEQ ID NO 49; 245pp; English.
XX This invention relates to novel domains of non-ribosomal peptide
XX CC synthetases (NRPSs) that exhibit dual condensation and epimerisation
XX CC activities. Specifically, these domains allow incorporation of non-
XX CC proteinogenic substrates (e.g. D-amino acids) into peptide products.
XX CC Furthermore, they can be used in vivo to modify the stereochemistry of
XX CC synthesised peptides (e.g. ramoplanin or complestatin) at selected amino
XX CC acid sites by the addition of non-chiral residues. The present invention
XX CC describes the identification of isolated polynucleotide NRPS domains in
XX CC various organisms from the actinomycetes taxon, and the encoded
XX CC polypeptide sequence, as well as suitable expression vectors. This
XX CC polypeptide sequence is a dual condensation/epimerisation NRPS domain
XX CC protein of the invention.
XX SQ Sequence 469 AA;

Query Match 39.4%; Score 50; DB 7; Length 469;
Best Local Similarity 64.3%; Pred. No. 2.9e+02;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 10 ITVELKQLEQWN 23
DB 432 LPLNERKQLEQWN 445

RESULT 36
AAB35470
ID AAB35470 standard; protein; 516 AA.
XX AAB35470;
DT 06-JUN-2001 (first entry)
DE Human cyclic nucleic acid phosphodiesterase PDE1B2.
XX Human; cyclic nucleic acid phosphodiesterase; PDE1B2; spleen;
XX KW cardiovascular disease; gastrointestinal disorder; sexual dysfunction.
XX Homo sapiens.
XX EP1085092-A1.
XX 21-MAR-2001.
PD

XX 14-SEP-2000; 2000EP-00307982.
 PF 17-SEP-1999; 99GB-00022125.
 PR (PF12) PFIZER LTD.
 PA (PF12) PFIZER INC.
 XX
 PI Fldock MD;
 XX
 DR WPI; 2001-246901/26.
 DR N-PSDB; AAF62301.
 XX
 PT Human cyclic nucleotide phosphodiesterase 1B2 and its nucleotide sequence
 PT useful for treating cardiovascular, gastrointestinal and spleen disorders
 PT and screening for drugs to treat associated disorders.
 PS
 PS Claim 1; Page 42-45; 58pp; English.
 CC The present invention provides the protein and coding sequences for the
 CC human cyclic nucleic acid phosphodiesterase PDE1B2. This is thought to be
 CC a splice variant of PDE1, and capable of catalysing the degradation of
 CC cAMP and/or cGMP. The sequences are useful in the treatment of
 CC cardiovascular, gastrointestinal and spleen disorders, and in the
 CC enhancement of the male erectile response and treatment of female sexual
 CC dysfunction. The present sequence is the PDE1B2 protein
 XX
 SQ Sequence 516 AA;
 XX
 Query Match 39.4%; Score 50; DB 4; Length 516;
 Best Local Similarity 55.6%; Pred. No. 3.2e+02;
 Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 QY 3 KXADNGTIVEELKQLE 20
 Db | : | | : | | | : | |
 24 KQLENGEINIEELKKNLE 41
 XX
 RESULT 37
 ABM83406
 ID ABM83406 standard; protein; 534 AA.
 XX
 AC ABM83406;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Human diagnostic and therapeutic protein SEQ ID NO:3655.
 XX
 KM gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
 XX
 OS Homo sapiens.
 XX
 PN WO2004023973-A2.
 XX
 PD 25-MAR-2004.
 XX
 PF 12-SEP-2003; 2003WO-US028227.
 XX
 PR 12-SEP-2002; 2002US-0410259P.
 PR 12-SEP-2002; 2002US-0410260P.
 XX
 PA (INCY-) INCYTE CORP.
 XX
 PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic NM, Shen F;
 PI Hartshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
 PI Mooney EM, Deleage AM, Panesar IS, Barville SC, Reddy TP;
 PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH;
 PI Beralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve IL;
 PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vilt UA, Kitton ES,
 PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
 PI Fatury S, Shi X, Suarez CJ;
 XX
 WPI; 2004-329368/30.

DR N-PSDB; ACN42058.
 XX
 PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
 PT in diagnosing a condition, disease or disorder associated with human
 PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
 PT in gene mapping.
 XX
 PS Claim 27; Page; 190pp; English.
 XX
 CC The invention relates to novel diagnostic and therapeutic polynucleotides
 CC selected from one of the 2722 sequences defined in the specification. A
 CC polynucleotide of the invention may have a use in gene therapy. The human
 CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
 CC used to diagnose a particular condition, disease or disorder associated
 CC with human molecules, e.g. cell proliferative disorders,
 CC autoimmune/inflammatory disorder, developmental disorder, endocrine
 CC disorder, neurological disorders, gastrointestinal disorders, or
 CC infections caused by virus, bacteria, fungi or parasite. The dithp
 CC molecules may also be used in genetic mapping, in identifying individuals
 CC from minute biological samples, in detecting single nucleotide
 CC polymorphisms, as molecular weight markers, and for somatic or germline
 CC gene therapy. The present sequence represents a dithp protein of the
 CC invention. Note: The sequence data for this patent is not represented in
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
 XX
 SQ Sequence 534 AA;
 XX
 Query Match 39.4%; Score 50; DB 8; Length 534;
 Best Local Similarity 55.6%; Pred. No. 3.4e+02;
 Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 QY 3 KXADNGTIVEELKQLE 20
 Db | : | | : | | | : | |
 24 KQLENGEINIEELKKNLE 41
 XX
 RESULT 38
 AAW95110
 ID AAW95110 standard; protein; 536 AA.
 XX
 AC AAW95110;
 XX
 DT 26-MAY-1999 (first entry)
 XX
 DE Human RPMI 8392 cell phosphodiesterase, PDE1B1.
 XX
 KM Antisense oligodeoxynucleotide; phosphodiesterase; PDE1B1; enzyme; PDE;
 KM cell death; apoptosis; cancer; Ca2+-calmodulin; lymphoblastoid; RNase H;
 KM RPMI 8392; RNA degradation; cAMP; immunoproliferative disorder; breast;
 KM immune dysfunction; acute lympholytic leukemia; prostate; human.
 XX
 OS Homo sapiens.
 XX
 PN US5885834-A.
 XX
 PD 23-MAR-1999.
 XX
 PF 30-SEP-1997; 97US-00940332.
 XX
 PR 30-SEP-1996; 96US-0027207P.
 XX
 PA (EPST/) EPSTEIN P M.
 XX
 PI Epstein PM;
 PI WPI; 1999-228548/19.
 DR N-PSDB; AAX6288.
 XX
 PT Antisense oligodeoxynucleotides specific for mRNA encoding
 PT phosphodiesterase PDE1B1 enzymes and method for using them to induce
 PT apoptosis of cells - useful in the treatment of immunoproliferative
 PT disorders and immune dysfunctions.

XX Disclosure; Fig 8A-D; 35pp; English.
PS
XX
CC The invention relates to antisense oligodeoxynucleotides (AS-ODN) which
CC will bind to mRNA encoding phosphodiesterase PDE1B1 enzymes and their use
CC in inducing programmed cell death (apoptosis) in cancer cells. PDE1 is a
CC Ca2+-calmodulin dependent phosphodiesterase found in cytosolic extracts
CC of human lymphoblastoid cell line, RPMI 8392. The method in which
CC programmed cell death is induced in cancer cells comprises: (1)
CC identifying the phosphodiesterase enzyme PDE1B1 in a cell line containing
CC the cancer cells; (2) synthesizing an AS-ODN inhibitor which will bind to
CC mRNA encoding PDE1B1; and (3) applying the AS-ODN to the cell line to
CC inhibit the enzymatic activity of the PDE1B1 and induce apoptosis in the
CC cells. The AS-ODNs inhibit the expression of a protein by two mechanisms:
CC (i) by degradation of RNA by the ubiquitous enzyme RNase H, which
CC selectively cleaves the RNA of DNA-RNA heteroduplexes; and (ii) the
CC arrest of translation initiation caused by AS-ODN hybridization to the 5'
CC un-translated region or the translation initiation site on the mRNA.
CC Inhibition of phosphodiesterase (PDE) enzyme expression results in
CC elevated levels of cAMP in the cells due to PDE1B1 being involved in the
CC metabolism of cAMP. The elevated cAMP levels result in apoptosis by
CC inhibition of DNA synthesis. The method and AS-ODN are useful in inducing
CC cAMP stimulated apoptosis and in the treatment of immunoproliferative
CC disorders and immune dysfunction such as acute lympholytic leukemia,
CC breast and prostate cancer. The present sequence represents a human RPMI
CC 8392 cell PDE1B1
CC
XX
SQ Sequence 536 AA;
Query Match 39.4%; Score 50; DB 2; Length 536;
Best Local Similarity 55.6%; Pred. No. 3.4e+02;
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
Oy 3 KXADNGTIVBEIKKOLE 20
| : | | : | | | : | |
Db 44 KOLENCEINIEBKKNLE 61
RESULT 39
ADE58253
ID ADE58253 standard; protein; 536 AA.
XX
AC ADE58253;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein Q01064, SEQ ID NO 4124.
XX
DE Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-033347P.
XX
PA (GENO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
XX DR GENBANK: Q01064.
XX
PT New composition comprising two or more isolated polypeptides, useful for

PT preparing a medicament for treating pain in an animal.
XX
XX Claim 1; Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
CC
XX
SQ Sequence 536 AA;
Query Match 39.4%; Score 50; DB 7; Length 536;
Best Local Similarity 55.6%; Pred. No. 3.4e+02;
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
Oy 3 KXADNGTIVBEIKKOLE 20
| : | | : | | | : | |
Db 44 KOLENCEINIEBKKNLE 61
RESULT 40
ADO40394
ID ADO40394 standard; protein; 536 AA.
XX
AC ADO40394;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human phosphodiesterase 1B protein.
XX
DE Phosphodiesterase 1B; PDE1B; calmodulin-dependent phosphodiesterase 1B;
KW hyperproliferative disorder; gene therapy; human; enzyme.
XX
OS Homo sapiens.
XX
PN US2004092461-A1.
XX
PD 13-MAY-2004.
XX
PF 11-NOV-2002; 2002US-00292312.
XX
PR 11-NOV-2002; 2002US-00292312.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Dobie KW;
XX WPI: 2004-374979/35.
XX DR N-PSDB; ADO40339.
XX
XX

PT New compound that modulates phosphodiesterase 1B expression, useful in
PT treating an animal having a disease or condition, i.e. hyperproliferative
PT disorder.
XX
XX Disclosure, Page 21-23; 34pp; English.
XX
CC The present invention is directed to antisense oligonucleotides which are
CC targeted to nucleic acid molecule encoding phosphodiesterase 1B (also
CC known as PDE1B and calmodulin-dependent phosphodiesterase 1B) and which
CC modulate the expression of phosphodiesterase 1B. The invention is
CC useful in treating an animal having a disease or condition such as
CC hyperproliferative disorder. The invention is also useful in gene
CC therapy. The present sequence is human phosphodiesterase 1B protein.
XX
XX Sequence 536 AA;
SQ
Query Match 39.4%; Score 50; DB 8; Length 536;
Best Local Similarity 55.6%; Pred. No. 3.4e+02;
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
OY 3 KMADNGTIVEELKQLE 20
DB 44 KQLENGEINIEELKKNLE 61
RESULT 41
ADSF75985
ID ADSF75985 standard; protein; 536 AA.
XX
XX ADSF75985;
AC
XX
XX 16-DEC-2004 (first entry)
DT
XX
XX Human phosphodiesterase 1B protein.
DE
XX
XX cardiant; neuroprotective; nephrotropic; cytosolic; gastrointestinal;
XX respiratory; gene therapy; cancer; hematological disease;
XX metabolic disease; cardiovascular disease; gastrointestinal disease;
XX hepatic disease; neurological disease; urological disease;
XX respiratory disease; phosphodiesterase 1B; PDE1B; human.
XX
XX Homo sapiens.
OS
XX
XX WO2004080270-A2.
PN
XX
XX 23-SEP-2004.
PD
XX
XX 27-FEB-2004; 2004WO-EP002065.
PF
XX
XX 13-MAR-2003; 2003EP-00005386.
PR
XX
XX (FARB) BAYER HEALTHCARE AG.
PA
XX
XX Golz S, Brueggemeier U, Geerts A;
PI
XX
XX WPI; 2004-690439/67.
DR
XX
XX N-PSDB; ADSF75984.
PT
XX
XX Screening for therapeutic agents for treating e.g., cardiovascular or
PT neurological diseases by contacting a test compound with a
PT phosphodiesterase 1B (PDE1B) polypeptide or polynucleotide and detecting
PT binding of the test compound.
XX
XX Disclosure; SEQ ID NO 2; 131pp; English.
XX
XX The invention relates to a method of screening for therapeutic agents for
XX treating a disease consisting of cancer or hematological, metabolic,
XX cardiovascular, gastrointestinal, hepatic, neurological, urological or
XX respiratory diseases in a mammal by: (a) contacting a test compound with
XX a phosphodiesterase 1B (PDE1B) polypeptide or polynucleotide; and (b)
XX detecting binding of the test compound to the PDE1B polypeptide or
XX polynucleotide. Screening for therapeutic agents for treating a disease
XX consisting of cancer or hematological, metabolic, cardiovascular,

CC gastrointestinal, hepatic, neurological, urological or respiratory
CC diseases in a mammal. The regulators of PDE1B are useful in regulating
CC PDE1B activity in a mammal having a disease comprising cancer or
CC hematological, metabolic, cardiovascular, gastrointestinal, hepatic,
CC neurological, urological or respiratory diseases. This sequence
CC represents the human phosphodiesterase 1B protein.
XX
XX Sequence 536 AA;
SQ
Query Match 39.4%; Score 50; DB 8; Length 536;
Best Local Similarity 55.6%; Pred. No. 3.4e+02;
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
OY 3 KMADNGTIVEELKQLE 20
DB 44 KQLENGEINIEELKKNLE 61
RESULT 42
ADF04444
ID ADF04444 standard; protein; 537 AA.
XX
XX ADF04444;
AC
XX
XX 12-FEB-2004 (first entry)
DT
XX
XX Bacterial polypeptide #557.
DE
XX
XX Proteus mirabilis infection; bacterial infection; antibacterial;
XX immunostimulant.
XX
XX Proteus mirabilis.
OS
XX
XX US6605709-B1.
PN
XX
XX 12-AUG-2003.
PD
XX
XX 05-APR-2000; 2000US-00543681.
PF
XX
XX 09-APR-1999; 99US-0128706P.
PR
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
PA
XX
XX Breton GL;
PI
XX
XX WPI; 2003-895291/82.
DR
XX
XX N-PSDB; ADF00272.
PT
XX
XX New Proteus mirabilis polypeptides and polynucleotides, useful as
PT reagents for diagnosis of bacterial disease, as components of
PT antibacterial vaccines, as targets for antibacterial drugs, or as
PT biocontrol agents for plants.
XX
XX Disclosure; SEQ ID NO 4729; 870pp; English.
XX
XX The invention relates to new Proteus mirabilis polypeptides and
XX polynucleotides. The invention also relates to antibodies against the
XX polypeptides, methods for producing the polypeptides, a method of
XX generating vaccines for immunising an individual against P. mirabilis, a
XX method for evaluating a compound for the ability to bind a P. mirabilis
XX polypeptide and a method for screening test compounds for anti-bacterial
XX activity. The polypeptides and polynucleotides are useful as molecular
XX targets for diagnosing, preventing and treating pathological conditions
XX resulting from bacterial infection, as reagents for diagnosis of
XX bacterial diseases, as components of antibacterial vaccines, as targets
XX for antibacterial drugs or as bio-control agents for plants. This
XX sequence represents a Proteus mirabilis polypeptide of the invention.
XX
XX Sequence 537 AA;
SQ
Query Match 39.4%; Score 50; DB 7; Length 537;
Best Local Similarity 36.4%; Pred. No. 3.4e+02;
Matches 8; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

OY 3 KMAADNGTIVTEELKOLLEQWNL 24
 DB 111 KRVYNGSASLEDEPPELLEDKWHL 132

RESULT 43

AA19080
 ID AAB19080 standard; protein; 545 AA.

AC AAB19080;

DT 08-FEB-2001 (first entry)

DE Amino acid sequence of a 60 kDa protein from Campylobacter jejuni.

KM Antigenic protein; flagellaeless mutant; vaccine; poultry; Campylobacter.

OS Campylobacter jejuni.

PN EP1043029-A1.

PD 11-OCT-2000.

PF 03-APR-2000; 2000EP-00201203.

PR 09-APR-1999; 99EP-00201086.

XX (ALKU) AKZO NOBEL NV.

PI Jacobs AAC, Van Den Bosch JF, Nuijten PWM;

DR WPI; 2000-589147/56.

XX Novel Campylobacter antigenic proteins, useful for the production of

PT vaccines for protecting poultry form Campylobacter infection.

PS Disclosure; Page 12-14; 21pp; English.

CC The present sequence represents a 60 kDa protein of Campylobacter jejuni.

CC The protein is antigenic, and is visible on a Western blot of C. jejuni

CC protein after incubation of the blot with antibodies against a

CC flagellaeless mutant of C. jejuni but not visible after incubation with

CC antibodies against wild type C. jejuni. The proteins are used to produce

CC vaccines which are useful for protecting animals, especially poultry,

CC against Campylobacter, especially C. jejuni

XX Sequence 545 AA;

SQ

Query Match 39.4%; Score 50; DB 3; Length 545;

Best Local Similarity 41.7%; Pred. No. 3.4e+02;

Matches 10; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

OY 2 KMAADNGTIVTEELKOLLEQWNLV 25

DB 166 EKVGKDGIVTEEPKSIINDELNV 189

RESULT 44

ABM83407

AC ABM83407 standard; protein; 554 AA.

DT 18-NOV-2004 (first entry)

DE Human diagnostic and therapeutic protein SEQ ID NO:3656.

KM gene therapy; human diagnostic and therapeutic polynucleotide; dthp.

OS Homo sapiens.

PN WO2004023973-A2.

XX 25-MAR-2004.

XX 12-SEP-2003; 2003WO-US028227.

XX 12-SEP-2002; 2002US-0410259P.

XX 12-SEP-2002; 2002US-0410260P.

XX (INCY-) INCYTE CORP.

PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;

PI Harthorne TA, Suchorolski MT, Altus CM, Pits SJ, Rider LV;

PI Mooney EM, Degeane AM, Pansar IS, Barville SC, Reddy TP;

PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH;

PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;

PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vilt UA, Kilton ES;

PI Lu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;

PI Patury S, Shi X, Suarez CJ;

XX WPI; 2004-329368/30.

XX N-PSDB; ACN42059.

XX New diagnostic and therapeutic polynucleotides and polypeptides, useful

PT in diagnosing a condition, disease or disorder associated with human

PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or

PT in gene mapping.

PS Claim 27; Page; 190pp; English.

XX The invention relates to novel diagnostic and therapeutic polynucleotides

CC selected from one of the 2722 sequences defined in the specification. A

CC polynucleotide of the invention may have a use in gene therapy. The human

CC diagnostic and therapeutic polynucleotides (dthp) or polypeptides may be

CC used to diagnose a particular condition, disease or disorder associated

CC with human molecules, e.g. cell proliferative disorders, endocrine

CC autoimmune/inflammatory disorder, developmental disorders, or

CC disorders, neurological disorders, gastrointestinal disorders, or

CC infections caused by virus, bacteria, fungi or parasite. The dthp

CC molecules may also be used in genetic mapping, in identifying individuals

CC from minute biological samples, in detecting single nucleotide

CC polymorphisms, as molecular weight markers, and for somatic or germline

CC gene therapy. The present sequence represents a dthp protein of the

CC invention. Note: The sequence data for this patent is not represented in

CC the printed specification, but was obtained in electronic format directly

CC from WIPO at www.wipo.int/pct/en/sequences/11sting.htm

SQ Sequence 554 AA;

Query Match 39.4%; Score 50; DB 8; Length 554;

Best Local Similarity 55.6%; Pred. No. 3.5e+02;

Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 3 KMAADNGTIVTEELKOLLE 20

DB 44 KQLENGEINTEELKKNLE 61

RESULT 45

ABU48797

AC ABU48797 standard; protein; 673 AA.

DT 19-JUN-2003 (first entry)

DE Protein encoded by prokaryotic essential gene #34324.

KM Antisense; prokaryotic essential gene; cell proliferation; drug design.

OS Ureaplasma urealyticum.

PN WO200277183-A2.

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PD 03-OCT-2002.
PF
PR 21-MAR-2002; 2002WO-US009107.
XX
XX 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0349292P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zykkind JM;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
X1 WPI; 2003-029926/02.
DR N-PSDB; ACA52667.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 25; SEQ ID NO 76721; 1766bp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 623 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway; (8)
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-regulated gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 673 AA:
OY
Query Match 39.4% Score 50. DB 6; Length 673;
Best Local Similarity 66.7%; Pred. No. 4.3e+02;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0
Db 12 VEELKQLEOWN 23
::||| |::|||
8 IDELKQKDDOWN 19
RESULT 46
ADB64170
ID ADB64170 standard; protein; 808 AA.
AC ADB64170;
XX

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DT 04-DEC-2003 (first entry)
XX
DE Human protein encoded by clone CTONG20060040.
XX
KW Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration;
KW cell regeneration; membrane protein; signal transduction-related protein;
KW transcription-related protein; osteoporosis; neurological disease;
KW cancer; tumour.
XX
OS Homo sapiens.
XX
PN EP1308459-A2.
XX
PD 07-MAY-2003.
XX
PF 28-MAR-2002; 2002EP-00007401.
XX
PR 05-NOV-2001; 2001JP-00379298.
XX
PR 25-JAN-2002; 2002JP-00350978.
XX
PA (HELI-) HELIX RES INST.
XX
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Isegaki T, Sugiyama T, Otsuki T, Makamaru A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Maeno Y;
XX
WP1: 2003-450961/43.
DR N-PSDB; ADB62200.
XX
PT New polynucleotides and polypeptides, useful for developing a diagnostic
PT marker or medicines for regulation of their expression and activity, or
PT as targets of gene therapy.
XX
PS Claim 1, Page: 222pp; English.
XX
CC The invention discloses a polynucleotide comprising a sequence selected
CC from 1970 fully defined nucleotide sequences which encode novel
CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide
CC or its partial peptide, an antibody binding to the polypeptide or peptide
CC of the polynucleotide, immunologically assaying the polypeptide or
CC peptide of the polynucleotide by contacting the polypeptide or peptide
CC with the antibody of the encoded protein, and observing the binding
CC between the two, a transformant carrying the polynucleotide in an
CC expressible manner and an antisense polynucleotide. The oligonucleotide
CC is useful as a primer for synthesizing the polynucleotide, or as a probe
CC for detecting the polynucleotide. The polynucleotides and encoded
CC proteins are useful as pharmaceutical agents and many disease-related
CC genes may be included in them, for developing a diagnostic marker or
CC medicines for regulation of their expression and activity, or as targets
CC of gene therapy. The genes are involved in tissue and/or cell
CC regeneration. Membrane proteins, signal transduction-related proteins,
CC transcription-related proteins, disease-related proteins and genes
CC encoding them can be used as indicators for diseases (e.g. osteoporosis,
CC neurological diseases, cancer, tumours). The cDNA may be used to regulate
CC the activity or expression of the encoded protein to treat diseases. The
CC sequence presented is a protein of the invention. Note: Some of the
CC sequence data for this patent is not represented in the printed
CC specification, but is based on sequence information supplied by the
CC European Patent Office.
XX
SQ Sequence 808 AA;
XX
Query Match 39.4%; Score 50; DB 7; Length 808;
Best Local Similarity 48.0%; Pred. No. 5.2e+02;
Matches 12; Conservative 3; Mismatches 8; Indels 2; Gaps 1;
XX
CY 3 KMAADGTTTVEELKQLLEQ--WNLV 25
|:|:| | | | | | | | | |
Db 32 KLAADGKTTTEELVLLLEGGTWSNI 56

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ADE71288
ID ADE71288 standard; protein; 867 AA.
XX
AC ADE71288;
XX
DT 29-JAN-2004 (first entry)
XX
DE Novel human protein #42.
XX
KM human; novel protein; drug.
XX
OS Homo sapiens.
XX
PN JP2002345493-A.
XX
PD 03-DEC-2002.
XX
PF 29-MAR-2001; 2002JP-00049046.
XX
PR 29-MAR-2001; 2001JP-00095524.
XX
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.
XX
DR WPI; 2003-460885/44.
XX
DR N-PSDB; ADE71226.
XX
PT A gene and a protein encoded by it, used in drugs.
XX
PS Disclosure; Page 189-192; 257pp; Japanese.
XX
CC The invention comprises the amino acid and coding sequences of novel
CC human proteins. The DNA and protein sequences of the invention are used
CC in drugs. The present amino acid sequence represents a novel human
CC protein of the invention.
XX
SQ Sequence 867 AA;

Query Match          39.4%; Score 50; DB 7; Length 867;
Best Local Similarity 48.0%; Pred. No. 5.7e+02;
Matches 12; Conservative 3; Mismatches 8; Indels 2; Gaps 1;

QY 3 KXADNGTITVEBELKOLEQ--KMLV 25
DB 297 KXADGKTYTEBELVLLEBGTWNSI 321

RESULT 48
ABB77073
ID ABB77073 standard; protein; 1803 AA.
XX
AC ABB77073;
XX
DT 15-JUL-2002 (first entry)
XX
DE Euglena gracilis pyruvate:NADP+ oxidoreductase #2.
XX
KM PNO; pyruvate:NADP+ oxidoreductase; antiparasitic; transgenic plant;
KM nicotinamide adenine dinucleotide phosphate; enzyme.
XX
OS Euglena gracilis.
XX
FH Key
FH Peptide 1..37
FT /label= Signal_peptide
FT Protein 38..1803
FT /label= Mature_PNO
XX
PN WO200214522-A1.
XX
PD 21-FEB-2002.
XX
PF 11-AUG-2001; 2001WO-EP009317.
XX

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PR 17-AUG-2000; 2000EP-00117730.
XX
PA (BADI ) BASF PLANT SCI GMBH.
XX
PI Cirpus P, Lerchl J, Martin W, Rotte C;
XX
DR WPI; 2002-329577/36.
XX
DR N-PSDB; ABL55676.
XX
PT Polynucleotide encoding pyruvate:nicotinamide adenine dinucleotide
PT phosphate+ oxidoreductases and polypeptide for identifying of an agonist
PT or antagonist of PNO activity useful for treating parasite infections.
XX
PS Claim 1; Page 102-105; 112pp; English.
XX
CC The sequence represents Euglena gracilis pyruvate:NADP+ oxidoreductase.
CC CC The invention relates to a novel polynucleotide encoding pyruvate:
CC nicotinamide adenine dinucleotide phosphate (NADP)+ oxidoreductases
CC (PNO). The PNO of the invention has antiparasitic activity. The
CC polynucleotide and polypeptide are useful for production of transgenic
CC plants, plant cells or plant tissue
XX
SQ Sequence 1803 AA;

Query Match          39.4%; Score 50; DB 5; Length 1803;
Best Local Similarity 47.8%; Pred. No. 1.2e+03;
Matches 11; Conservative 4; Mismatches 6; Indels 2; Gaps 1;

QY 1 KXKADNGTITVEBELKOLEQOWN 23
DB 963 EKXVADGKTYTE--LAQMLQDMN 983

RESULT 49
ABB77072
ID ABB77072 standard; protein; 1805 AA.
XX
AC ABB77072;
XX
DT 15-JUL-2002 (first entry)
XX
DE Euglena gracilis pyruvate:NADP+ oxidoreductase #1.
XX
KM PNO; pyruvate:NADP+ oxidoreductase; antiparasitic; transgenic plant;
KM nicotinamide adenine dinucleotide phosphate; enzyme.
XX
OS Euglena gracilis.
XX
FH Key
FH Peptide 1..39
FT /label= Signal_peptide
FT Protein 40..1805
FT /label= Mature_PNO
XX
PN WO200214522-A1.
XX
PD 21-FEB-2002.
XX
PF 11-AUG-2001; 2001WO-EP009317.
XX
PR 17-AUG-2000; 2000EP-00117730.
XX
PA (BADI ) BASF PLANT SCI GMBH.
XX
PI Cirpus P, Lerchl J, Martin W, Rotte C;
XX
DR WPI; 2002-329577/36.
XX
PT Polynucleotide encoding pyruvate:nicotinamide adenine dinucleotide
PT phosphate+ oxidoreductases and polypeptide for identifying of an agonist
PT or antagonist of PNO activity useful for treating parasite infections.
XX
PS Claim 1; Fig 5A; 112pp; English.
XX

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Job time : 154.511 secs

XX The sequence represents Euglena gracilis pyruvate:NADP+ oxidoreductase.
 CC The invention relates to a novel polynucleotide encoding pyruvate:
 CC nicotinamide adenine dinucleotide phosphate (NADP) + oxidoreductases
 CC (PNO). The PNO of the invention has antiparasitic activity. The
 CC polynucleotide and polypeptide are useful for production of transgenic
 CC plants, plant cells or plant tissue

SQ Sequence 1805 AA;

Query Match 39.4%; Score 50; DB 5; Length 1805;
 Best Local Similarity 47.8%; Pred. No. 1.2e+03;

Matches 11; Conservative 4; Mismatches 6; Indels 2; Gaps 1;

QY 1 KKKMADNGTITVEELKOLLEQWN 23

DB 965 EKKVADGELTTL--LAQWLQDWN 985

RESULT 50

ADN04333

ID ADN04333 standard; protein; 2000 AA.

XX ADN04333;

DT 01-JUL-2004 (first entry)

DE Antiparasitic protein sequence #361.

XX antiparasitic; gene therapy; psoriasis; diagnosis.

XX Homo sapiens.

XX PN. WO2004028479-A2.

XX 08-APR-2004.

XX 25-SEP-2003; 2003WO-US030907.

XX 25-SEP-2002; 2002US-0414006P.

XX (GETH) GENENTECH INC.

XX Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WT;

XX WIPI; 2004-305105/28.

XX N-PSDB; ADN04332.

XX New PRO nucleic acid or polypeptide, useful for preparing a

XX pharmaceutical composition for diagnosing or treating psoriasis in a

XX Claim 9; SEQ ID NO 727; 3069pp; English.

XX The invention relates to novel polynucleotide and polypeptides for

XX creating psoriasis or a sequence having at least 80% identity to the

XX above sequences. The nucleic acid is useful for preparing a composition

XX for diagnosing or treating psoriasis in a mammal. This sequence

XX corresponds to one of the polypeptides of the invention.

XX Sequence 2000 AA;

QY 2 KKKMADNGTITVEELKOLLEQWN 22

DB 1828 KKLSDNTIGKEIQRLAQF 1848

Search completed: May 11, 2005, 21:22:54

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OM protein - protein search, using sw model

Run on: May 11, 2005, 21:13:34 ; Search time 25 Seconds
(without alignments)
96.217 Million cell updates/sec

Title: US-10-712-812-6
Perfect score: 127
Sequence: 1 KKKMADNGTIVEELKQLLEQMNLY 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 62 | 48.8 | 376 | 2 T51170 | homocitrate syntha |
| 2 | 55 | 43.3 | 206 | 1 TVH0UA | transferring prote |
| 3 | 53 | 41.7 | 351 | 2 E97225 | carbamoylphosphate |
| 4 | 52 | 40.9 | 206 | 1 TVCJRA | transferring prote |
| 5 | 52 | 40.9 | 206 | 2 JN0622 | GTP-binding protei |
| 6 | 52 | 40.9 | 545 | 2 G81328 | 60 kd chaperonin (|
| 7 | 51 | 40.2 | 105 | 2 T22980 | hypothetical prote |
| 8 | 51 | 40.2 | 344 | 2 D83894 | hypothetical prote |
| 9 | 51 | 40.2 | 546 | 2 S35311 | heat shock cognate |
| 10 | 51 | 40.2 | 626 | 2 AC1619 | DNA primase (impor |
| 11 | 51 | 40.2 | 626 | 2 AG1256 | conserved uncharac |
| 12 | 50 | 39.4 | 264 | 2 T38795 | hypothetical prote |
| 13 | 50 | 39.4 | 294 | 2 T25085 | hypothetical prote |
| 14 | 50 | 39.4 | 323 | 2 C64087 | exopolysphatase |
| 15 | 50 | 39.4 | 536 | 1 JC6129 | 3',5'-cyclic-nucle |
| 16 | 50 | 39.4 | 550 | 2 S35309 | heat shock protein |
| 17 | 50 | 39.4 | 673 | 2 F82930 | DNA ligase (U121) |
| 18 | 50 | 39.4 | 819 | 2 S61217 | spectrin alpha II |
| 19 | 50 | 39.4 | 882 | 2 S41034 | hypothetical prote |
| 20 | 50 | 39.4 | 1030 | 2 A32612 | spectrin alpha cha |
| 21 | 50 | 39.4 | 1325 | 2 T14790 | hypothetical prote |
| 22 | 50 | 39.4 | 2472 | 2 A35715 | fodrin alpha chain |
| 23 | 50 | 39.4 | 2477 | 1 SUC8A | spectrin alpha cha |
| 24 | 49 | 38.6 | 36 | 2 S16552 | hypothetical prote |
| 25 | 49 | 38.6 | 218 | 2 S50566 | hypothetical prote |
| 26 | 49 | 38.6 | 462 | 2 B32840 | anthranilate synth |
| 27 | 49 | 38.6 | 475 | 2 B27671 | spectrin alpha cha |
| 28 | 49 | 38.6 | 485 | 2 C97022 | glutamy1-cRNA synt |
| 29 | 49 | 38.6 | 506 | 2 AC0845 | probable sigma-54- |

| | | | | | |
|-----|------|------|------|----------|---------------------|
| 30 | 49 | 38.6 | 529 | 2 A65051 | ygaA protein - Esc |
| 31 | 49 | 38.6 | 529 | 2 E91074 | probable 2-compone |
| 32 | 49 | 38.6 | 529 | 2 D85919 | probable 2-compone |
| 33 | 49 | 38.6 | 534 | 1 A44162 | 3',5'-cyclic-nucle |
| 34 | 49 | 38.6 | 535 | 1 A44151 | 3',5'-cyclic-nucle |
| 35 | 49 | 38.6 | 535 | 1 A46378 | 3',5'-cyclic-nucle |
| 36 | 49 | 38.6 | 643 | 2 H64119 | threonine-cRNA lig |
| 37 | 48 | 37.8 | 159 | 1 S56237 | glucosamine-phosph |
| 38 | 48 | 37.8 | 299 | 2 D83010 | probable binding p |
| 39 | 48 | 37.8 | 309 | 2 T23021 | hypothetical prote |
| 40 | 48 | 37.8 | 312 | 2 AC0897 | TDC operon transcr |
| 41 | 48 | 37.8 | 335 | 2 AG2311 | hypothetical prote |
| 42 | 48 | 37.8 | 423 | 2 T29549 | ATP-dependent prote |
| 43 | 48 | 37.8 | 441 | 2 AB1290 | ATP-dependent RNA |
| 44 | 48 | 37.8 | 442 | 2 AH1661 | ATP-dependent RNA |
| 45 | 48 | 37.8 | 447 | 2 F90248 | hypothetical prote |
| 46 | 48 | 37.8 | 462 | 2 S52528 | UtlA protein - yea |
| 47 | 48 | 37.8 | 914 | 2 B75017 | alanyl-tRNA synth |
| 48 | 48 | 37.8 | 1273 | 2 T42405 | baa-3 protein - Ca |
| 49 | 48 | 37.8 | 1964 | 2 A59282 | nonmuscle myosin I |
| 50 | 47.5 | 37.4 | 294 | 2 S60545 | envelope polypept |
| 51 | 47.5 | 37.4 | 294 | 2 S60524 | envelope polypept |
| 52 | 47 | 37.0 | 190 | 2 T08258 | conserved hypotet |
| 53 | 47 | 37.0 | 281 | 2 T01445 | hypothetical prote |
| 54 | 47 | 37.0 | 407 | 2 S27774 | transferring prote |
| 55 | 47 | 37.0 | 472 | 2 H90563 | hypothetical prote |
| 56 | 47 | 37.0 | 627 | 2 B83692 | hypothetical prote |
| 57 | 47 | 37.0 | 659 | 2 S74435 | arginine decarboxy |
| 58 | 47 | 37.0 | 667 | 2 S75959 | nitrate transport |
| 59 | 47 | 37.0 | 749 | 2 JC7729 | replication protei |
| 60 | 47 | 37.0 | 1067 | 2 T06312 | hypothetical prote |
| 61 | 47 | 37.0 | 1198 | 2 D96723 | hypothetical prote |
| 62 | 46.5 | 36.6 | 201 | 2 E97339 | HAD superfamily hy |
| 63 | 46.5 | 36.6 | 428 | 2 G82238 | adenosylmethionine |
| 64 | 46.5 | 36.6 | 594 | 2 A82913 | hypothetical prote |
| 65 | 46 | 36.2 | 118 | 2 E90178 | hypothetical prote |
| 66 | 46 | 36.2 | 335 | 2 F72404 | flagellar motor sw |
| 67 | 46 | 36.2 | 340 | 2 E69527 | hypothetical prote |
| 68 | 46 | 36.2 | 420 | 2 C71407 | hypothetical prote |
| 69 | 46 | 36.2 | 473 | 2 I50420 | nonerythroid alpha |
| 70 | 46 | 36.2 | 474 | 2 H72403 | glycine dehydrogen |
| 71 | 46 | 36.2 | 475 | 2 A27671 | spectrin alpha cha |
| 72 | 46 | 36.2 | 477 | 2 E64595 | hypothetical prote |
| 73 | 46 | 36.2 | 477 | 2 F71918 | hypothetical prote |
| 74 | 46 | 36.2 | 544 | 2 I40731 | heat shock protein |
| 75 | 46 | 36.2 | 544 | 2 B41479 | 60k heat shock pro |
| 76 | 46 | 36.2 | 544 | 2 JL0117 | hspB protein - Chl |
| 77 | 46 | 36.2 | 544 | 2 B81556 | 60 kDa chaperonin |
| 78 | 46 | 36.2 | 544 | 2 F86507 | heat shock protein |
| 79 | 46 | 36.2 | 544 | 2 S19023 | chaperonin groEL - |
| 80 | 46 | 36.2 | 544 | 2 D81709 | 60 kDa chaperonin |
| 81 | 46 | 36.2 | 544 | 2 A71555 | probable hsp-60 - |
| 82 | 46 | 36.2 | 560 | 2 AB2043 | chaperonin GroEL (|
| 83 | 46 | 36.2 | 963 | 2 B83502 | ribonucleoside red |
| 84 | 45.5 | 35.8 | 88 | 2 AB2591 | conserved hypotet |
| 85 | 45.5 | 35.8 | 88 | 2 B87373 | hypothetical prote |
| 86 | 45.5 | 35.8 | 138 | 2 H90461 | hypothetical prote |
| 87 | 45.5 | 35.8 | 206 | 1 E64317 | hypothetical prote |
| 88 | 45.5 | 35.8 | 422 | 1 AD0141 | adenosylmethionine |
| 89 | 45.5 | 35.8 | 490 | 2 T08873 | calcium-dependent |
| 90 | 45.5 | 35.8 | 490 | 2 T02366 | hypothetical prote |
| 91 | 45.5 | 35.8 | 759 | 2 D89946 | hypothetical prote |
| 92 | 45.5 | 35.8 | 3488 | 2 T74418 | protein-export mem |
| 93 | 45 | 35.4 | 104 | 2 F30183 | hypothetical prote |
| 94 | 45 | 35.4 | 106 | 2 F90468 | hypothetical prote |
| 95 | 45 | 35.4 | 118 | 2 G70478 | hypothetical prote |
| 96 | 45 | 35.4 | 128 | 2 C69183 | hypothetical prote |
| 97 | 45 | 35.4 | 150 | 2 T47315 | hypothetical prote |
| 98 | 45 | 35.4 | 207 | 2 A69349 | conserved hypotet |
| 99 | 45 | 35.4 | 226 | 2 S37434 | membrane glycoprot |
| 100 | 45 | 35.4 | 226 | 2 D49591 | membrane protein M |
| 101 | 45 | 35.4 | 260 | 1 A38585 | deoxycytidine kina |
| 102 | 45 | 35.4 | 307 | 2 T45998 | hypothetical prote |

| | | | | | | | | | | | | | |
|-----|------|------|------|---|--------|----------------------|-----|------|------|------|---|--------|---------------------|
| 103 | 45 | 35.4 | 318 | 2 | T43492 | hypothetical prote | 176 | 43.5 | 34.3 | 501 | 2 | G85097 | hypothetical prote |
| 104 | 45 | 35.4 | 376 | 2 | S55892 | endo-1,4-beta-xylo | 177 | 43.5 | 34.3 | 516 | 2 | T33061 | hypothetical prote |
| 105 | 45 | 35.4 | 401 | 2 | E72213 | probable 2,3-bisph | 178 | 43.5 | 34.3 | 571 | 2 | T00835 | calcium-dependent |
| 106 | 45 | 35.4 | 459 | 2 | H82426 | probable regulator | 179 | 43.5 | 34.3 | 635 | 2 | T49694 | hypothetical prote |
| 107 | 45 | 35.4 | 468 | 2 | H82012 | hypothetical prote | 180 | 43.5 | 34.3 | 761 | 2 | H69797 | transcription regu |
| 108 | 45 | 35.4 | 470 | 2 | T31049 | hypothetical prote | 181 | 43.5 | 34.3 | 1165 | 2 | S58236 | pyruvate (flavodox |
| 109 | 45 | 35.4 | 473 | 2 | T15998 | calcium-dependent | 182 | 43 | 33.9 | 71 | 2 | B98040 | degenerative trans |
| 110 | 45 | 35.4 | 514 | 2 | T10938 | chaperonin-like pr | 183 | 43 | 33.9 | 80 | 2 | B82267 | exodeoxyribonuclea |
| 111 | 45 | 35.4 | 543 | 2 | S70013 | chaperonin-groEL | 184 | 43 | 33.9 | 145 | 2 | A56085 | regulatory protein |
| 112 | 45 | 35.4 | 546 | 2 | S36237 | chaperonin groEL - | 185 | 43 | 33.9 | 146 | 2 | D83676 | transcription regu |
| 113 | 45 | 35.4 | 546 | 2 | B71986 | 60kDa chaperone - | 186 | 43 | 33.9 | 163 | 2 | G69035 | hypothetical prote |
| 114 | 45 | 35.4 | 560 | 1 | DOCGA | NAD-diphthamide AD | 187 | 43 | 33.9 | 178 | 2 | AG0049 | hypothetical prote |
| 115 | 45 | 35.4 | 560 | 1 | DOCGPO | NAD-diphthamide AD | 188 | 43 | 33.9 | 184 | 2 | S41960 | ras-related GTP-bi |
| 116 | 45 | 35.4 | 755 | 2 | T47806 | hypothetical prote | 189 | 43 | 33.9 | 184 | 2 | I55401 | ras-related protei |
| 117 | 45 | 35.4 | 897 | 2 | AC2001 | hypothetical prote | 190 | 43 | 33.9 | 186 | 2 | F89831 | hypothetical prote |
| 118 | 45 | 35.4 | 897 | 2 | AC2001 | intraluminal subti | 191 | 43 | 33.9 | 192 | 2 | S16509 | DNA-invertase - St |
| 119 | 45 | 35.4 | 1052 | 2 | T17093 | hypothetical prote | 192 | 43 | 33.9 | 197 | 2 | S11781 | DNA-invertase - St |
| 120 | 45 | 35.4 | 1549 | 2 | T21809 | hypothetical prote | 193 | 43 | 33.9 | 199 | 2 | A44033 | ubiquinol-cytochro |
| 121 | 45 | 35.4 | 1596 | 2 | T00057 | genome polyprotein | 194 | 43 | 33.9 | 237 | 2 | D97801 | hypothetical prote |
| 122 | 45 | 35.4 | 146 | 2 | G90201 | conserved hypotet | 195 | 43 | 33.9 | 267 | 2 | H69373 | hypothetical prote |
| 123 | 44.5 | 35.0 | 146 | 2 | G90201 | transcription regu | 196 | 43 | 33.9 | 278 | 2 | T24444 | hypothetical prote |
| 124 | 44.5 | 35.0 | 260 | 2 | A80330 | transcription regu | 197 | 43 | 33.9 | 279 | 2 | B72255 | dimethyladenosine |
| 125 | 44.5 | 35.0 | 271 | 2 | A82209 | hypothetical prote | 198 | 43 | 33.9 | 292 | 2 | D85863 | probable regulator |
| 126 | 44.5 | 35.0 | 280 | 2 | G68881 | rRNA (adenine-N6,N | 199 | 43 | 33.9 | 292 | 2 | B91019 | probable transcrip |
| 127 | 44.5 | 35.0 | 314 | 2 | G97050 | hypothetical prote | 200 | 43 | 33.9 | 306 | 2 | A48118 | major epidermal ca |
| 128 | 44.5 | 35.0 | 532 | 2 | S22662 | DNA-methyltransfer | 201 | 43 | 33.9 | 322 | 2 | S52032 | ribose-phosphate 1 |
| 129 | 44.5 | 35.0 | 536 | 2 | T05500 | calcium-dependent | 202 | 43 | 33.9 | 325 | 2 | T32838 | hypothetical prote |
| 130 | 44.5 | 35.0 | 852 | 2 | T12016 | envelope glycoprot | 203 | 43 | 33.9 | 336 | 2 | S74424 | sphx protein - Syn |
| 131 | 44.5 | 35.0 | 1384 | 2 | S78132 | delta-directed RNA p | 204 | 43 | 33.9 | 353 | 2 | T15429 | hypothetical prote |
| 132 | 44.5 | 35.0 | 3770 | 2 | A40889 | hypothetical prote | 205 | 43 | 33.9 | 364 | 2 | A84099 | hypothetical prote |
| 133 | 44 | 34.6 | 100 | 2 | D68691 | hypothetical prote | 206 | 43 | 33.9 | 370 | 2 | A49360 | pyruvate dehydroge |
| 134 | 44 | 34.6 | 151 | 2 | D86891 | hypothetical prote | 207 | 43 | 33.9 | 379 | 2 | H84398 | phosphate ABC tran |
| 135 | 44 | 34.6 | 182 | 2 | B70335 | conserved hypotet | 208 | 43 | 33.9 | 382 | 2 | F82428 | iron-containing al |
| 136 | 44 | 34.6 | 183 | 2 | A96605 | unknown protein FI | 209 | 43 | 33.9 | 389 | 2 | A86706 | hypothetical prote |
| 137 | 44 | 34.6 | 186 | 2 | P82508 | hypothetical prote | 210 | 43 | 33.9 | 394 | 2 | D83002 | multidrug resistan |
| 138 | 44 | 34.6 | 258 | 2 | A59369 | ubiquinol-cytochro | 211 | 43 | 33.9 | 399 | 2 | A82351 | DNA/pantothenate m |
| 139 | 44 | 34.6 | 271 | 2 | A30592 | 33k cytoskeletal p | 212 | 43 | 33.9 | 404 | 2 | S6573 | transcription init |
| 140 | 44 | 34.6 | 308 | 1 | F69752 | 5-dehydro-4-deoxyg | 213 | 43 | 33.9 | 414 | 2 | G70360 | hypothetical prote |
| 141 | 44 | 34.6 | 407 | 2 | T24951 | hypothetical prote | 214 | 43 | 33.9 | 420 | 2 | A72377 | two-component sens |
| 142 | 44 | 34.6 | 429 | 2 | D70763 | threonine ammonia- | 215 | 43 | 33.9 | 460 | 2 | D70435 | hypothetical prote |
| 143 | 44 | 34.6 | 443 | 2 | B75165 | signal recognition | 216 | 43 | 33.9 | 468 | 2 | D85828 | gluconate-6-phosph |
| 144 | 44 | 34.6 | 500 | 2 | A71874 | hypothetical prote | 217 | 43 | 33.9 | 468 | 2 | F90982 | gluconate-6-phosph |
| 145 | 44 | 34.6 | 511 | 2 | H89758 | histidine ammonia- | 218 | 43 | 33.9 | 469 | 2 | A72377 | 6-phosphogluconate |
| 146 | 44 | 34.6 | 530 | 2 | D82412 | chaperonin, 60 kD | 219 | 43 | 33.9 | 473 | 2 | D83508 | two-component resp |
| 147 | 44 | 34.6 | 540 | 2 | D81192 | gamma-glutamyltran | 220 | 43 | 33.9 | 481 | 2 | UJ1147 | N-acetylmutamoyl-L |
| 148 | 44 | 34.6 | 553 | 2 | D84133 | oligoendopeptidase | 221 | 43 | 33.9 | 499 | 2 | AH0485 | probable insulinlas |
| 149 | 44 | 34.6 | 555 | 2 | S12639 | hypothetical prote | 222 | 43 | 33.9 | 510 | 2 | B70368 | L-aspartate oxidas |
| 150 | 44 | 34.6 | 571 | 2 | C70353 | ATP-binding protei | 223 | 43 | 33.9 | 521 | 2 | B71717 | hypothetical prote |
| 151 | 44 | 34.6 | 601 | 2 | C81044 | succinate dehydrog | 224 | 43 | 33.9 | 526 | 2 | B86149 | TlN6.20 protein - |
| 152 | 44 | 34.6 | 603 | 2 | G82738 | gamma-glutamyltran | 225 | 43 | 33.9 | 539 | 2 | S22342 | chaperonin HSP60 - |
| 153 | 44 | 34.6 | 611 | 1 | S62811 | oligoendopeptidase | 226 | 43 | 33.9 | 541 | 2 | S68249 | chaperonin groEL, h |
| 154 | 44 | 34.6 | 750 | 2 | S34683 | hypothetical prote | 227 | 43 | 33.9 | 543 | 2 | F97232 | chaperonin groEL, |
| 155 | 44 | 34.6 | 919 | 2 | B83212 | probable sensor/re | 228 | 43 | 33.9 | 543 | 2 | B41872 | heat shock protein |
| 156 | 44 | 34.6 | 940 | 2 | B81852 | probable type III | 229 | 43 | 33.9 | 543 | 2 | T30186 | hypothetical prote |
| 157 | 44 | 34.6 | 1019 | 2 | F70342 | cation efflux syst | 230 | 43 | 33.9 | 552 | 2 | S74322 | chaperonin groEL-2 |
| 158 | 44 | 34.6 | 1415 | 2 | C86438 | hypothetical prote | 231 | 43 | 33.9 | 565 | 2 | T47625 | glutathione-disulf |
| 159 | 44 | 34.6 | 1577 | 2 | T30858 | glycosyltransferas | 232 | 43 | 33.9 | 577 | 2 | T51264 | calcium-dependent |
| 160 | 44 | 34.6 | 1905 | 2 | T51553 | Placxin - African c | 233 | 43 | 33.9 | 589 | 2 | H90112 | CPB60 protein [lmp |
| 161 | 44 | 34.6 | 2094 | 2 | S33124 | lpr protein - huma | 234 | 43 | 33.9 | 591 | 2 | A45135 | profilaggrin - hum |
| 162 | 44 | 34.6 | 5369 | 2 | T44807 | myosubtilin synth | 235 | 43 | 33.9 | 602 | 2 | T13219 | major capsid prote |
| 163 | 43.5 | 34.3 | 209 | 2 | H69901 | general stress pro | 236 | 43 | 33.9 | 602 | 2 | S60052 | calcium-dependent |
| 164 | 43.5 | 34.3 | 248 | 2 | E90295 | hypothetical prote | 237 | 43 | 33.9 | 615 | 2 | F64572 | arginine decarboxy |
| 165 | 43.5 | 34.3 | 249 | 2 | C90468 | hypothetical prote | 238 | 43 | 33.9 | 615 | 2 | C71867 | arginine decarboxy |
| 166 | 43.5 | 34.3 | 279 | 2 | A86312 | hypothetical prote | 239 | 43 | 33.9 | 642 | 2 | C81345 | hypothetical prote |
| 167 | 43.5 | 34.3 | 316 | 2 | E90401 | FlA6.5 protein - | 240 | 43 | 33.9 | 821 | 1 | S76330 | endopeptidase Clp |
| 168 | 43.5 | 34.3 | 316 | 2 | E90401 | hypothetical prote | 241 | 43 | 33.9 | 890 | 2 | C98101 | alcohol-acetaldehy |
| 169 | 43.5 | 34.3 | 316 | 2 | H90426 | hypothetical prote | 242 | 43 | 33.9 | 1187 | 2 | T46637 | transcription fac |
| 170 | 43.5 | 34.3 | 355 | 2 | S74678 | hypothetical prote | 243 | 43 | 33.9 | 1188 | 2 | T46608 | zinc finger protei |
| 171 | 43.5 | 34.3 | 370 | 2 | G97277 | glycosyltransferas | 244 | 43 | 33.9 | 1245 | 2 | C88104 | protein P40E12.2 [|
| 172 | 43.5 | 34.3 | 429 | 1 | UC5005 | adenosylmethionine | 245 | 43 | 33.9 | 1245 | 2 | T11953 | hypothetical prote |
| 173 | 43.5 | 34.3 | 429 | 1 | AG0596 | geranylgeranyl red | 246 | 43 | 33.9 | 1247 | 2 | C89583 | protein K07E3.1 [i |
| 174 | 43.5 | 34.3 | 467 | 2 | F96773 | calcium-dependent | 247 | 43 | 33.9 | 1374 | 2 | S62524 | probable RNA helic |
| 175 | 43.5 | 34.3 | 495 | 1 | S46284 | | 248 | 43 | 33.9 | 1495 | 2 | S61023 | hypothetical prote |

| | | | | | | |
|-----|------|------|------|---|--------|----------------------|
| 249 | 42.5 | 33.5 | 58 | 2 | T04616 | hypothetical prote |
| 250 | 42.5 | 33.5 | 147 | 2 | A29910 | myosin calcium-bin |
| 251 | 42.5 | 33.5 | 189 | 2 | S39864 | late competence op |
| 252 | 42.5 | 33.5 | 224 | 2 | D89836 | hypothetical prote |
| 253 | 42.5 | 33.5 | 265 | 2 | S73334 | probable lipoprote |
| 254 | 42.5 | 33.5 | 321 | 2 | A63088 | conserved hypotet |
| 255 | 42.5 | 33.5 | 340 | 2 | PH0217 | reverse transcript |
| 256 | 42.5 | 33.5 | 376 | 2 | T16050 | hypothetical prote |
| 257 | 42.5 | 33.5 | 428 | 2 | S09134 | gene ND4L intron 1 |
| 258 | 42.5 | 33.5 | 429 | 1 | XNEDCP | adenosylmethionine |
| 259 | 42.5 | 33.5 | 429 | 2 | B85585 | 7,8-diaminopelarg |
| 260 | 42.5 | 33.5 | 429 | 2 | D90735 | calcium-dependent |
| 261 | 42.5 | 33.5 | 490 | 1 | S71776 | probable RNA-direc |
| 262 | 42.5 | 33.5 | 513 | 2 | S21976 | hypothetical prote |
| 263 | 42.5 | 33.5 | 523 | 2 | S2347 | dihydroxy-acid deh |
| 264 | 42.5 | 33.5 | 558 | 2 | B99494 | flageellar hook-ase |
| 265 | 42.5 | 33.5 | 666 | 2 | S71032 | probable RNA-direc |
| 266 | 42.5 | 33.5 | 685 | 2 | S16783 | hypothetical prote |
| 267 | 42.5 | 33.5 | 821 | 2 | T24728 | hypothetical prote |
| 268 | 42.5 | 33.5 | 932 | 2 | H86325 | ncca protein - Alc |
| 269 | 42.5 | 33.5 | 1076 | 2 | T39580 | DNA-directed RNA p |
| 270 | 42.5 | 33.5 | 1481 | 2 | S78373 | hypothetical prote |
| 271 | 42.5 | 33.5 | 1601 | 2 | AE2011 | tubercous sclerosis |
| 272 | 42.5 | 33.5 | 1809 | 2 | S57329 | transfer complex p |
| 273 | 42 | 33.1 | 55 | 2 | F56976 | hypothetical prote |
| 274 | 42 | 33.1 | 82 | 2 | A99836 | unknown protein en |
| 275 | 42 | 33.1 | 82 | 2 | C85694 | hypothetical prote |
| 276 | 42 | 33.1 | 103 | 2 | F69110 | transposase alr714 |
| 277 | 42 | 33.1 | 134 | 2 | AE2496 | hypothetical prote |
| 278 | 42 | 33.1 | 135 | 2 | T29428 | hypothetical prote |
| 279 | 42 | 33.1 | 158 | 2 | A72562 | probable resistanc |
| 280 | 42 | 33.1 | 159 | 2 | T10826 | probable resistanc |
| 281 | 42 | 33.1 | 159 | 2 | T10837 | conserved hypotet |
| 282 | 42 | 33.1 | 172 | 2 | G69087 | ribosome recycling |
| 283 | 42 | 33.1 | 185 | 2 | G69626 | conserved hypotet |
| 284 | 42 | 33.1 | 189 | 2 | B69044 | epoxidase - Methan |
| 285 | 42 | 33.1 | 190 | 2 | F69187 | probable calcium-b |
| 286 | 42 | 33.1 | 191 | 2 | T10620 | hypothetical prote |
| 287 | 42 | 33.1 | 204 | 2 | T25760 | GTP-binding protei |
| 288 | 42 | 33.1 | 207 | 2 | E38625 | phage shock protei |
| 289 | 42 | 33.1 | 222 | 2 | H82169 | basal-body rod mod |
| 290 | 42 | 33.1 | 225 | 2 | AF0219 | nonstructural - Sen |
| 291 | 42 | 33.1 | 229 | 1 | B43685 | somolactacin - Sen |
| 292 | 42 | 33.1 | 230 | 2 | JC2582 | ABC transporter. A |
| 293 | 42 | 33.1 | 244 | 2 | E72364 | nitrogenase (EC 1. |
| 294 | 42 | 33.1 | 282 | 2 | H70671 | probable membrane |
| 295 | 42 | 33.1 | 290 | 1 | N1A1V | hypothetical prote |
| 296 | 42 | 33.1 | 292 | 2 | S60950 | ldca protein - Bac |
| 297 | 42 | 33.1 | 297 | 2 | H72670 | transcription acti |
| 298 | 42 | 33.1 | 312 | 1 | QOECRG | transcription acti |
| 299 | 42 | 33.1 | 312 | 2 | B85973 | glycerol-3-phospha |
| 300 | 42 | 33.1 | 312 | 2 | F91128 | H+-transporting AT |
| 301 | 42 | 33.1 | 321 | 2 | E69147 | conserved hypotet |
| 302 | 42 | 33.1 | 364 | 1 | T44672 | probable enzyme wi |
| 303 | 42 | 33.1 | 367 | 1 | D70395 | G box-binding prot |
| 304 | 42 | 33.1 | 368 | 1 | B97198 | tRNA-splicing endo |
| 305 | 42 | 33.1 | 374 | 2 | T07887 | hypothetical prote |
| 306 | 42 | 33.1 | 376 | 2 | A38862 | cell division cont |
| 307 | 42 | 33.1 | 377 | 2 | A38862 | theonine deaminas |
| 308 | 42 | 33.1 | 379 | 1 | S42543 | probable pyruvate |
| 309 | 42 | 33.1 | 389 | 1 | A48329 | probable signal re |
| 310 | 42 | 33.1 | 390 | 2 | T25996 | calcium-dependent |
| 311 | 42 | 33.1 | 390 | 1 | A43685 | argininosuccinate |
| 312 | 42 | 33.1 | 399 | 1 | A43685 | hypothetical prote |
| 313 | 42 | 33.1 | 407 | 2 | T36204 | hypothetical prote |
| 314 | 42 | 33.1 | 408 | 2 | AG1745 | aminotransferase h |
| 315 | 42 | 33.1 | 412 | 2 | S07537 | myosin heavy chain |
| 316 | 42 | 33.1 | 420 | 2 | T43932 | cell division cont |
| 317 | 42 | 33.1 | 427 | 2 | C87060 | theonine deaminas |
| 318 | 42 | 33.1 | 431 | 2 | A72549 | probable pyruvate |
| 319 | 42 | 33.1 | 445 | 2 | H71176 | probable signal re |
| 320 | 42 | 33.1 | 451 | 2 | S56717 | calcium-dependent |
| 321 | 42 | 33.1 | 459 | 2 | E86640 | argininosuccinate |
| 322 | 42 | 33.1 | 466 | 2 | T30040 | hypothetical prote |
| 323 | 42 | 33.1 | 482 | 2 | T01659 | phosphoglucanate d |
| 324 | 42 | 33.1 | 484 | 2 | T01658 | phosphoglucanate d |
| 325 | 42 | 33.1 | 494 | 2 | B33501 | myosin heavy chain |
| 326 | 42 | 33.1 | 494 | 2 | S75398 | lysine-tRNA ligase |
| 327 | 42 | 33.1 | 509 | 2 | AE1295 | Bitfunctional phosp |
| 328 | 42 | 33.1 | 509 | 2 | AC1667 | Cytochrome P450 92 |
| 329 | 42 | 33.1 | 510 | 2 | JC7886 | calcium-dependent |
| 330 | 42 | 33.1 | 521 | 2 | G96543 | calcium-dependent |
| 331 | 42 | 33.1 | 529 | 1 | S71774 | calcium-dependent |
| 332 | 42 | 33.1 | 553 | 1 | T02139 | calcium-dependent |
| 333 | 42 | 33.1 | 554 | 1 | T03263 | calcium-dependent |
| 334 | 42 | 33.1 | 604 | 2 | G89864 | hypothetical prote |
| 335 | 42 | 33.1 | 611 | 2 | T21747 | hypothetical prote |
| 336 | 42 | 33.1 | 621 | 2 | S10450 | myosin heavy chain |
| 337 | 42 | 33.1 | 624 | 2 | A55220 | penicillin-binding |
| 338 | 42 | 33.1 | 654 | 2 | T17959 | hypothetical prote |
| 339 | 42 | 33.1 | 667 | 2 | B97012 | methy1-accepting c |
| 340 | 42 | 33.1 | 674 | 2 | S74506 | ribonuclease E - S |
| 341 | 42 | 33.1 | 684 | 2 | S60266 | novel antigen rece |
| 342 | 42 | 33.1 | 692 | 1 | S46953 | phosphotransferase |
| 343 | 42 | 33.1 | 712 | 1 | A47331 | ribonuclease-eri |
| 344 | 42 | 33.1 | 712 | 2 | AC1058 | ribonuclease-eri |
| 345 | 42 | 33.1 | 712 | 2 | G91280 | anaerobic ribonuci |
| 346 | 42 | 33.1 | 712 | 2 | G86121 | polypeptide synthet |
| 347 | 42 | 33.1 | 750 | 2 | AG3008 | hypothetical prote |
| 348 | 42 | 33.1 | 757 | 2 | T24266 | hypothetical prote |
| 349 | 42 | 33.1 | 770 | 2 | F88275 | 2-oxoglutarate deh |
| 350 | 42 | 33.1 | 910 | 2 | B89918 | clostritipain-relate |
| 351 | 42 | 33.1 | 979 | 2 | E72236 | dynein heavy chain |
| 352 | 42 | 33.1 | 1125 | 2 | T30298 | p115 homolog - Met |
| 353 | 42 | 33.1 | 1169 | 2 | A64505 | chromosomal protei |
| 354 | 42 | 33.1 | 1203 | 2 | B55094 | flightless-I homol |
| 355 | 42 | 33.1 | 1268 | 2 | A49674 | protein M01E10.2 (|
| 356 | 42 | 33.1 | 1286 | 2 | A88396 | probable inositol |
| 357 | 42 | 33.1 | 1305 | 2 | T00670 | DNA-directed RNA p |
| 358 | 42 | 33.1 | 1365 | 1 | RNLVC2 | hypothetical prote |
| 359 | 42 | 33.1 | 1409 | 2 | T29594 | hypothetical prote |
| 360 | 42 | 33.1 | 1583 | 2 | AB2137 | probable polypeptid |
| 361 | 42 | 33.1 | 1733 | 2 | D70887 | smooth muscle myos |
| 362 | 42 | 33.1 | 1938 | 2 | UC5421 | myosin heavy chain |
| 363 | 42 | 33.1 | 1972 | 1 | A41604 | smooth muscle myos |
| 364 | 42 | 33.1 | 1972 | 2 | UC5420 | variant surface pr |
| 365 | 42 | 33.1 | 3026 | 2 | T28431 | trithorax protein |
| 366 | 42 | 33.1 | 3759 | 2 | A35085 | hypothetical prote |
| 367 | 42 | 32.7 | 82 | 2 | DC4329 | hypothetical prote |
| 368 | 42 | 32.7 | 184 | 2 | T40305 | nitroreductase hom |
| 369 | 42 | 32.7 | 202 | 2 | H69902 | conserved hypotet |
| 370 | 42 | 32.7 | 226 | 1 | H69474 | probable transcript |
| 371 | 42 | 32.7 | 236 | 2 | A86075 | hypothetical prote |
| 372 | 42 | 32.7 | 236 | 2 | S40817 | probable transcript |
| 373 | 42 | 32.7 | 236 | 2 | B81228 | conserved hypotet |
| 374 | 42 | 32.7 | 239 | 2 | D70359 | amino acid ABC tra |
| 375 | 42 | 32.7 | 255 | 2 | F69962 | ATP phosphoribosyl |
| 376 | 42 | 32.7 | 281 | 2 | F69323 | transposase - fru1 |
| 377 | 42 | 32.7 | 345 | 2 | S60466 | adenosylmethionine |
| 378 | 42 | 32.7 | 428 | 2 | B84964 | hypothetical prote |
| 379 | 42 | 32.7 | 450 | 2 | D86356 | hypothetical prote |
| 380 | 42 | 32.7 | 489 | 2 | H86356 | probable UDP-gluc |
| 381 | 42 | 32.7 | 508 | 1 | A43713 | calcium-dependent |
| 382 | 42 | 32.7 | 532 | 2 | AD2420 | hypothetical prote |
| 383 | 42 | 32.7 | 559 | 2 | T09038 | NADH dehydrogenase |
| 384 | 42 | 32.7 | 583 | 2 | H84810 | hypothetical prote |
| 385 | 42 | 32.7 | 634 | 2 | E86880 | hypothetical prote |
| 386 | 42 | 32.7 | 639 | 1 | T02784 | calcium-dependent |
| 387 | 42 | 32.7 | 678 | 2 | S56284 | hypothetical prote |
| 388 | 42 | 32.7 | 836 | 2 | B84417 | cell surface glyco |
| 389 | 42 | 32.7 | 846 | 1 | VCLJND | env polyprotein pr |
| 390 | 42 | 32.7 | 852 | 2 | A28459 | cell surface glyco |
| 391 | 42 | 32.7 | 886 | 2 | F83862 | penicillin-binding |
| 392 | 42 | 32.7 | 886 | 2 | S67200 | hypothetical prote |
| 393 | 42 | 32.7 | 1289 | 2 | S67200 | eye development pr |
| 394 | 42 | 32.7 | 1893 | 2 | A56158 | probable acetyl-Co |
| 394 | 42 | 32.7 | 2123 | 2 | S55089 | |

| | | | | | | |
|-----|------|------|------|---|--------|----------------------|
| 395 | 41.5 | 32.7 | 2339 | 2 | A45597 | DNA-directed RNA p |
| 396 | 41.5 | 32.7 | 3119 | 2 | T18414 | protein g377 - mal |
| 397 | 41 | 32.3 | 71 | 1 | RGBOG2 | GTP-binding regula |
| 398 | 41 | 32.3 | 71 | 2 | JC7290 | guanine nucleotide |
| 399 | 41 | 32.3 | 126 | 2 | B82184 | hypothetical prote |
| 400 | 41 | 32.3 | 140 | 2 | A10114 | conserved hypotnet |
| 401 | 41 | 32.3 | 150 | 1 | MC2P | calmodulin - flasi |
| 402 | 41 | 32.3 | 150 | 2 | S18394 | tropomycin C isoform |
| 403 | 41 | 32.3 | 152 | 2 | A11018 | SoxR protein limpo |
| 404 | 41 | 32.3 | 154 | 2 | B91259 | redox-sensing acti |
| 405 | 41 | 32.3 | 154 | 2 | A86100 | redox-sensing acti |
| 406 | 41 | 32.3 | 154 | 2 | JS0577 | soxR protein - Esc |
| 407 | 41 | 32.3 | 156 | 2 | T32236 | hypothetical prote |
| 408 | 41 | 32.3 | 159 | 2 | T32233 | hypothetical prote |
| 409 | 41 | 32.3 | 161 | 2 | S47549 | cell division cont |
| 410 | 41 | 32.3 | 169 | 2 | D84864 | probable calcium b |
| 411 | 41 | 32.3 | 169 | 2 | H75387 | hypothetical prote |
| 412 | 41 | 32.3 | 172 | 2 | G69432 | hypothetical prote |
| 413 | 41 | 32.3 | 206 | 2 | S73817 | type 1 restriction |
| 414 | 41 | 32.3 | 211 | 2 | T32591 | hypothetical prote |
| 415 | 41 | 32.3 | 214 | 2 | T00879 | MADS-box protein A |
| 416 | 41 | 32.3 | 240 | 2 | T22210 | hypothetical prote |
| 417 | 41 | 32.3 | 253 | 1 | F71233 | hypothetical prote |
| 418 | 41 | 32.3 | 260 | 2 | S73040 | hypothetical prote |
| 419 | 41 | 32.3 | 280 | 2 | P96768 | hypothetical prote |
| 420 | 41 | 32.3 | 292 | 2 | AG0791 | probable transcrip |
| 421 | 41 | 32.3 | 296 | 2 | I52860 | smooth muscle myos |
| 422 | 41 | 32.3 | 307 | 2 | B69837 | hypothetical prote |
| 423 | 41 | 32.3 | 325 | 2 | B83165 | hypothetical prote |
| 424 | 41 | 32.3 | 329 | 2 | G72319 | hypothetical prote |
| 425 | 41 | 32.3 | 330 | 2 | I65768 | smooth muscle myos |
| 426 | 41 | 32.3 | 338 | 2 | G71220 | response regulator |
| 427 | 41 | 32.3 | 344 | 2 | G75260 | hypothetical prote |
| 428 | 41 | 32.3 | 344 | 2 | T48827 | hypothetical prote |
| 429 | 41 | 32.3 | 364 | 2 | T25086 | hypothetical prote |
| 430 | 41 | 32.3 | 364 | 2 | T09011 | probable transpos |
| 431 | 41 | 32.3 | 383 | 2 | AB1567 | teichoic acid bios |
| 432 | 41 | 32.3 | 390 | 2 | AC2169 | molybdopterin bios |
| 433 | 41 | 32.3 | 398 | 2 | AE4390 | N-acetylornithine |
| 434 | 41 | 32.3 | 410 | 2 | AE2621 | conserved hypotet |
| 435 | 41 | 32.3 | 410 | 2 | B97403 | hypothetical prote |
| 436 | 41 | 32.3 | 416 | 2 | C47017 | probable transcrip |
| 437 | 41 | 32.3 | 416 | 2 | AE2017 | RNA polymerase sig |
| 438 | 41 | 32.3 | 416 | 2 | F71869 | hypothetical prote |
| 439 | 41 | 32.3 | 443 | 2 | H96841 | hypothetical prote |
| 440 | 41 | 32.3 | 444 | 2 | B90192 | DNA repair protein |
| 441 | 41 | 32.3 | 448 | 2 | C82936 | signal recognition |
| 442 | 41 | 32.3 | 455 | 2 | H89896 | hypothetical prote |
| 443 | 41 | 32.3 | 455 | 2 | H71028 | hypothetical prote |
| 444 | 41 | 32.3 | 456 | 2 | F81215 | signal recognition |
| 445 | 41 | 32.3 | 456 | 2 | B81792 | signal recognition |
| 446 | 41 | 32.3 | 461 | 2 | SS0864 | avermectin-sensiti |
| 447 | 41 | 32.3 | 465 | 2 | D83598 | probable zinc prot |
| 448 | 41 | 32.3 | 468 | 2 | I41250 | phosphoglucosate d |
| 449 | 41 | 32.3 | 472 | 1 | B53236 | transcription fact |
| 450 | 41 | 32.3 | 472 | 1 | AD1889 | adenylate cyclase |
| 451 | 41 | 32.3 | 478 | 1 | S73919 | pet112 protein hom |
| 452 | 41 | 32.3 | 486 | 1 | SS7786 | phosphoglucosate d |
| 453 | 41 | 32.3 | 486 | 2 | AC2424 | hypothetical prote |
| 454 | 41 | 32.3 | 492 | 2 | SS0554 | hypothetical prote |
| 455 | 41 | 32.3 | 495 | 2 | T20754 | hypothetical prote |
| 456 | 41 | 32.3 | 520 | 2 | C84774 | probable calcium-d |
| 457 | 41 | 32.3 | 525 | 2 | D70747 | probable effh prote |
| 458 | 41 | 32.3 | 534 | 2 | H82244 | sensor histidine k |
| 459 | 41 | 32.3 | 537 | 2 | AG2259 | transposase all363 |
| 460 | 41 | 32.3 | 538 | 2 | H72367 | groEL protein - Th |
| 461 | 41 | 32.3 | 538 | 2 | A70485 | single-strand-DNA- |
| 462 | 41 | 32.3 | 541 | 2 | JN0511 | heat shock protein |
| 463 | 41 | 32.3 | 541 | 2 | JN0512 | heat shock protein |
| 464 | 41 | 32.3 | 541 | 2 | S72614 | chaperonin 60 - Th |
| 465 | 41 | 32.3 | 542 | 2 | F95967 | probable heat choc |
| 466 | 41 | 32.3 | 544 | 1 | B43827 | chaperonin groEL - |
| 467 | 41 | 32.3 | 544 | 2 | B82048 | chaperonin, 60 Kd |
| 468 | 41 | 32.3 | 544 | 2 | S37039 | groEL protein - Ba |
| 469 | 41 | 32.3 | 544 | 2 | T43364 | potassium channel |
| 470 | 41 | 32.3 | 545 | 2 | JN0509 | heat shock protein |
| 471 | 41 | 32.3 | 545 | 2 | C95311 | groEL2 chaperonin |
| 472 | 41 | 32.3 | 546 | 2 | S34938 | heat shock protein |
| 473 | 41 | 32.3 | 546 | 2 | S65596 | heat shock protein |
| 474 | 41 | 32.3 | 546 | 2 | S22347 | heat shock protein |
| 475 | 41 | 32.3 | 546 | 2 | I40342 | groEL - Brucella a |
| 476 | 41 | 32.3 | 546 | 2 | AG3640 | heat shock protein |
| 477 | 41 | 32.3 | 557 | 2 | AC2137 | 60K chaperonin gro |
| 478 | 41 | 32.3 | 557 | 2 | AC2137 | ABC transporter AT |
| 479 | 41 | 32.3 | 572 | 2 | SS5889 | collapsin response |
| 480 | 41 | 32.3 | 576 | 2 | T43353 | potassium channel |
| 481 | 41 | 32.3 | 581 | 2 | T50841 | phosphoinositide-s |
| 482 | 41 | 32.3 | 603 | 2 | A84584 | hypothetical prote |
| 483 | 41 | 32.3 | 622 | 2 | AC1236 | acylttransferase (t |
| 484 | 41 | 32.3 | 627 | 2 | C98148 | acetoin catabolism |
| 485 | 41 | 32.3 | 627 | 2 | A13139 | transcription regu |
| 486 | 41 | 32.3 | 630 | 2 | AC1309 | probable ABC trans |
| 487 | 41 | 32.3 | 640 | 2 | T32885 | hypothetical prote |
| 488 | 41 | 32.3 | 695 | 2 | T13639 | probable tail-host |
| 489 | 41 | 32.3 | 749 | 2 | H82691 | topoisomerase IV s |
| 490 | 41 | 32.3 | 754 | 2 | G83025 | topoisomerase IV s |
| 491 | 41 | 32.3 | 765 | 2 | S76795 | hypothetical prote |
| 492 | 41 | 32.3 | 772 | 2 | D75002 | chemotaxis histidi |
| 493 | 41 | 32.3 | 784 | 2 | G95112 | exoribonuclease, V |
| 494 | 41 | 32.3 | 785 | 2 | F97981 | exoribonuclease, R |
| 495 | 41 | 32.3 | 785 | 2 | A82123 | chemotaxis protein |
| 496 | 41 | 32.3 | 818 | 2 | H83904 | hypothetical prote |
| 497 | 41 | 32.3 | 821 | 2 | H84600 | probable vacuolar |
| 498 | 41 | 32.3 | 831 | 2 | H84368 | MCM / cell divisio |
| 499 | 41 | 32.3 | 838 | 1 | UC7860 | glucoylesteramidase |
| 500 | 41 | 32.3 | 847 | 2 | AG1949 | starch phosphoryla |
| 501 | 41 | 32.3 | 847 | 2 | T13334 | probable tail-host |
| 502 | 41 | 32.3 | 864 | 2 | S71741 | hypothetical prote |
| 503 | 41 | 32.3 | 883 | 2 | B95237 | DNA ligase (ATP) (|
| 504 | 41 | 32.3 | 895 | 2 | A55514 | alcohol dehydrogen |
| 505 | 41 | 32.3 | 913 | 2 | C71455 | pyruvate dehydroge |
| 506 | 41 | 32.3 | 943 | 2 | S59317 | alanine-tRNA ligas |
| 507 | 41 | 32.3 | 949 | 2 | T38543 | DLP2 protein - yea |
| 508 | 41 | 32.3 | 953 | 1 | B30169 | hypothetical prote |
| 509 | 41 | 32.3 | 954 | 2 | AP2756 | leukotoxin A - Pas |
| 510 | 41 | 32.3 | 954 | 2 | B97537 | glycine cleavage s |
| 511 | 41 | 32.3 | 1154 | 2 | A39577 | protein-cytosine k |
| 512 | 41 | 32.3 | 1182 | 2 | T33089 | myelin transcripti |
| 513 | 41 | 32.3 | 1271 | 2 | T43269 | microcystin synthe |
| 514 | 41 | 32.3 | 1411 | 2 | SS5123 | hypothetical prote |
| 515 | 41 | 32.3 | 1525 | 2 | T14961 | hypothetical prote |
| 516 | 41 | 32.3 | 1557 | 2 | T29132 | hypothetical prote |
| 517 | 41 | 32.3 | 1613 | 2 | A43081 | vitellinogen vit-2 |
| 518 | 41 | 32.3 | 1613 | 2 | F89528 | protein vit-2 [imp |
| 519 | 41 | 32.3 | 1732 | 2 | E71442 | hypothetical prote |
| 520 | 41 | 32.3 | 1795 | 2 | T30332 | avirulence protein |
| 521 | 41 | 32.3 | 1819 | 2 | D97033 | uncharacterized pr |
| 522 | 41 | 32.3 | 2396 | 2 | T13714 | kakapo gene, protei |
| 523 | 40.5 | 31.9 | 85 | 2 | C69418 | hypothetical prote |
| 524 | 40.5 | 31.9 | 98 | 2 | D95371 | hypothetical prote |
| 525 | 40.5 | 31.9 | 156 | 2 | A83952 | hypothetical prote |
| 526 | 40.5 | 31.9 | 165 | 2 | AG2184 | hypothetical prote |
| 527 | 40.5 | 31.9 | 234 | 2 | S27956 | arginine-rich prot |
| 528 | 40.5 | 31.9 | 243 | 2 | S43887 | restriction endonu |
| 529 | 40.5 | 31.9 | 243 | 2 | F81130 | type II restrictio |
| 530 | 40.5 | 31.9 | 243 | 2 | H86487 | hypothetical prote |
| 531 | 40.5 | 31.9 | 261 | 2 | B97589 | 1-2,3-butanediol d |
| 532 | 40.5 | 31.9 | 261 | 2 | AG2810 | short chain dehydr |
| 533 | 40.5 | 31.9 | 261 | 2 | S60521 | envelope polyprote |
| 534 | 40.5 | 31.9 | 299 | 2 | S60552 | envelope polyprote |
| 535 | 40.5 | 31.9 | 299 | 2 | S60551 | envelope polyprote |
| 536 | 40.5 | 31.9 | 299 | 2 | S60523 | envelope polyprote |
| 537 | 40.5 | 31.9 | 299 | 2 | S60554 | envelope polyprote |
| 538 | 40.5 | 31.9 | 299 | 2 | S60553 | envelope polyprote |
| 539 | 40.5 | 31.9 | 331 | 2 | E90121 | DNA repair protein |
| 540 | 40.5 | 31.9 | 427 | 2 | F87465 | GTP-binding protei |

| | | | | | | |
|-----|------|------|------|---|--------|----------------------|
| 541 | 40.5 | 31.9 | 452 | 2 | S10840 | gene ND4L intron p |
| 542 | 40.5 | 31.9 | 459 | 2 | T39668 | amino transferase - |
| 543 | 40.5 | 31.9 | 479 | 2 | R6356 | TL6E15.2 protein - |
| 544 | 40.5 | 31.9 | 523 | 2 | C62289 | exopolysphatase |
| 545 | 40.5 | 31.9 | 614 | 2 | T33149 | hypothetical prote |
| 546 | 40.5 | 31.9 | 685 | 2 | S65974 | conserved hypotet |
| 547 | 40.5 | 31.9 | 808 | 2 | H64474 | hypothetical prote |
| 548 | 40.5 | 31.9 | 866 | 2 | A11466 | phosphoenolpyruvat |
| 549 | 40.5 | 31.9 | 917 | 2 | G02529 | dyein heavy chain |
| 550 | 40.5 | 31.9 | 922 | 2 | T31223 | tag protein homol |
| 551 | 40.5 | 31.9 | 1343 | 2 | T20718 | hypothetical prote |
| 552 | 40.5 | 31.9 | 1518 | 2 | A44811 | glucosyltransferas |
| 553 | 40.5 | 31.9 | 1634 | 2 | E64410 | DNA-directed DNA p |
| 554 | 40.5 | 31.9 | 1784 | 2 | A49420 | tuberos sclerosi |
| 555 | 40.5 | 31.9 | 3746 | 1 | VGPIV3 | alpha-aminoadipyl- |
| 556 | 40.5 | 31.9 | 3791 | 1 | VGPIV8 | alpha-aminoadipyl- |
| 557 | 40.5 | 31.9 | 4644 | 1 | A38905 | dynein heavy chain |
| 558 | 40.5 | 31.9 | 4767 | 1 | T31345 | hypothetical prote |
| 559 | 40 | 31.5 | 50 | 2 | E48518 | PEB1 3'-region hyp |
| 560 | 40 | 31.5 | 64 | 2 | H81811 | hypothetical prote |
| 561 | 40 | 31.5 | 65 | 2 | E97099 | hypothetical prote |
| 562 | 40 | 31.5 | 66 | 2 | B87516 | hypothetical prote |
| 563 | 40 | 31.5 | 86 | 2 | D67774 | hypothetical prote |
| 564 | 40 | 31.5 | 88 | 2 | E75144 | hypothetical prote |
| 565 | 40 | 31.5 | 102 | 2 | F69475 | conserved hypotet |
| 566 | 40 | 31.5 | 116 | 1 | A69043 | conserved hypotet |
| 567 | 40 | 31.5 | 134 | 2 | T22275 | hypothetical prote |
| 568 | 40 | 31.5 | 134 | 2 | F72638 | hypothetical prote |
| 569 | 40 | 31.5 | 150 | 2 | H66194 | hypothetical prote |
| 570 | 40 | 31.5 | 151 | 2 | A97008 | transcription regu |
| 571 | 40 | 31.5 | 154 | 2 | G85041 | probable calmoduli |
| 572 | 40 | 31.5 | 155 | 2 | G83774 | hypothetical prote |
| 573 | 40 | 31.5 | 156 | 2 | T16066 | hypothetical prote |
| 574 | 40 | 31.5 | 177 | 2 | U01691 | gamma B protein - |
| 575 | 40 | 31.5 | 177 | 2 | H83323 | hypothetical prote |
| 576 | 40 | 31.5 | 188 | 2 | E82370 | Sna5/YicO/YidC fam |
| 577 | 40 | 31.5 | 190 | 2 | A90354 | conserved hypotet |
| 578 | 40 | 31.5 | 191 | 1 | W6M1R1 | E6 protein - rhesu |
| 579 | 40 | 31.5 | 192 | 2 | T17331 | hypothetical prote |
| 580 | 40 | 31.5 | 194 | 2 | E69999 | hypothetical prote |
| 581 | 40 | 31.5 | 198 | 2 | T20305 | hypothetical prote |
| 582 | 40 | 31.5 | 204 | 2 | S6256 | hypothetical prote |
| 583 | 40 | 31.5 | 211 | 2 | H70443 | rRNA methylase Spo |
| 584 | 40 | 31.5 | 218 | 2 | C81423 | hypothetical prote |
| 585 | 40 | 31.5 | 229 | 1 | D43685 | nonstructural prot |
| 586 | 40 | 31.5 | 231 | 1 | D64170 | hypothetical prote |
| 587 | 40 | 31.5 | 231 | 2 | H70157 | hypothetical prote |
| 588 | 40 | 31.5 | 231 | 2 | B83060 | hypothetical prote |
| 589 | 40 | 31.5 | 235 | 2 | A81515 | probable phosphopr |
| 590 | 40 | 31.5 | 248 | 2 | T04170 | MADS box protein - |
| 591 | 40 | 31.5 | 250 | 2 | G81365 | probable ABC-type |
| 592 | 40 | 31.5 | 269 | 2 | B97113 | protein serine/thr |
| 593 | 40 | 31.5 | 270 | 2 | A42882 | mobility protein (|
| 594 | 40 | 31.5 | 291 | 2 | D90491 | ABC transporter, A |
| 595 | 40 | 31.5 | 294 | 2 | R86731 | hypothetical prote |
| 596 | 40 | 31.5 | 296 | 1 | J02155 | nitrogenase (Ec 1. |
| 597 | 40 | 31.5 | 306 | 2 | A81238 | aspartate carboxy |
| 598 | 40 | 31.5 | 307 | 2 | S16390 | auxin-induced prot |
| 599 | 40 | 31.5 | 315 | 2 | AH0897 | probable carboxydr |
| 600 | 40 | 31.5 | 327 | 2 | A11422 | hypothetical prote |
| 601 | 40 | 31.5 | 328 | 2 | C90196 | conserved hypotet |
| 602 | 40 | 31.5 | 332 | 2 | AR3265 | asparaginase (Ec 3 |
| 603 | 40 | 31.5 | 333 | 2 | H82245 | glyceraledehyde 3-p |
| 604 | 40 | 31.5 | 336 | 2 | D71016 | probable chlorodox |
| 605 | 40 | 31.5 | 339 | 2 | H75187 | hypothetical prote |
| 606 | 40 | 31.5 | 340 | 2 | D97170 | probable nucleosid |
| 607 | 40 | 31.5 | 341 | 2 | A75313 | DNA-directed RNA p |
| 608 | 40 | 31.5 | 341 | 2 | T45124 | hypothetical prote |
| 609 | 40 | 31.5 | 345 | 2 | D75116 | thioredoxin reduct |
| 610 | 40 | 31.5 | 351 | 2 | A87716 | uroporphyrinogen d |
| 611 | 40 | 31.5 | 352 | 1 | S76448 | transcription releas |
| 612 | 40 | 31.5 | 373 | 1 | E90241 | soluble hydrogenas |
| 613 | 40 | 31.5 | 374 | 2 | E70346 | mannosyltransferas |
| 614 | 40 | 31.5 | 377 | 2 | S44844 | K6H7.4 protein - |
| 615 | 40 | 31.5 | 382 | 2 | S58138 | gene 8 protein - p |
| 616 | 40 | 31.5 | 386 | 2 | G97316 | NADH-dependent but |
| 617 | 40 | 31.5 | 389 | 2 | C62027 | conserved hypotet |
| 618 | 40 | 31.5 | 389 | 2 | C86597 | CT712 hypotet |
| 619 | 40 | 31.5 | 391 | 2 | S31416 | pyruvate dehydroge |
| 620 | 40 | 31.5 | 391 | 2 | T20752 | hypothetical prote |
| 621 | 40 | 31.5 | 394 | 2 | S57332 | NADH2 dehydrogenas |
| 622 | 40 | 31.5 | 394 | 2 | S46437 | NADH2 dehydrogenas |
| 623 | 40 | 31.5 | 399 | 1 | C43685 | polymerase-associ |
| 624 | 40 | 31.5 | 401 | 2 | C71483 | probable nifS-rela |
| 625 | 40 | 31.5 | 416 | 2 | T25101 | hypothetical prote |
| 626 | 40 | 31.5 | 418 | 2 | T39279 | probable homocitra |
| 627 | 40 | 31.5 | 425 | 2 | T11619 | probable nucleopor |
| 628 | 40 | 31.5 | 427 | 2 | A53964 | carboxyl-terminal |
| 629 | 40 | 31.5 | 433 | 2 | S74753 | hypothetical prote |
| 630 | 40 | 31.5 | 438 | 2 | S62453 | hypothetical prote |
| 631 | 40 | 31.5 | 442 | 2 | D70315 | transcription regu |
| 632 | 40 | 31.5 | 445 | 2 | T36069 | hypothetical prote |
| 633 | 40 | 31.5 | 446 | 2 | C64205 | signal recognition |
| 634 | 40 | 31.5 | 446 | 2 | B47154 | signal recognition |
| 635 | 40 | 31.5 | 448 | 2 | T32575 | hypothetical prote |
| 636 | 40 | 31.5 | 450 | 2 | H82495 | C4-dicarboxylate c |
| 637 | 40 | 31.5 | 451 | 2 | T21036 | hypothetical prote |
| 638 | 40 | 31.5 | 455 | 2 | H97237 | membrane associate |
| 639 | 40 | 31.5 | 459 | 2 | F75049 | hypothetical prote |
| 640 | 40 | 31.5 | 462 | 2 | G96506 | hypothetical prote |
| 641 | 40 | 31.5 | 468 | 1 | D5ECC | phosphogluconate d |
| 642 | 40 | 31.5 | 468 | 2 | I62465 | phosphogluconate d |
| 643 | 40 | 31.5 | 468 | 2 | I62463 | phosphogluconate d |
| 644 | 40 | 31.5 | 469 | 1 | TVH082 | transcription fact |
| 645 | 40 | 31.5 | 470 | 1 | S6565 | hypothetical 53K p |
| 646 | 40 | 31.5 | 470 | 2 | P91291 | probable regulator |
| 647 | 40 | 31.5 | 470 | 2 | H86132 | probable regulator |
| 648 | 40 | 31.5 | 478 | 2 | C70416 | trigger factor tlg |
| 649 | 40 | 31.5 | 479 | 2 | S65466 | xylose isomerase (|
| 650 | 40 | 31.5 | 479 | 2 | T49871 | peroxisomal Ca-dep |
| 651 | 40 | 31.5 | 485 | 2 | A84859 | probable cytochrom |
| 652 | 40 | 31.5 | 486 | 2 | AF1575 | acetaldehyde dehyd |
| 653 | 40 | 31.5 | 486 | 2 | AC1222 | acetaldehyde dehyd |
| 654 | 40 | 31.5 | 487 | 1 | S71770 | calcium-dependent |
| 655 | 40 | 31.5 | 493 | 2 | A33809 | embryonic callus |
| 656 | 40 | 31.5 | 502 | 2 | T14286 | probable tpr prote |
| 657 | 40 | 31.5 | 505 | 2 | F71266 | probable tpr prote |
| 658 | 40 | 31.5 | 508 | 2 | F71895 | hypothetical prote |
| 659 | 40 | 31.5 | 508 | 2 | AB2236 | protochlorophyllid |
| 660 | 40 | 31.5 | 511 | 1 | B89775 | 2',3'-cyclic-nucle |
| 661 | 40 | 31.5 | 511 | 2 | T05363 | phosphogluconate d |
| 662 | 40 | 31.5 | 513 | 1 | T02259 | calcium-dependent |
| 663 | 40 | 31.5 | 513 | 2 | S48981 | hypothetical prote |
| 664 | 40 | 31.5 | 513 | 2 | S53392 | probable membrane |
| 665 | 40 | 31.5 | 531 | 1 | T02993 | calcium-dependent |
| 666 | 40 | 31.5 | 533 | 1 | S56652 | calcium-dependent |
| 667 | 40 | 31.5 | 536 | 2 | T23346 | hypothetical prote |
| 668 | 40 | 31.5 | 538 | 2 | T08874 | calcium-dependent |
| 669 | 40 | 31.5 | 540 | 1 | T01989 | calcium-dependent |
| 670 | 40 | 31.5 | 541 | 2 | S61301 | heat shock protein |
| 671 | 40 | 31.5 | 541 | 2 | AB2320 | heat shock protein |
| 672 | 40 | 31.5 | 544 | 2 | S70667 | methyl-accepting c |
| 673 | 40 | 31.5 | 544 | 2 | S61302 | chaperonin groEL - |
| 674 | 40 | 31.5 | 544 | 2 | S61300 | heat shock protein |
| 675 | 40 | 31.5 | 544 | 2 | C81021 | chaperonin, 60 kDa |
| 676 | 40 | 31.5 | 544 | 2 | S61303 | chaperonin, 60 kDa |
| 677 | 40 | 31.5 | 544 | 2 | H81964 | heat shock protein |
| 678 | 40 | 31.5 | 547 | 2 | H87334 | chaperonin, 60 kDa |
| 679 | 40 | 31.5 | 548 | 2 | B84932 | chaperonin, 60 kDa |
| 680 | 40 | 31.5 | 548 | 2 | B42281 | symblonin symL - p |
| 681 | 40 | 31.5 | 548 | 2 | H95066 | helicase, probable |
| 682 | 40 | 31.5 | 548 | 2 | T10393 | chitinase (Ec 3.2. |
| 683 | 40 | 31.5 | 550 | 2 | T25902 | hypothetical prote |
| 684 | 40 | 31.5 | 564 | 2 | F86879 | arginine-cRNA liga |
| 685 | 40 | 31.5 | 572 | 2 | JC5316 | dihydropyrimidinas |
| 686 | 40 | 31.5 | 573 | 2 | T40474 | hypothetical prote |

| | | | | | | | | | | | | | |
|-----|----|------|------|---|--------|----------------------|-----|------|------|------|---|--------|---------------------|
| 687 | 40 | 31.5 | 581 | 1 | S71170 | phosphoinositide-s | 760 | 39.5 | 31.1 | 368 | 2 | SE5475 | hypothetical prote |
| 688 | 40 | 31.5 | 582 | 2 | H97326 | methy1-accepting c | 761 | 39.5 | 31.1 | 424 | 1 | B40905 | inhibin beta-A cha |
| 689 | 40 | 31.5 | 584 | 2 | T08678 | hypothetical prote | 762 | 39.5 | 31.1 | 424 | 1 | S31440 | inhibin beta-A cha |
| 690 | 40 | 31.5 | 601 | 2 | T38200 | spliceosome associ | 763 | 39.5 | 31.1 | 425 | 1 | S50898 | inhibin beta-A cha |
| 691 | 40 | 31.5 | 606 | 2 | B69805 | conserved hypotnet | 764 | 39.5 | 31.1 | 425 | 1 | T47072 | inhibin beta-A cha |
| 692 | 40 | 31.5 | 608 | 2 | H72292 | hypothetical prote | 765 | 39.5 | 31.1 | 426 | 1 | B24248 | inhibin beta-A cha |
| 693 | 40 | 31.5 | 619 | 2 | B81117 | dihydroxy-acid deh | 766 | 39.5 | 31.1 | 481 | 2 | B86356 | hypothetical prote |
| 694 | 40 | 31.5 | 624 | 2 | A64150 | hypothetical prote | 767 | 39.5 | 31.1 | 482 | 2 | T33651 | hypothetical prote |
| 695 | 40 | 31.5 | 629 | 2 | A65536 | plastin, intestina | 768 | 39.5 | 31.1 | 490 | 2 | D84592 | hypothetical prote |
| 696 | 40 | 31.5 | 633 | 2 | AH1598 | acyltransferase (t | 769 | 39.5 | 31.1 | 503 | 2 | T52172 | probable cytochrom |
| 697 | 40 | 31.5 | 642 | 2 | SE9306 | probable membrane | 770 | 39.5 | 31.1 | 548 | 2 | AC0871 | probable integrase |
| 698 | 40 | 31.5 | 645 | 2 | BE4444 | hypothetical prote | 771 | 39.5 | 31.1 | 552 | 2 | T33511 | hypothetical prote |
| 699 | 40 | 31.5 | 647 | 2 | CT1534 | probable transglyc | 772 | 39.5 | 31.1 | 552 | 2 | UC4030 | DnaU-like protein |
| 700 | 40 | 31.5 | 650 | 2 | T49523 | tumor necrosis fac | 773 | 39.5 | 31.1 | 567 | 2 | T33650 | hypothetical prote |
| 701 | 40 | 31.5 | 656 | 2 | JC7222 | 77k muscle-derived | 774 | 39.5 | 31.1 | 575 | 2 | H72752 | probable dihydroxy |
| 702 | 40 | 31.5 | 680 | 2 | H90558 | hypothetical prote | 775 | 39.5 | 31.1 | 657 | 2 | CT1905 | conserved outer mem |
| 703 | 40 | 31.5 | 744 | 2 | A70385 | DNA gyrase A subun | 776 | 39.5 | 31.1 | 660 | 2 | F64608 | conserved hypotnet |
| 704 | 40 | 31.5 | 774 | 2 | A28392 | penicillin amidase | 777 | 39.5 | 31.1 | 662 | 2 | G89909 | transketolase [amp |
| 705 | 40 | 31.5 | 777 | 2 | T21048 | hypothetical prote | 778 | 39.5 | 31.1 | 672 | 2 | S75001 | hypothetical prote |
| 706 | 40 | 31.5 | 796 | 2 | D97065 | transketolase [amp | 779 | 39.5 | 31.1 | 707 | 2 | T42239 | probable phosphopr |
| 707 | 40 | 31.5 | 810 | 1 | I40508 | endopeptidase Clp (| 780 | 39.5 | 31.1 | 722 | 2 | VCPVCN | coat protein VP1 - |
| 708 | 40 | 31.5 | 819 | 1 | B72128 | endopeptidase Ia (| 781 | 39.5 | 31.1 | 722 | 2 | T34072 | hypothetical prote |
| 709 | 40 | 31.5 | 819 | 2 | B86494 | Ion ATP-dependent | 782 | 39.5 | 31.1 | 732 | 1 | JU0132 | acylaminoacyl-pept |
| 710 | 40 | 31.5 | 845 | 2 | S77383 | hypothetical prote | 783 | 39.5 | 31.1 | 732 | 1 | S07624 | coat protein VP1 - |
| 711 | 40 | 31.5 | 845 | 2 | I48176 | synaptonemal compl | 784 | 39.5 | 31.1 | 737 | 1 | VCPVCD | coat protein VP1 - |
| 712 | 40 | 31.5 | 868 | 2 | SE5186 | NIP80 protein - ye | 785 | 39.5 | 31.1 | 748 | 1 | VCPVCP | phytochrome-like p |
| 713 | 40 | 31.5 | 880 | 2 | AC2108 | alanyl-tRNA synthe | 786 | 39.5 | 31.1 | 751 | 2 | AD2168 | probable sucrose s |
| 714 | 40 | 31.5 | 969 | 2 | T32566 | hypothetical prote | 787 | 39.5 | 31.1 | 809 | 2 | T06497 | DNA polymerase I (|
| 715 | 40 | 31.5 | 976 | 2 | S40697 | processing endopro | 788 | 39.5 | 31.1 | 875 | 2 | AE1270 | hypothetical prote |
| 716 | 40 | 31.5 | 1002 | 2 | T46033 | receptor protein k | 789 | 39.5 | 31.1 | 888 | 2 | S78288 | preprotein translo |
| 717 | 40 | 31.5 | 1007 | 2 | S48535 | rho-type GTPase-ac | 790 | 39.5 | 31.1 | 888 | 2 | H84105 | hypothetical prote |
| 718 | 40 | 31.5 | 1013 | 2 | A69226 | type I restriction | 791 | 39.5 | 31.1 | 1113 | 2 | B84105 | p-glycoprotein iso |
| 719 | 40 | 31.5 | 1021 | 2 | AC2202 | hypothetical prote | 792 | 39.5 | 31.1 | 1281 | 2 | I48123 | xanthine dehydroge |
| 720 | 40 | 31.5 | 1039 | 2 | AI2284 | translational initia | 793 | 39.5 | 31.1 | 1331 | 1 | XORTDH | cytochrome L - Clo |
| 721 | 40 | 31.5 | 1054 | 2 | D70425 | conserved hypotnet | 794 | 39.5 | 31.1 | 2364 | 2 | I40884 | orf Ia protein - L |
| 722 | 40 | 31.5 | 1097 | 2 | AD2572 | hypothetical prote | 795 | 39.5 | 31.1 | 2396 | 2 | B38651 | regulatory extrace |
| 723 | 40 | 31.5 | 1116 | 2 | D97001 | probable membrane | 796 | 39.5 | 30.7 | 40 | 2 | I39944 | ascQ protein - Bac |
| 724 | 40 | 31.5 | 1136 | 2 | AH1227 | different proteins | 797 | 39.5 | 30.7 | 46 | 2 | A26929 | GTP-binding regula |
| 725 | 40 | 31.5 | 1154 | 2 | SE9206 | neural cell adhesi | 798 | 39.5 | 30.7 | 75 | 2 | I39157 | GTP-binding regula |
| 726 | 40 | 31.5 | 1232 | 2 | T43027 | hypothetical prote | 799 | 39.5 | 30.7 | 75 | 2 | UC4339 | calcium-binding pr |
| 727 | 40 | 31.5 | 1295 | 2 | T21720 | hypothetical prote | 800 | 39.5 | 30.7 | 79 | 1 | KLPGI | calcium-binding pr |
| 728 | 40 | 31.5 | 1334 | 1 | AB1775 | hypothetical prote | 801 | 39.5 | 30.7 | 81 | 2 | F90454 | hypothetical prote |
| 729 | 40 | 31.5 | 1441 | 1 | GNVUSV | W polyprotein prec | 802 | 39.5 | 30.7 | 89 | 2 | A54314 | calcyclin - mouse |
| 730 | 40 | 31.5 | 1607 | 2 | T04583 | ATM resistance fac | 803 | 39.5 | 30.7 | 89 | 2 | E47758 | retrovirus-related |
| 731 | 40 | 31.5 | 1690 | 2 | T35694 | ATP dependent DNA | 804 | 39.5 | 30.7 | 90 | 1 | S27011 | calcyclin - rat |
| 732 | 40 | 31.5 | 1979 | 1 | S03166 | mpsin heavy chain | 805 | 39.5 | 30.7 | 90 | 2 | B28363 | calcyclin - rat |
| 733 | 40 | 31.5 | 2150 | 1 | S27802 | zinc finger protei | 806 | 39.5 | 30.7 | 92 | 2 | E69408 | transcription regu |
| 734 | 40 | 31.5 | 2150 | 2 | T19450 | hypothetical prote | 807 | 39.5 | 30.7 | 95 | 1 | LUPG10 | calcipactin I light |
| 735 | 40 | 31.5 | 2186 | 2 | TI3169 | liggrin - fruit fl | 808 | 39.5 | 30.7 | 95 | 2 | TI2718 | hypothetical prote |
| 736 | 40 | 31.5 | 3006 | 2 | T28625 | variant-specific s | 809 | 39.5 | 30.7 | 97 | 2 | UC1139 | calcipactin I light |
| 737 | 40 | 31.5 | 3190 | 2 | T13828 | CRFB-binding prote | 810 | 39.5 | 30.7 | 97 | 2 | B28489 | calcipactin I light |
| 738 | 40 | 31.5 | 3228 | 2 | T21381 | hypothetical prote | 811 | 39.5 | 30.7 | 103 | 2 | D83678 | hypothetical prote |
| 739 | 40 | 31.5 | 4930 | 2 | BE9679 | polyketide synthet | 812 | 39.5 | 30.7 | 105 | 2 | B86755 | prophage p12 prote |
| 740 | 40 | 31.5 | 5126 | 2 | S40450 | transcine receptor | 813 | 39.5 | 30.7 | 114 | 2 | E86353 | protein P2E2.12 [i |
| 741 | 40 | 31.5 | 5149 | 2 | F83345 | probable non-ribos | 814 | 39.5 | 30.7 | 119 | 1 | A69481 | conserved hypotnet |
| 742 | 40 | 31.1 | 78 | 2 | B97045 | hypothetical prote | 815 | 39.5 | 30.7 | 119 | 2 | E84085 | arsenate reductase |
| 743 | 40 | 31.1 | 135 | 2 | AB1429 | hypothetical prote | 816 | 39.5 | 30.7 | 122 | 2 | T04090 | probable thioredox |
| 744 | 40 | 31.1 | 139 | 2 | SE3353 | hypothetical prote | 817 | 39.5 | 30.7 | 122 | 2 | A43885 | translation repres |
| 745 | 40 | 31.1 | 169 | 2 | C89919 | hypothetical prote | 818 | 39.5 | 30.7 | 127 | 2 | B97269 | hypothetical prote |
| 746 | 40 | 31.1 | 192 | 1 | KLSS8S | conserved hypotnet | 819 | 39.5 | 30.7 | 132 | 2 | S76503 | hypothetical prote |
| 747 | 40 | 31.1 | 206 | 2 | AD1898 | calcium-binding pr | 820 | 39.5 | 30.7 | 148 | 2 | G70312 | transcription term |
| 748 | 40 | 31.1 | 208 | 2 | GG9744 | uracil accessory p | 821 | 39.5 | 30.7 | 148 | 2 | A39268 | conserved hypotnet |
| 749 | 40 | 31.1 | 240 | 2 | D75203 | hypothetical prote | 822 | 39.5 | 30.7 | 149 | 2 | A33553 | calcium-binding pr |
| 750 | 40 | 31.1 | 284 | 1 | S74516 | (adenine-N6, N6-) -d | 823 | 39.5 | 30.7 | 151 | 2 | SE6246 | hypothetical prote |
| 751 | 40 | 31.1 | 291 | 2 | A70475 | H+-transporting tw | 824 | 39.5 | 30.7 | 155 | 2 | T13308 | hypothetical prote |
| 752 | 40 | 31.1 | 301 | 2 | SE6032 | envelope polypote | 825 | 39.5 | 30.7 | 158 | 2 | UC5434 | larva muscle tropo |
| 753 | 40 | 31.1 | 301 | 2 | SE6051 | envelope polypote | 826 | 39.5 | 30.7 | 158 | 2 | A38357 | tropom C-1 - gia |
| 754 | 40 | 31.1 | 301 | 2 | AB1307 | dehydrogenase and | 827 | 39.5 | 30.7 | 161 | 2 | E70381 | glycine cleavage s |
| 755 | 40 | 31.1 | 306 | 2 | AB1518 | conserved hypotnet | 828 | 39.5 | 30.7 | 166 | 2 | A45119 | transcription fact |
| 756 | 40 | 31.1 | 309 | 2 | F70217 | conserved hypotnet | 829 | 39.5 | 30.7 | 167 | 2 | A55438 | hypothetical prote |
| 757 | 40 | 31.1 | 314 | 2 | D89958 | catabolic control | 830 | 39.5 | 30.7 | 167 | 2 | T43621 | hypothetical prote |
| 758 | 40 | 31.1 | 317 | 2 | SE4548 | hypothetical prote | 831 | 39.5 | 30.7 | 176 | 2 | T30025 | hypothetical prote |
| 759 | 40 | 31.1 | 347 | 2 | C90412 | 2-isopropylmalate | 832 | 39.5 | 30.7 | 178 | 2 | T22802 | hypothetical prote |

| | | | | | | |
|-----|----|------|-----|---|--------|----------------------|
| 833 | 39 | 30.7 | 180 | 2 | 575356 | sensory transducti |
| 834 | 39 | 30.7 | 185 | 2 | H88709 | protein C43c2.3 [1 |
| 835 | 39 | 30.7 | 185 | 2 | H90540 | hypothetical prote |
| 836 | 39 | 30.7 | 188 | 2 | AB0044 | elongation factor |
| 837 | 39 | 30.7 | 190 | 2 | C84152 | hypothetical prote |
| 838 | 39 | 30.7 | 192 | 2 | B86679 | prophage p11 prote |
| 839 | 39 | 30.7 | 204 | 2 | C84122 | thymidine kinase (|
| 840 | 39 | 30.7 | 208 | 2 | B70208 | conserved hypotet |
| 841 | 39 | 30.7 | 208 | 2 | A97011 | probable Zn-finger |
| 842 | 39 | 30.7 | 209 | 2 | S09885 | hypothetical prote |
| 843 | 39 | 30.7 | 211 | 2 | AB0118 | hypothetical prote |
| 844 | 39 | 30.7 | 219 | 2 | F70474 | conserved hypotet |
| 845 | 39 | 30.7 | 229 | 2 | T18629 | hypothetical prote |
| 846 | 39 | 30.7 | 231 | 2 | B69756 | ABC transporter (A |
| 847 | 39 | 30.7 | 233 | 2 | T41263 | hypothetical prote |
| 848 | 39 | 30.7 | 238 | 2 | F81221 | probable phosphat |
| 849 | 39 | 30.7 | 238 | 2 | AB6068 | hypothetical prote |
| 850 | 39 | 30.7 | 238 | 2 | D37841 | hypothetical 27.1k |
| 851 | 39 | 30.7 | 240 | 2 | AC1921 | hypothetical prote |
| 852 | 39 | 30.7 | 247 | 2 | C71229 | hypothetical prote |
| 853 | 39 | 30.7 | 248 | 2 | T20037 | hypothetical prote |
| 854 | 39 | 30.7 | 257 | 2 | T23332 | hypothetical prote |
| 855 | 39 | 30.7 | 260 | 2 | A55122 | deoxycytidine kina |
| 856 | 39 | 30.7 | 260 | 2 | A10934 | glutamate racemase |
| 857 | 39 | 30.7 | 262 | 2 | A99417 | conserved hypotet |
| 858 | 39 | 30.7 | 269 | 2 | C82080 | dihydrodipicolinat |
| 859 | 39 | 30.7 | 270 | 2 | S67389 | conserved hypotet |
| 860 | 39 | 30.7 | 278 | 2 | AB1266 | probable biotin by |
| 861 | 39 | 30.7 | 280 | 1 | PRSAEA | epidermolysin toxi |
| 862 | 39 | 30.7 | 282 | 2 | T44699 | probable oxidoredu |
| 863 | 39 | 30.7 | 286 | 2 | C82143 | conserved hypotet |
| 864 | 39 | 30.7 | 297 | 2 | S52726 | syntaxin-4 - human |
| 865 | 39 | 30.7 | 298 | 2 | E48213 | syntaxin 4 - rat |
| 866 | 39 | 30.7 | 300 | 2 | S60558 | envelope polypote |
| 867 | 39 | 30.7 | 300 | 2 | S60526 | envelope polypote |
| 868 | 39 | 30.7 | 301 | 2 | G01817 | syntaxin 5 - human |
| 869 | 39 | 30.7 | 301 | 2 | F48213 | syntaxin 5 - rat |
| 870 | 39 | 30.7 | 303 | 2 | AF1304 | aspartate carboxamoy |
| 871 | 39 | 30.7 | 303 | 2 | AF1676 | aspartate carboxamoy |
| 872 | 39 | 30.7 | 303 | 2 | S34966 | rfkQ protein - Shi |
| 873 | 39 | 30.7 | 303 | 2 | E97850 | cell division prot |
| 874 | 39 | 30.7 | 309 | 2 | B82137 | transcription regu |
| 875 | 39 | 30.7 | 312 | 2 | T20932 | hypothetical prote |
| 876 | 39 | 30.7 | 314 | 2 | C90038 | hypothetical prote |
| 877 | 39 | 30.7 | 315 | 2 | A84598 | probable triosepho |
| 878 | 39 | 30.7 | 323 | 2 | UT0755 | ethylene-forming e |
| 879 | 39 | 30.7 | 323 | 2 | AB6184 | hypothetical prote |
| 880 | 39 | 30.7 | 324 | 2 | G69515 | transcription regu |
| 881 | 39 | 30.7 | 325 | 2 | AC1333 | conjugated bile ac |
| 882 | 39 | 30.7 | 334 | 2 | B69888 | GMP-binding protei |
| 883 | 39 | 30.7 | 334 | 2 | P86226 | hypothetical prote |
| 884 | 39 | 30.7 | 335 | 2 | E72344 | conserved hypotet |
| 885 | 39 | 30.7 | 336 | 2 | T03959 | A1ei protein homol |
| 886 | 39 | 30.7 | 336 | 2 | D72327 | heat shock operon |
| 887 | 39 | 30.7 | 340 | 2 | I15147 | probable RNA-bindi |
| 888 | 39 | 30.7 | 342 | 2 | S14432 | heterogeneous ribo |
| 889 | 39 | 30.7 | 343 | 2 | AB2105 | hypothetical prote |
| 890 | 39 | 30.7 | 344 | 2 | B84204 | hypothetical prote |
| 891 | 39 | 30.7 | 345 | 2 | AH3131 | malate dehydrogena |
| 892 | 39 | 30.7 | 346 | 2 | AH3358 | pyruvate dehydroge |
| 893 | 39 | 30.7 | 346 | 2 | C98156 | probable l-malate |
| 894 | 39 | 30.7 | 347 | 2 | I15146 | probable RNA-bindi |
| 895 | 39 | 30.7 | 353 | 2 | A41558 | N-syndecan - rat (|
| 896 | 39 | 30.7 | 356 | 2 | A12317 | two-component hydr |
| 897 | 39 | 30.7 | 362 | 2 | A49506 | protein kinase ERK |
| 898 | 39 | 30.7 | 362 | 2 | A49506 | MSPI protein - yea |
| 899 | 39 | 30.7 | 369 | 2 | F81125 | glutamate 5-kinase |
| 900 | 39 | 30.7 | 369 | 2 | B81895 | probable glutamate |
| 901 | 39 | 30.7 | 371 | 2 | T02284 | hypothetical prote |
| 902 | 39 | 30.7 | 374 | 2 | H75002 | methyl-accepting c |
| 903 | 39 | 30.7 | 383 | 2 | AG1216 | hypothetical prote |
| 904 | 39 | 30.7 | 384 | 2 | A44146 | syndecan-3 - chick |
| 905 | 39 | 30.7 | 387 | 1 | BRADY4 | 41k fiber protein |
| 906 | 39 | 30.7 | 389 | 1 | DEBPA | pyruvate dehydroge |
| 907 | 39 | 30.7 | 390 | 1 | DEHUPA | pyruvate dehydroge |
| 908 | 39 | 30.7 | 390 | 1 | DETRP1 | pyruvate dehydroge |
| 909 | 39 | 30.7 | 390 | 1 | DETRPA | pyruvate dehydroge |
| 910 | 39 | 30.7 | 390 | 2 | S23506 | pyruvate dehydroge |
| 911 | 39 | 30.7 | 390 | 2 | B69483 | hypothetical prote |
| 912 | 39 | 30.7 | 391 | 2 | A82801 | conserved hypotet |
| 913 | 39 | 30.7 | 393 | 2 | S04408 | hydroxyneurosporen |
| 914 | 39 | 30.7 | 393 | 2 | B81438 | helicase-like prot |
| 915 | 39 | 30.7 | 394 | 2 | H97825 | elongation factor |
| 916 | 39 | 30.7 | 394 | 2 | F82507 | proteinase VCA0045 |
| 917 | 39 | 30.7 | 398 | 2 | A59371 | Ig V-region-like B |
| 918 | 39 | 30.7 | 405 | 1 | A64314 | corrinoid/iron-gu1 |
| 919 | 39 | 30.7 | 406 | 2 | F86576 | Nifs-related amino |
| 920 | 39 | 30.7 | 406 | 2 | G72047 | nifs-related amino |
| 921 | 39 | 30.7 | 407 | 2 | E83873 | hypothetical prote |
| 922 | 39 | 30.7 | 408 | 2 | AB0103 | probable regulator |
| 923 | 39 | 30.7 | 412 | 2 | H90244 | pre mRNA splicing |
| 924 | 39 | 30.7 | 413 | 2 | AE2163 | hypothetical prote |
| 925 | 39 | 30.7 | 416 | 2 | T13514 | hypothetical prote |
| 926 | 39 | 30.7 | 417 | 2 | S58193 | adenosylhomocyste1 |
| 927 | 39 | 30.7 | 424 | 2 | E64450 | hypothetical prote |
| 928 | 39 | 30.7 | 425 | 2 | S17759 | protein kinase, ca |
| 929 | 39 | 30.7 | 429 | 2 | AB2936 | hypothetical prote |
| 930 | 39 | 30.7 | 429 | 2 | E98346 | hypothetical prote |
| 931 | 39 | 30.7 | 431 | 2 | AB1150 | histidyl-tRNA synt |
| 932 | 39 | 30.7 | 433 | 2 | A69735 | phage P88X termina |
| 933 | 39 | 30.7 | 442 | 2 | C90224 | B-adenosyl-L-homoc |
| 934 | 39 | 30.7 | 442 | 2 | D82936 | hemolysin U0072 [1 |
| 935 | 39 | 30.7 | 445 | 2 | H64067 | hypothetical prote |
| 936 | 39 | 30.7 | 452 | 2 | UC4100 | hydroxyindole O-me |
| 937 | 39 | 30.7 | 453 | 2 | AD0400 | signal recognition |
| 938 | 39 | 30.7 | 453 | 2 | F82702 | conserved hypotet |
| 939 | 39 | 30.7 | 455 | 2 | T29555 | hypothetical prote |
| 940 | 39 | 30.7 | 456 | 2 | C71402 | probable glucosylc |
| 941 | 39 | 30.7 | 456 | 2 | E86903 | hypothetical prote |
| 942 | 39 | 30.7 | 465 | 1 | T03024 | calcium-dependent |
| 943 | 39 | 30.7 | 469 | 2 | B70486 | hypothetical prote |
| 944 | 39 | 30.7 | 472 | 1 | A53236 | transcription fact |
| 945 | 39 | 30.7 | 472 | 2 | AH1246 | 6-phosphogluconate |
| 946 | 39 | 30.7 | 472 | 2 | AD1609 | 6-phosphogluconate |
| 947 | 39 | 30.7 | 475 | 2 | C72538 | probable cyte1nyl |
| 948 | 39 | 30.7 | 476 | 2 | D71200 | probable glutamate |
| 949 | 39 | 30.7 | 479 | 1 | A42241 | glycine hydroxymet |
| 950 | 39 | 30.7 | 482 | 2 | E69629 | spore germination |
| 951 | 39 | 30.7 | 485 | 2 | F90182 | conserved hypotet |
| 952 | 39 | 30.7 | 488 | 2 | A87660 | hypothetical prote |
| 953 | 39 | 30.7 | 494 | 2 | E70352 | anthranilate synth |
| 954 | 39 | 30.7 | 503 | 2 | A97802 | n utilization subs |
| 955 | 39 | 30.7 | 503 | 2 | H71659 | transcription term |
| 956 | 39 | 30.7 | 514 | 2 | F64019 | hypothetical prote |
| 957 | 39 | 30.7 | 516 | 2 | S44181 | carboxypeptidase D |
| 958 | 39 | 30.7 | 531 | 2 | D85059 | probable calcium d |
| 959 | 39 | 30.7 | 532 | 2 | T14335 | protein kinase, ca |
| 960 | 39 | 30.7 | 532 | 2 | PN0108 | RNA-directed RNA p |
| 961 | 39 | 30.7 | 534 | 2 | T23425 | hypothetical prote |
| 962 | 39 | 30.7 | 536 | 2 | S62110 | lysophospholipase |
| 963 | 39 | 30.7 | 539 | 2 | A54294 | cell division cont |
| 964 | 39 | 30.7 | 542 | 2 | JN0661 | heat shock protein |
| 965 | 39 | 30.7 | 542 | 2 | S32106 | groEL protein - la |
| 966 | 39 | 30.7 | 542 | 2 | B86674 | 60 kD chaperonin [|
| 967 | 39 | 30.7 | 542 | 2 | AD1333 | class I heat-shock |
| 968 | 39 | 30.7 | 542 | 2 | AC1704 | class I heat-shock |
| 969 | 39 | 30.7 | 545 | 2 | T43893 | DNA gyrase chain A |
| 970 | 39 | 30.7 | 545 | 2 | S47530 | chaperonin groEL - |
| 971 | 39 | 30.7 | 545 | 2 | D69679 | polyketide synthas |
| 972 | 39 | 30.7 | 547 | 2 | F82763 | 60kDa chaperonin X |
| 973 | 39 | 30.7 | 547 | 2 | I40331 | Cn60 protein (Gro |
| 974 | 39 | 30.7 | 548 | 2 | AG0064 | 60 kDa chaperonin |
| 975 | 39 | 30.7 | 549 | 2 | UC2564 | heat shock protein |
| 976 | 39 | 30.7 | 550 | 2 | S52901 | heat shock protein |
| 977 | 39 | 30.7 | 553 | 2 | F96982 | fission threonyl-tr |
| 978 | 39 | 30.7 | 554 | 2 | T05476 | calcium-dependent |

| | | | | | | |
|------|----|------|-----|---|--------|--------------------|
| 979 | 39 | 30.7 | 554 | 2 | T43466 | hypothetical prote |
| 980 | 39 | 30.7 | 555 | 2 | AG1914 | carbon dioxide con |
| 981 | 39 | 30.7 | 557 | 2 | E95945 | probable urocanate |
| 982 | 39 | 30.7 | 559 | 2 | CG4137 | transcription regu |
| 983 | 39 | 30.7 | 561 | 2 | G71597 | carboxylase (|
| 984 | 39 | 30.7 | 564 | 2 | CG4188 | hypothetical prote |
| 985 | 39 | 30.7 | 566 | 2 | A72254 | methyl-accepting c |
| 986 | 39 | 30.7 | 573 | 1 | A32800 | chaperonin GroEL p |
| 987 | 39 | 30.7 | 573 | 1 | HHMS60 | chaperonin groEL p |
| 988 | 39 | 30.7 | 573 | 1 | HHRT60 | chaperonin groEL p |
| 989 | 39 | 30.7 | 573 | 2 | A34173 | mitochondrial proc |
| 990 | 39 | 30.7 | 573 | 2 | AD2361 | flavoprotein (limp |
| 991 | 39 | 30.7 | 583 | 2 | S57721 | csbp protein - C10 |
| 992 | 39 | 30.7 | 587 | 2 | T14360 | H+-exporting ATPas |
| 993 | 39 | 30.7 | 595 | 2 | G64233 | dhak-type molecula |
| 994 | 39 | 30.7 | 595 | 2 | S73733 | dhak-type molecula |
| 995 | 39 | 30.7 | 597 | 2 | A32440 | RNA-directed RNA p |
| 996 | 39 | 30.7 | 597 | 2 | T45676 | hypothetical prote |
| 997 | 39 | 30.7 | 601 | 2 | T46084 | CDPK-related prote |
| 998 | 39 | 30.7 | 605 | 2 | T50842 | phospholipase C2 l |
| 999 | 39 | 30.7 | 606 | 2 | T11909 | NADH2 dehydrogenas |
| 1000 | 39 | 30.7 | 608 | 2 | T03476 | conserved hypothet |

ALIGNMENTS

RESULT 1

homocitrate synthase (EC 4.1.3.21) [validated] - Thermus aquaticus

C/Species: Thermus aquaticus

C/Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 09-Jul-2004

C/Accession: T51170

R/Kosuge, T.; Hoshino, T.

submitted to the EMBL Data Library, October 1998

A/Description: Lysoine is synthesized through the alpha-aminoadipate pathway in Thermus

A/Reference number: 225321

A/Accession: T51170

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-376 <KOS>

A/Cross-references: UNIPROT:O87198; EMBL:AB018379; PDB:BAA33785.1

A/Experimental source: strain HB27

C/Genetics:

A/Gene: lys20

C/Function:

A/Description: EC 4.1.3.21 [validated, MUID:99085673]

A/Superfamily: hydroxymethylglutaryl-CoA lyase

C/Keywords: carbon-carbon lyase; coenzyme A; oxo-acid-lyase

Query Match 48.8%; Score 62; DB 2; Length 376;
Best Local Similarity 47.6%; Pred. No. 1.5;
Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 2 KKMADNGTIVTEELKQLLEQW 22

Db 353 KALADRGQLTEELDRIRRW 373

RESULT 2

TVHUA

transforming protein ralA - human

N/Alternate names: GTP-binding protein ral

C/Species: Homo sapiens (man)

C/Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004

C/Accession: S04596; A34387

R/Chardin, P.; Tavittian, A.

Nucleic Acids Res. 17, 4380, 1989

A/Title: Coding sequences of human ralA and ralB cDNAs.

A/Reference number: S04596; MUID:89296492; PMID:2662142

A/Accession: S04596

A/Molecule type: mRNA

A/Residues: 1-206 <CHA>

A/Cross-references: UNIPROT:P11233; GB:X15014; NID:935845; PDB:CAA33118.1; PID:935846
R/Polakis, P.G.; Weber, R.F.; Nevins, B.; Didsbury, J.R.; Evans, T.; Snyderman, R.
J. Biol. Chem. 264, 16383-16389, 1989
A/Title: Identification of the ral and rac1 gene products, low molecular mass GTP-binding
A/Reference number: A34387; MUID:89380251; PMID:2550440
A/Accession: A34387
A/Molecule type: mRNA
A/Residues: 1, 'VDYL', 3-206 <POL>
A/Cross-references: GB:M29893; NID:9190849; PDB:AAA36542.1; PID:9190850
A/Note: parts of this sequence were confirmed by peptide sequencing
C/Genetics:
A/Gene: GDB:RALA
A/Cross-references: GDB:120723; OMIM:179550
A/Map position: 1pter-7cen
C/Superfamily: ras transforming protein; translation elongation factor Tu homology
C/Keywords: GTP binding; lipoprotein; membrane protein; methylated carboxyl end; nucleoti
F/15-130/Domain: translation elongation factor Tu homology <RTU>
F/21-28/Region: nucleotide-binding motif A (P-loop)
F/127-130/Region: GTP-binding NKXD motif
F/157-159/Region: GTP-binding SAK/L motif
F/127,28,46,127,128,130,157/Binding site: Mg-GTP (Lys, Ser, Thr, Asn, Lys, Asp, Ser) #stat
F/203/Binding site: geranyl-geranyl (Cys) (covalent) #status predicted
F/203/Modified site: methyl ester carboxyl end (Cys) (in mature form) #status predicted

Query Match

43.3%; Score 55; DB 1; Length 206;
Best Local Similarity 41.7%; Pred. No. 6.7;

Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 KKMADNGTIVTEELKQLLEQW 24

Db 128 KSDLEKROVSVEAKRRAEQWNV 151

RESULT 3

E97225

carbamoylphosphate synthase small chain [imported] - Clostridium acetobutylicum

C/Species: Clostridium acetobutylicum

C/Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004

C/Accession: E97225

R/Nolling, J.; Breton, G.; Ometchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,

J. Bacteriol. 183, 4823-4838, 2001

A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo

A/Reference number: A96900; MUID:21359325; PMID:21359325

A/Accession: E97225

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-351 <KUR>

A/Cross-references: UNIPROT:Q97FT3; GB:AF001437; PDB:AAK0592.1; PID:915025673; GSPDB:GT

A/Experimental source: Clostridium acetobutylicum ATCC824

C/Genetics:

A/Gene: CAC2645

C/Superfamily: carbamoyl-phosphate synthase (glutamine-hydrolyzing) small chain; carbamo

Query Match 41.7%; Score 53; DB 2; Length 351;
Best Local Similarity 37.5%; Pred. No. 21;
Matches 9; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

QY 2 KKMADNGTIVTEELKQLLEQW 25

Db 127 KCIISNGELISELKKMDASNTV 150

RESULT 4

TVICRA

transforming protein ral - cotton-top tamarin

C/Species: Saguinus oedipus (cotton-top tamarin)

C/Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 19-Jan-2001

C/Accession: A25261; A24893

R/Chardin, P.; Tavittian, A.

EMBO J. 5, 2203-2208, 1986

A/Title: The ral gene: a new ras related gene isolated by the use of a synthetic probe.

A/Reference number: A91050; MUID:87053859; PMID:3023062

A:Accession: A25261
A:Molecule type: mRNA
A:Residues: 1-206 <CRA>
A:Cross-references: EMBL:X04328; NID:G38256; PIDN:CAA27859.1; PID:G38257
C:Genetics: rat
A:Gene: rat
C:Superfamily: ras transforming protein; translation elongation factor Tu homology
C:Keywords: GTP binding; lipoprotein; membrane protein; methylated carboxyl end; nucleot
F:15-130/Domain: translation elongation factor Tu homology <ETU>
F:21-28/Region: nucleotide-binding motif A (P-loop)
F:127-130/Region: GTP-binding NKXD motif
F:157-159/Region: GTP-binding SAK/L motif
F:27,28,46,127,128,130,157/Binding site: Mg-GTP (Lys, Ser, Thr, Asn, Lys, Asp, Ser) #sta
F:203/Modified site: methyl ester carboxyl end (Cys) (in mature form) #status predicted
F:203/Binding site: geranyl-geranyl (Cys) (covalent) #status predicted

Query Match 40.9%; Score 52; DB 1; Length 206;
Best Local Similarity 37.5%; Pred. No. 17;
Matches 9; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

Oy 1 KKKKADNGTITVEELKQLLEQNL 24
Db 128 KSDLEDKQVSVBEAKRRADQMN 151

RESULT 5
JN0622
GTP-binding protein ral A - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C:Accession: JN0622
R:Wiley, G.M.; Vagstad, M.; Rim, S.; Denker, J.K.
Biochem. Biophys. Res. Commun. 194, 552-559, 1993
A:Title: Isolation of cDNA clones and tissue expression of rat ral A and ral B GTP-bind
A:Reference number: JN0622; MUID:93326173; PMID:7687439
A:Accession: JN0622
A:Molecule type: mRNA
A:Residues: 1-206 <MIL>
A:Cross-references: UNIPROT:P05810; GB:L19698; NID:G310209; PIDN:AAA42003.1; PID:G310210
C:Genetics: rat
A:Gene: ral A
C:Superfamily: ras transforming protein; translation elongation factor Tu homology
C:Keywords: GTP binding; nucleotide binding; P-loop; proto-oncogene; transforming protei
F:15-130/Domain: translation elongation factor Tu homology <ETU>
F:21-28/Region: nucleotide-binding motif A (P-loop)
F:127-130/Region: GTP-binding NKXD motif
F:157-159/Region: GTP-binding SAK/L motif
F:27,28,46,127,128,130,157/Binding site: Mg-GTP (Lys, Ser, Thr, Asn, Lys, Asp, Ser) #sta

Query Match 40.9%; Score 52; DB 2; Length 206;
Best Local Similarity 37.5%; Pred. No. 17;
Matches 9; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

Oy 1 KKKKADNGTITVEELKQLLEQNL 24
Db 128 KSDLEDKQVSVBEAKRRADQMN 151

RESULT 6
G81328
60 kD chaperonin (cpn60) Cj1221 [imported] - Campylobacter jejuni (strain NCTC 11168)
C:Species: Campylobacter jejuni
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: G81328
R:Perkhill, J.; Wren, B.W.; Murgall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVlier, A.; Whitehead, S.; Barre
Nature 403, 665-668, 2000
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hy
A:Reference number: A81250; MUID:20150912; PMID:10688204
A:Accession: G81328
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-545 <PAR>

A:Cross-references: UNIPROT:O69289; GB:A1139077; GB:A1111168; NID:96968444; PIDN:CA87347
A:Experimental source: serotype O2, strain NCTC 11168
C:Genetics: rat
A:Gene: groEL; Cj1221
C:Superfamily: chaperonin groEL

Query Match 40.9%; Score 52; DB 2; Length 545;
Best Local Similarity 41.7%; Pred. No. 45;
Matches 10; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Oy 2 KKKADNGTITVEELKQLLEQNL 25
Db 166 EKKVGDVITVEEAKSINDELNV 189

RESULT 7
T22980
hypothetical protein F59B10.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T22980
R:Lloyd, C.
submitted to the EMBL Data Library, March 1995
A:Reference number: Z19646
A:Accession: T22980
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-105 <MIL>
A:Cross-references: UNIPROT:Q09954; EMBL:Z48716; PIDN:CA88600.1; GSPDB:GN00020; CESP:F5
A:Experimental source: clone F59B10
C:Genetics: rat
A:Gene: CESP:F59B10.6
A:Map position: 2
A:introns: 54/2; 75/2

Query Match 40.2%; Score 51; DB 2; Length 105;
Best Local Similarity 36.0%; Pred. No. 11;
Matches 9; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Oy 1 KKKKADNGTITVEELKQLLEQNL 25
Db 60 EKKIENGVARSKELRLDPAVYKI 84

RESULT 8
D83894
hypothetical protein BH1956 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: D83894
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Saeki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: D83894
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-344 <STO>
A:Cross-references: UNIPROT:Q95BH1; GB:AP001513; GB:BA000004; NID:G10174345; PIDN:BA0056
A:Experimental source: strain C-125
C:Genetics: rat
A:Gene: BH1956

Query Match 40.2%; Score 51; DB 2; Length 344;
Best Local Similarity 41.4%; Pred. No. 38;
Matches 12; Conservative 3; Mismatches 6; Indels 8; Gaps 1;

Oy 4 MADNGTITVEE-----LKQLLEQNL 24
Db 273 MGDNGATVGENKEQALVDLRLLPEPKI 301

RESULT 9

A:Residues: 1-819 <KAL>
A:Cross-references: EMBL:X90845
A:Superfamily: spectrin alpha chain; calmodulin repeat homology; SH3 homology; spectrin/
C:Keywords: EF hand
F:284-389/Domain: spectrin/dystrophin repeat homology <SP12>

Query Match 39.4%; Score 50; DB 2; Length 819;
Best Local Similarity 47.6%; Pred. No. 1.2e+02;
Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Oy 2 KKMADNGTITVEELKQLEQW 22
Db 774 KKLSDNMTIGQEELIQRLAQF 794

RESULT 19

hypochemical protein R10E12.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004

C:Accession: S41034

R:Smith, A.
submitted to the EMBL Data Library, January 1994

A:Accession: S41034

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-882 <SMT>

A:Cross-references: UNIPROT:Q81115; EMBL:Z29561; NID:9450897; PID:9450898

C:Genetics:

A:Insertions: 72/2; 324/3; 359/1; 400/2; 722/1; 743/1; 782/1; 818/1

Query Match 39.4%; Score 50; DB 2; Length 882;
Best Local Similarity 47.6%; Pred. No. 1.3e+02;
Matches 10; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Oy 5 ADNGTITVEELKQLEQW 25
Db 548 ATGETDTYRQLRQRMSCWNEV 568

RESULT 20

spectrin alpha chain, nonerythroid - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C>Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 09-Jul-2004

C:Accession: A32612

R:Hong, W.; Doyle, D.

J. Biol. Chem. 264, 12758-12764, 1989

A:Title: Cloning and analysis of cDNA clones for rat kidney alpha-spectrin.

A:Reference number: A32612; MUID:89327227; PMID:2753883

A:Accession: A32612

A:Molecule type: mRNA

A:Residues: 1-1030 <HON>

A:Cross-references: UNIPROT:P16086; GB:J04828; NID:9203013; PID:AAA40770.1; PID:9203014

C:Superfamily: spectrin alpha chain; calmodulin repeat homology; SH3 homology; spectrin/
C:Keywords: actin binding; cytoskeleton; EF hand

F:47-152/Domain: spectrin/dystrophin repeat homology <SP12>

F:799-904/Domain: spectrin/dystrophin repeat homology <SP19>

F:913-1019/Domain: spectrin/dystrophin repeat homology <SP20>

Query Match 39.4%; Score 50; DB 2; Length 1030;
Best Local Similarity 47.6%; Pred. No. 1.6e+02;
Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Oy 2 KKMADNGTITVEELKQLEQW 22
Db 537 KKLSDNMTIGQEELIQRLAQF 557

RESULT 21

hypochemical protein DKFZp564P0562.1 - human (fragment)

C:Species: Homo sapiens (man)
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T14790
R:Blum, H.; Baerach, S.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, August 1999

A:Reference number: Z18179

A:Accession: T14790

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1325 <BLU>

A:Cross-references: UNIPROT:Q9UG16; EMBL:AL110273

A:Experimental source: fetal brain; clone DKFZp564P0562

C:Genetics:

A:Note: DKFZp564P0562.1

C:Superfamily: spectrin alpha chain; calmodulin repeat homology; SH3 homology; spectrin/
C:Keywords: EF hand

Query Match 39.4%; Score 50; DB 2; Length 1325;
Best Local Similarity 47.6%; Pred. No. 2e+02;
Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Oy 2 KKMADNGTITVEELKQLEQW 22
Db 817 KKLSDNMTIGQEELIQRLAQF 837

RESULT 22

fodrin alpha chain - human

N:Alternate names: alpha II spectrin; nonerythroid alpha-spectrin

C:Species: Homo sapiens (man)

C>Date: 05-Oct-1990 #sequence_revision 05-Oct-1990 #text_change 09-Jul-2004

C:Accession: A35715; A28580; I52382; A61369; G01810; S54877; S65689

R:Moore, R.T.; McMahon, A.P.

J. Biol. Chem. 265, 4427-4433, 1990

A:Title: Generation of diversity in nonerythroid spectrins. Multiple polypeptides are pr

A:Reference number: A35715; MUID:90170948; PMID:2307671

A:Accession: A35715

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-2472 <MOO>

A:Cross-references: UNIPROT:Q13813; GB:J05243; NID:9179105; PID:AAA51790.1; PID:9179106

R:McMahon, A.P.; Giebelhaus, D.H.; Champion, J.E.; Balles, J.A.; Lacey, S.; Carrillo, B.;

Differentiation 34, 68-78, 1987

A:Title: cDNA cloning, sequencing and chromosome mapping of a non-erythroid spectrin, hu

A:Reference number: A28580; MUID:87277023; PMID:3038643

A:Accession: A28580

A:Molecule type: mRNA

A:Residues: 676-1594 <MCN>

R:McMahon, A.P.; Moon, R.T.

Biochem. Soc. Trans. 15, 804-807, 1987

A:Title: Structure and evolution of a non-erythroid spectrin, human alpha-fodrin.

A:Reference number: I52382; MUID:88083942; PMID:3631949

A:Accession: I52382

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Cross-references: GB:M24773; NID:9537330; PID:AAA52468.1; PID:9537331

R:Mutha, S.; Langston, A.; Bonifae, J.M.; Epstein Jr., E.H.

U. Invest. Dermatol. 97, 383-388, 1991

A:Title: Biochemical identification of alpha-fodrin and protein 4.1 in human keratinocy.

A:Reference number: A61369; MUID:91341201; PMID:1875039

A:Accession: A61369

A:Molecule type: mRNA

A:Residues: 'R',1595-1610,'E',1612-1614,'P',1616-1624,'S',1626-1638,'P',1640,'E',1642-16

2-1813,'R',1815-1820,'K',1822-1844,'V',1846-1850 <MUT>

A:Note: the sequence in Fig. 4 is inconsistent with the sequence in Fig. 3 at several po

R:Morrow, J.S.

submitted to the EMBL Data Library, May 1995

A:Reference number: G08473

A:Accession: G01810

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 811-1299, 'I', 1301-1529 <MOR>
A:Cross-references: EMBL:U26396; NID:G83668; PIDD:AAB60364.1; PID:G83666
R:Lundberg, S.; Bjoerk, J.; Loevenberg, L.; Backman, L.
submitted to the EMBL Data Library, May 1995
A:Description: Cloning and characterization of two putative calcium-binding sites in human
A:Reference number: S54877
A:Accession: S54877
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 2059-2312, 'P', 2314-2346, 'EF', 2349-2433 <LU2>
A:Cross-references: EMBL:X86901
R:Lundberg, S.; Bjoerk, J.; Loevenberg, L.; Backman, L.
Eur. J. Biochem. 230, 658-665, 1995
A>Title: Cloning, expression and characterization of two putative calcium-binding sites
A:Reference number: S55689; MUID:95331304; PMID:7607240
A:Accession: S55689
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 2320-2346, 'EF', 2349-2406 <LU2>
A:Cross-references: EMBL:X86901
C:Gene: GDB:SPTAN1
A:Cross-references: GDB:I20385; OMIM:182810
A:Map position: 9q34.1-9q34.1
C:Superfamily: spectrin alpha chain; calmodulin repeat homology; SH3 homology; spectrin,
C:Keywords: actin binding; EF hand
F:466-571/Domain: spectrin/dystrophin repeat homology <SP5>
F:572-676/Domain: spectrin/dystrophin repeat homology <SP6>
F:677-782/Domain: spectrin/dystrophin repeat homology <SP7>
F:974-1021/Domain: SH3 homology <SH3>
F:2080-2195/Domain: spectrin/dystrophin repeat homology <SP19>
F:2204-2310/Domain: spectrin/dystrophin repeat homology <SP20>
F:2323-2355/Domain: calmodulin repeat homology <EF1>
F:2366-2398/Domain: calmodulin repeat homology <EF2>

Query Match 39.4%; Score 50; DB 2; Length 2472;
Best Local Similarity 47.6%; Pred. No. 3.9e+02;
Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

OY 2 KKMADNGTIVTEELKQLLEQW 22
Db 1828 KKLDNDNTIGKEFIQGRRAQF 1848

RESULT 23
SUCHA
spectrin alpha chain, brain - chicken
N:Alternate names: calspectin alpha chain; fodrin alpha chain
C:Species: Gallus gallus (chicken)
C>Date: 30-Jun-1991 #sequence revision 30-Jun-1991 #text_change 09-Jul-2004
C:Accession: A30122; A31866; A22723; S02425; S03190
R:Maenken, V.M.; Saraste, M.; Salven, P.; Eraamaa, M.; Holm, L.; Lehto, V.P.
J. Cell Biol. 108, 1177-1178, 1989
A:Reference number: A30122
A:Contents: extratum
A:Accession: A30122
A:Molecule type: mRNA
A:Residues: 1-2477 <MAS>
A:Cross-references: UNIPROT:P07751; GB:X14519
R:Maenken, V.M.; Saraste, M.; Salven, P.; Eraamaa, M.; Holm, L.; Lehto, V.P.
Cell Biol. 108, 79-93, 1989
A>Title: Primary structure of the brain alpha-spectrin.
A:Reference number: A31866; MUID:89093238; PMID:2910879
A:Accession: A31866
A:Molecule type: mRNA
A:Residues: 1-2477 <MA2>
A:Cross-references: EMBL:X13701
A>Note: residues 1880-2359 are shown between residues 1399 and 1400 in Fig. 2
C:Superfamily: spectrin alpha chain; calmodulin repeat homology; SH3 homology; spectrin/heterodimer
C:Keywords: actin binding; calcium binding; cytoskeleton; duplication; EF hand; heterodimer
F:43-147/Domain: spectrin/dystrophin repeat homology <SP1>
F:148-253/Domain: spectrin/dystrophin repeat homology <SP2>
F:254-359/Domain: spectrin/dystrophin repeat homology <SP3>

Query Match
Best Local Similarity 39.4%; Score 50; DB 1; Length 2477;
Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 2 KKMADNGITTVBELKQLDEW 22
 ||::|||::|||::|||:
Db 1833 KKLSDNTIGKEIKOQLAOF 1853

RESULT 24

S16552
Hypotheetical protein - Yersinia enterocolitica
CSpecies: Yersinia enterocolitica
CDate: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Jan-1995
JAccession: S16552
R.Seoane, A.; Garcia Lobo, J.M.
Mol. Gen. Genet. 228, 215-220, 1991
A.Title: Nucleotide sequence of a new class A beta-lactamase gene from the chromosome of
A.Reference number: S16552; NCID:91360067; PMID:1866608
A.Accession: S16552
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-36 <SEO>
A.Cross-references: EMBL:X57074

Query Match
Best Local Similarity 38.6%; Score 49; DB 2; Length 36;
Matches 10; Conservative 58.8%; Pred. No. 6.9; Mismatches 5; Indels 0; Gaps 0;

QY 2 KKMADNGITTVBELKQL 18
 ||::|||::|||::|||:
Db 14 KKLDEGTTTSEHYQL 30

RESULT 25

S50566
Hypotheetical protein YER063w - yeast (*Saccharomyces cerevisiae*)
CSpecies: Saccharomyces cerevisiae
CDate: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 09-Jul-2004
JAccession: S50566
R.Dietrich, F.S.
Submitted to the EMBL Data Library, December 1994
A.Description: The sequence of S. cerevisiae lambda clones 6592, 4676, 4742, and 3612.
A.Reference number: S50427
A.Accession: S50566
A.Molecule type: DNA
A.Residues: 1-218 <DIB>
C.Genetics:
A.Gene: SGD:THO1; MIPS:YER063w
A.Cross-references: UNIPROT:P40040; EMBL:U18813; NID:G1381127; PID:G603299; GSPDB:GN0000
A.Map position: 5R

Query Match 38.6%; Score 49; DB 2; Length 218;
 Best Local Similarity 52.4%; Pred. No. 43;
 Matches 11; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 4 MADNGTIVBELKOLLEQNTL 24
 ||| :|| :|| :|| :|| :||
 Db 1 MADYSLTIVQLKDLTLTKRL 21

RESULT 26

B32840
 anthranilate synthase (EC 4.1.3.27) component I - *Leptospira biflexa*
 C:Species: *Leptospira biflexa*
 C:Date: 08-Dec-1989 #sequence_revision 08-Dec-1989 #text_change 09-Jul-2004
 C:Accession: B32840
 R:Yelton, D.B.; Peng, S.L.
 J. Bacteriol. 171, 2083-2089, 1989
 A:Title: Identification and nucleotide sequence of the *Leptospira biflexa* serovar patoc
 A:Reference number: A32840; MUID:89197778; PMID:2703466
 A:Accession: B32840
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-462 <YEL>
 A:Cross-references: UNIPROT:P20463; GB:M22468; NID:G149627; PIDN:AAA88216.1; PID:G149628
 C:Superfamily: anthranilate synthase component I
 C:Keywords: carbon-carbon lyase; oxo-acid-lyase

Query Match 38.6%; Score 49; DB 2; Length 462;
 Best Local Similarity 56.2%; Pred. No. 94;
 Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 6 DNGTIVBELKOLLEQ 21
 ||| :|| :|| :|| :|| :||
 Db 156 DNGTIRHEVQNLLEQ 171

RESULT 27

B27671
 spectrin alpha chain, nonerythroid - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 09-Jul-2004
 C:Accession: B27671
 R:Leao, T.L.; Fortugno-Erikson, D.; Barton, D.; Yang-Feng, T.L.; Francke, U.; Harris, A.
 Mol. Cell. Biol. 8, 1-9, 1988
 A:Title: Comparison of nonerythroid alpha-spectrin gene reveals strict homology among c
 A:Reference number: A53097; MUID:88094573; PMID:336352
 A:Accession: B27671
 A:Molecule type: mRNA
 A:Residues: 1-475 <LET>
 A:Cross-references: UNIPROT:Q14917
 A:Note: the authors translated the codon GGC for residue 18 as Ser
 C:Genetics:
 A:Gene: GDB:SPTAN1
 A:Cross-references: GDB:120385; OMIM:182810
 A:Map position: 9q34.1-9q34.1
 C:Superfamily: spectrin alpha chain, calmodulin repeat homology; SH3 homology; spectrin/
 C:Keywords: actin binding; EF hand
 F:205-311/Domain: spectrin/dystrophin repeat homology <SPI8>
 F:320-425/Domain: spectrin/dystrophin repeat homology <SPI9>

Query Match 38.6%; Score 49; DB 2; Length 475;
 Best Local Similarity 47.6%; Pred. No. 96;
 Matches 10; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 2 KKMADNGTIVBELKOLLEQW 22
 ||| :|| :|| :|| :|| :||
 Db 58 KKTLDNDNTIGKEIQORLAQF 78

RESULT 28

C97022
 glutamyl-tRNA synthetase [imported] - *Clostridium acetobutylicum*

C:Species: *Clostridium acetobutylicum*
 C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
 C:Accession: C97022
 R:Nolling, J.; Bretton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
 J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
 J. Bacteriol. 183, 4823-4838, 2001
 A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium *Clo*
 A:Reference number: A96900; MUID:21359325; PMID:21359325
 A:Accession: C97022
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-485 <KUR>
 A:Cross-references: UNIPROT:Q97KC9; GB:A5001437; PIDN:AAK78966.1; PID:G15023897; GSPDB:G
 A:Experimental source: *Clostridium acetobutylicum* ATCC824
 C:Genetics:
 A:Gene: CAC090
 C:Superfamily: glutamate-tRNA ligase; glutamine-tRNA ligase homology

Query Match 38.6%; Score 49; DB 2; Length 485;
 Best Local Similarity 41.4%; Pred. No. 98;
 Matches 12; Conservative 3; Mismatches 8; Indels 6; Gaps 1;

QY 2 KKMADNGTIVBELKOLLEQWNTL 24
 ||| :|| :|| :|| :|| :||
 Db 393 KKMKTNPBISLDSLNCPLPVYENIEDWNL 421

RESULT 29

AC0845
 probable sigma-54-dependent transcriptional regulator SRY2961 [imported] - *Salmonella ent*.
 C:Species: *Salmonella enterica* subsp. *enterica* serovar Typh
 A:Note: this species has also been called *Salmonella typh*
 C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 28-Apr-2003
 C:Accession: AC0845
 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher,
 Th, T.; Comerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
 S.; Moule, S.; O'Gaora, P.
 Nature 413, 848-852, 2001
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
 A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serov
 A:Reference number: AB0502; MUID:21534947; PMID:11677608
 A:Accession: AC0845
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-506 <PAR>
 A:Cross-references: GB:AL513382; PIDN:CAD05946.1; PID:G16503917; GSPDB:GN00176
 C:Genetics:
 A:Gene: SRY2961
 C:Superfamily: Response regulator (sigma54-dependent transcriptional activator), FlhA ty

Query Match 38.6%; Score 49; DB 2; Length 506;
 Best Local Similarity 50.0%; Pred. No. 1e+02;
 Matches 9; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 KKMADNGTIVBELKOL 18
 ||| :|| :|| :|| :|| :||
 Db 274 KFEWADNGTIFLDEIGEL 291

RESULT 30

A65051
 yjaA protein - *Escherichia coli* (strain K-12)
 C:Species: *Escherichia coli*
 C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
 C:Accession: A65051
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
 .A.; Rose, D.U.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A:Title: The complete genome sequence of *Escherichia coli* K-12.
 A:Reference number: A64720; MUID:97426617; PMID:9278503
 A:Accession: A65051
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA

A/Residues: 1-529 <BLAT>
A/Cross-references: UNIPROT:P37013; GB:AE000354; GB:U00096; NID:G2367149; PIDN:AAC75751.
A/Experimental source: strain K-12, substrain MG1655
C/Genetics:
A/Gene: ygaA
C/Superfamily: Response regulator (sigma54-dependent transcriptional activator), FhlA ty
F/212-434/Domain: RNA polymerase sigma factor interaction domain homology <SFI>
Query Match 38.6%; Score 49; DB 2; Length 529;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
Cy 1 KKMADNGTIVBELKOL 18
Db 299 KFEWADNGTFLDELIGEL 316

RESULT 31
B91074
probable 2-component transcription regulator [imported] - Escherichia coli (strain O157:
C/Species: Escherichia coli
C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C/Accession: B91074
R/Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhnara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A/Reference number: A99629; MUID:21156231; PMID:11258796
A/Accession: B91074
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-529 <HAY>
A/Cross-references: UNIPROT:O8X854; GB:BA000007; PIDN:BAH36988.1; PID:G13363036; GSPDB:C
C/Experimental source: strain O157:H7, substrain R1MD 0509552
C/Genetics:
A/Gene: EC93565
C/Superfamily: Response regulator (sigma54-dependent transcriptional activator), FhlA ty

Query Match 38.6%; Score 49; DB 2; Length 529;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
Cy 1 KKMADNGTIVBELKOL 18
Db 299 KFEWADNGTFLDELIGEL 316

RESULT 32
D85919
probable 2-component transcription regulator ygaA [imported] - Escherichia coli (strain
C/Species: Escherichia coli
C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C/Accession: D85919
R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A/Reference number: A85480; MUID:21074935; PMID:11206551
A/Accession: D85919
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-529 <STO>
A/Cross-references: UNIPROT:Q8X854; GB:AE005174; NID:G12517154; PIDN:AAG57816.1; GSPDB:C
A/Experimental source: strain O157:H7, substrain EDL933
C/Genetics:
A/Gene: ygaA
C/Superfamily: Response regulator (sigma54-dependent transcriptional activator), FhlA ty

Query Match 38.6%; Score 49; DB 2; Length 529;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
Cy 1 KKMADNGTIVBELKOL 18

Db 299 KFEWADNGTFLDELIGEL 316

RESULT 33
A44162
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 1B, calmodulin-dependent, 63k gp
N/Alternate names: 63k calmodulin-stimulated phosphodiesterase, brain; CAM-PDE1B1
C/Species: Bos primigenius taurus (cattle)
C/Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C/Accession: A44162; B40283
R/Bentley, J.K.; Kadlec, A.; Sherbert, C.H.; Seger, D.; Sonnenburg, W.K.; Charbonneau,
J. Biol. Chem. 267, 18676-18682, 1992
A/Title: Molecular cloning of cDNA encoding a "63"-kDa calmodulin-stimulated phosphodies
A/Reference number: A44162; MUID:92406781; PMID:1326531
A/Accession: A44162
A/Molecule type: mRNA
A/Residues: 1-534 <BEN>
A/Cross-references: UNIPROT:Q01061; GB:M94867; NID:G162782; PIDN:AAA74558.1; PID:G162783
A/Experimental source: brain
A/Note: sequence extracted from NCBI backbone (NCBI:P113352)
R/Novack, J.P.; Charbonneau, H.; Bentley, J.K.; Walsh, K.A.; Beavo, J.A.
Biochemistry 30, 7940-7947, 1991
A/Title: Sequence comparison of the 63-, 61-, and 59-kDa calmodulin-dependent cyclic nuc
A/Reference number: A40283; MUID:91329366; PMID:1651112
A/Accession: B40283
A/Molecule type: Protein
A/Residues: 29-45,'IP','48','R','50-52','IS','55-85;196-215;277','D','279','T','281-287','T','289-2
A/Experimental source: brain
C/Comment: This enzyme is a useful target for inducing the death of leukemic cells, and
C/Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent, 3',5'
C/Keywords: alternative splicing; calmodulin binding; cGMP binding; phosphoric diester h
F/220-437/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNPD>

Query Match 38.6%; Score 49; DB 1; Length 534;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
Cy 3 KMDNGTIVBELKOL 20
Db 43 KOLENGEVNIEELKONLE 60

RESULT 34
A44161
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 1B, calmodulin-dependent, 63k gp
N/Alternate names: 63k calmodulin-stimulated phosphodiesterase, brain; CAM-PDE1B1
C/Species: Rattus norvegicus (Norway rat)
C/Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C/Accession: A44161
R/Repaske, D.R.; Swinnen, J.V.; Jin, S.L.; Van Wyk, J.J.; Connel, M.
J. Biol. Chem. 267, 18683-18688, 1992
A/Title: A polymerase chain reaction strategy to identify and clone cyclic nucleotide ph
A/Reference number: A44161; MUID:92406782; PMID:1326532
A/Accession: A44161
A/Molecule type: mRNA
A/Residues: 1-535 <REP>
A/Cross-references: UNIPROT:Q01066; GB:M94537; NID:G203268; PIDN:AAA16530.1; PID:G203269
A/Experimental source: brain
A/Note: sequence extracted from NCBI backbone (NCBI:P113357)
C/Comment: This enzyme is a useful target for inducing the death of leukemic cells, and
C/Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent, 3',5'
C/Keywords: alternative splicing; calmodulin binding; cGMP binding; phosphoric diester h
F/221-438/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNPD>

Query Match 38.6%; Score 49; DB 1; Length 535;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
Cy 3 KMDNGTIVBELKOL 20
Db 43 KOLENGEVNIEELKONLE 60

RESULT 35

A46378

3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 1B, calmodulin-dependent, 63K sp

N/Alternate names: 63K calmodulin-stimulated phosphodiesterase, brain; CAM-PDE1B1

C/Species: Mus musculus (house mouse)

C/Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004

A/Accession: A46378; B44161

R/Polli, J.W.; Kincaid, R.L.

Proc. Natl. Acad. Sci. U.S.A. 89, 11079-11083, 1992

A/Title: Molecular cloning of DNA encoding a calmodulin-dependent phosphodiesterase enri

A/Reference number: A46378; MUID:99066388; PMID:1332068

A/Accession: A46378

A/Molecule type: mRNA; protein

A/Residues: 1-535 <POL>

A/Cross-references: UNIPROT:Q01065; GB:L01695; NID:G200269; PIDN:AAA39902.1; PID:G200270

A/Experimental source: brain

A/Note: sequence extracted from NCBI backbone (NCBI:118901, NCBI:118903)

R/Repaske, D.R.; Swinnen, J.V.; Jin, S.L.; Van Wyk, J.J.; Conti, M.

J. Biol. Chem. 267, 18683-18688, 1992

A/Title: A polymerase chain reaction strategy to identify and clone cyclic nucleotide ph

A/Reference number: A44161; MUID:92406782; PMID:1326532

A/Accession: B44161

A/Molecule type: mRNA

A/Residues: 221-223, R', 225-336 <REP>

A/Cross-references: GB:M94538; NID:G192366; PIDN:AAA37367.1; PID:G192369

A/Note: sequence extracted from NCBI backbone (NCBI:113365)

C/Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'

C/Keywords: alternative splicing; calmodulin binding; GMP binding; phosphoric diester h

F;221-438/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 38.6%; Score 49; DB 1; Length 535;

Best Local Similarity 50.0%; Pred. No. 1.1e+02;

Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Oy 3 KMA0NGTIVTEELKQLE 20

Db 43 KQLENGEVIIEELKKNLE 60

RESULT 36

H64119 chreonine-tRNA ligase (EC 6.1.1.3) - Haemophilus influenzae

N/Alternate names: threonyl-tRNA synthetase

C/Species: Haemophilus influenzae

C/Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004

A/Accession: H64119

R/Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirschner, E.F.; Kerlavage, A

; Gocayne, J.D.; Scott, J.; Shiley, R.; Liu, L.; Glodek, A.; Kelley, J.M.; McElman, J

; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Geoghagen, N.S.M.

Science 269, 496-512, 1995

A/Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,

A/Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A/Reference number: A64000; MUID:95350630; PMID:7542800

A/Accession: H64119

A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-643 <TIG>

A/Cross-references: UNIPROT:P43014; GB:U32816; GB:L42023; NID:G1574193; PIDN:AA23014.1;

A/Experimental source: strain Rd KW20

C/Genetics:

A/Function:

A/Description: activates L-threonine and transfers it to the specific tRNA

A/Pathway: protein biosynthesis

A/Note: belongs to class-II synthetases

C/Superfamily: threonine-tRNA ligase

C/Keywords: aminacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 38.6%; Score 49; DB 2; Length 643;

Best Local Similarity 52.6%; Pred. No. 1.3e+02;

Matches 10; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Oy 2 KMA0NGTIVTEELKQLE 20

Db 611 KQKADLTFTVEEFAELK 629

RESULT 37

S56237

glucosamine-phosphate N-acetyltransferase (EC 2.3.1.4) [validated] - Yeast (Saccharomyces

N/Alternate names: phosphoglucosamine acetylase; phosphoglucosamine transacetylase; prote

C/Species: Saccharomyces cerevisiae

C/Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 09-Jul-2004

A/Accession: S56237; S48321; S62296

R/Murakami, Y.; Naitou, M.; Hagihara, H.; Shibata, T.; Ozawa, M.; Sasamura, S.I.; Sasamu

submitted to the EMBL Data Library, May 1995

A/Description: Analysis of the nucleotide sequence of chromosome VI from Saccharomyces cer

A/Reference number: S56186

A/Accession: S56237

A/Molecule type: DNA

A/Residues: 1-159 <MUR>

A/Cross-references: UNIPROT:P43577; EMBL:D50617; NID:G836685; PIDN:BA09221.1; PID:G83672

R/Churcher, C.

submitted to the EMBL Data Library, September 1994

A/Reference number: S48310

A/Accession: S48321

A/Molecule type: DNA

A/Residues: 1-111, 'ASS' <CHU>

A/Cross-references: EMBL:Z46255; NID:G559925; PIDN:CA086352.1; PID:G559937; GSPDB:GN00006

R/Murakami, Y.

submitted to the EMBL Data Library, December 1994

A/Reference number: S62230

A/Accession: S62296

A/Molecule type: DNA

A/Residues: 1-159 <MUR>

A/Cross-references: EMBL:D44596; NID:G1100783; PIDN:BA08000.1; PID:G1100787

C/Genetics:

A/Map position: 6L

C/Function: EC 2.3.1.4 [validated, MUID:99085039]; glucosamine-phosphate N-acetyltran

A/Note: phosphoglucosamine acetyltransferase activity has been shown in vitro, by incubat

C/Superfamily: Saccharomyces glucosamine-phosphate N-acetyltransferase

C/Keywords: acyltransferase; coenzyme A

Query Match 37.8%; Score 48; DB 1; Length 159;

Best Local Similarity 40.9%; Pred. No. 42;

Matches 9; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Oy 2 KMA0NGTIVTEELKQLEON 23

Db 25 KVLTVGTTPESFKLTKWN 46

RESULT 38

DB3010 Probable binding protein component of ABC transporter PA5082 [imported] - Pseudomonas ae

C/Species: Pseudomonas aeruginosa

C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004

A/Accession: DB3010

R/Stover, C.K.; Pham, X.Q.; Ewlan, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,

; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathc

A/Reference number: A82950; MUID:20437337; PMID:10984043

A/Accession: DB3010

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-299 <STO>

A/Cross-references: UNIPROT:Q9HUAL; GB:AE004921; GB:AE004091; NID:G9951372; PIDN:AA08046

A:Experimental source: strain PA01
C:Gene: PA5082

Query Match 37.8%; Score 48; DB 2; Length 299;
Best Local Similarity 81.8%; Pred. No. 81;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 KKMADNGTITV 12
DB 30 KKMADNGTITL 40

RESULT 39

hypothetical protein H01G02.1 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T23021

R:Kershaw, J.

submitted to the EMBL Data Library, March 1997
A:Reference number: Z19655

A:Accession: T23021

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-309 <WIL>

A:Cross-references: UNIPROT:O17902; EMBL:Z92847; PIDN:GAB07421.1; GSPDB:GN00022; CESP:HO

A:Experimental source: clone H01G02

C:Gene: CESP:H01G02.1

A:Map position: 4

A:introns: 20/1; 52/3; 121/1; 162/3; 238/2

Query Match 37.8%; Score 48; DB 2; Length 309;
Best Local Similarity 40.9%; Pred. No. 84;
Matches 9; Conservative 9; Mismatches 2; Indels 2; Gaps 1;

OY 4 MADNGTIVE--ELKQLEOWN 23
DB 154 IAFNGTISVEMDQVEKIDWMS 175

RESULT 40

AC0897

TDC operon transcription activator STY3428 [imported] - *Salmonella enterica* subsp. enter

C:Species: *Salmonella enterica* subsp. *enterica* serovar Typh

A:Note: This species has also been called *Salmonella typhi*

C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

C:Accession: AC0897

R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,

Ch, T.; Conneron, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,

S.; Mole, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;

A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serov

A:Reference number: AB0502; MUID:21534947; PMID:11677608

A:Accession: AC0897

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-312 <PAR>

A:Cross-references: GB:AL513382; PIDN:CAD07769.1; PID:G16504318; GSPDB:GN00176

C:Gene: STY3428

C:Superfamily: regulatory protein 11v

Query Match 37.8%; Score 48; DB 2; Length 312;
Best Local Similarity 52.2%; Pred. No. 85;
Matches 12; Conservative 1; Mismatches 8; Indels 2; Gaps 1;

OY 2 KKMADNGTITVBEKQLEOWNL 24
DB 179 KSRCTGTITLESMD--EOWAL 199

RESULT 41

AG2311

hypothetical protein alr4046 [imported] - *Nostoc* sp. (strain PCC 7120)

C:Species: *Nostoc* sp. PCC 7120

A:Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120

C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C:Accession: AG2311

R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Matsumoto, A.; Iriuch

Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.

DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Ana*

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AG2311

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-335 <KUR>

A:Cross-references: UNIPROT:Q8YF24; GB:BA000019; PIDN:BA075745.1; PID:G1713181; GSPDB:G

A:Experimental source: strain PCC 7120

C:Gene: alr4046

C:Superfamily: glutathione S-transferase

Query Match 37.8%; Score 48; DB 2; Length 335;
Best Local Similarity 43.5%; Pred. No. 91;
Matches 10; Conservative 5; Mismatches 6; Indels 2; Gaps 1;

OY 3 KKMADNGTITV--BEKQLEOWN 23
DB 172 EFAKSTLNLVBEKQKIDWVN 194

RESULT 42

hypothetical protein ZK377.3 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

C:Accession: T29549

R:Nhan, M.; Hawkins, J.

submitted to the EMBL Data Library, February 1997

A:Description: The sequence of *C. elegans* cosmid ZK377.

A:Reference number: Z20639

A:Accession: T29549

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-423 <NHA>

A:Cross-references: EMBL:U88183; PIDN:AB52658.1; GSPDB:GN00028; CESP:ZK377.3

A:Experimental source: strain Bristol N2; clone ZK377

C:Gene: CESP:ZK377.3

A:Map position: X

A:introns: 24/1; 142/3; 229/3; 284/2; 408/3

Query Match 37.8%; Score 48; DB 2; Length 423;
Best Local Similarity 40.0%; Pred. No. 1.2e+02;
Matches 8; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

OY 1 KKMADNGTITVBEKQLE 20
DB 368 RTKVSPTGTITBEVRQVDE 387

RESULT 43

AB1290

ATP-dependent RNA helicase homolog lmo1722 [imported] - *Listeria monocytogenes* (strain

C:Species: *Listeria monocytogenes*

C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

C:Accession: AB1290

R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Bagner, F.; Berche, P.; Bioecker

; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurge, O.; Entian, K.D.; Fahn, H.

Science 294, 849-852, 2001

A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma

Ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of *Listeria species*.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AB1290
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-441 <GLA>
A:Cross-references: UNIPROT:Q8Y6G5; GB:NC_003210; PIDN:CAC99800.1; PID:g16411176; GSPDB:C
A:Experimental source: strain BGD-e
C:Genetics: 1m01722

Query Match 37.8%; Score 48; DB 2; Length 441;
Best Local Similarity 52.2%; Pred. No. 1.2e+02;
Matches 12; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 1 KKKMADNGTIVEELKQLEQWN 23
Db 135 KIKMHEIKTITLDECDQLLRQEN 157

RESULT 44
AH1661
ATP-dependent RNA helicases homolog lin1833 [imported] - *Listeria innocua* (strain Clip11
C:Species: *Listeria innocua*
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
A:Accession: AH1661
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bioecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurge, O.; Entlian, K.D.; Fshih, H.
D.; Jones, L.M.; Karet, U.
Science 294, 849-852, 2001
A:Authors: Krett, J.; Kuhn, M.; Kunst, F.; Kurapk, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A:Title: Comparative genomics of *Listeria species*.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AH1661
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-442 <GLA>
A:Cross-references: UNIPROT:Q92AT6; GB:AL592022; PIDN:CAC97064.1; PID:g16414335; GSPDB:C
A:Experimental source: strain Clip11262
C:Genetics: 1lin1833

Query Match 37.8%; Score 48; DB 2; Length 442;
Best Local Similarity 52.2%; Pred. No. 1.2e+02;
Matches 12; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 1 KKKMADNGTIVEELKQLEQWN 23
Db 135 KIKMHEIKTITLDECDQLLRQEN 157

RESULT 45
F90248
hypochemical protein srp54 [imported] - *Sulfolobus solfataricus*
C:Species: *Sulfolobus solfataricus*
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
A:Accession: F90248
R:Sho, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aweyer, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Mgoc, H.P.; Redder, F
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: *Sulfolobus solfataricus* complete genome.
A:Reference number: A99139
A:Accession: F90248
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-447 <KUD>
A:Cross-references: UNIPROT:Q97ZE7; GB:AE006641; NID:g13814155; PIDN:AA41245.1; GSPDB:C
C:Genetics: 1srp54
A:Gene: srp54
C:Superfamily: signal recognition particle 54K protein

Query Match 37.8%; Score 48; DB 2; Length 447;
Best Local Similarity 36.4%; Pred. No. 1.2e+02;
Matches 8; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

Qy 2 KKKMADNGTIVEELKQLEQWN 23
Db 401 RRIAGSGLEVEEVRLELWYN 422

RESULT 46
S52528
UTAI protein - yeast (*Saccharomyces cerevisiae*)
N:Alternate names: protein LP14w; protein YP8132.10; protein YPL003w
C:Species: *Saccharomyces cerevisiae*
C:Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
A:Accession: S52528; S59690
R:Badcock, K.; Churcher, C.
submitted to the EMBL Data Library, February 1995
A:Reference number: S52519
A:Accession: S52528
A:Molecule type: DNA
A:Residues: 1-462 <BAD>
A:Cross-references: UNIPROT:Q12059; EMBL:Z48483; NID:9683777; PID:9683787; MIPS:YPL003w
A:Experimental source: strain AB972
R:Hall, J.; Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, J.D.; Storms, R.K.; Vo, D.H.; Wa
submitted to the EMBL Data Library, August 1995
A:Description: The sequence of *Saccharomyces cerevisiae* chromosome XVI left arm.
A:Reference number: S59677
A:Accession: S59650
A:Molecule type: DNA
A:Residues: 1-462 <HAL>
A:Cross-references: EMBL:U33335; NID:965076; PID:965090; MIPS:YPL003w
C:Genetics: 1SGD:UTAI
A:Gene: SGD:UTAI
A:Cross-references: SGD:S0005924
A:Map position: 16L

Query Match 37.8%; Score 48; DB 2; Length 462;
Best Local Similarity 43.8%; Pred. No. 1.3e+02;
Matches 7; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

Qy 6 DNGTIVEELKQLEQ 21
Db 213 NNGRITIDQMKVLDQ 228

RESULT 47
B75017
alanyl-cRNA synthetase (alaS) PAB1245 - *Pyrococcus abyssi* (strain Orsay)
C:Species: *Pyrococcus abyssi*
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
A:Accession: B75017
R:Anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: *Pyrococcus abyssi* genome sequence: insights into archaeal chromosome stru
A:Reference number: A75001
A:Accession: B75017
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-914 <KMW>
A:Cross-references: UNIPROT:Q9UV36; GB:AJ248288; GB:AL096836; NID:95458960; PIDN:CAB5057
A:Experimental source: strain Orsay
C:Genetics: 1PAB1245
A:Gene: PAB1245
C:Superfamily: alanyl-cRNA ligase

Query Match 37.8%; Score 48; DB 2; Length 914;
Best Local Similarity 36.0%; Pred. No. 2.5e+02;
Matches 9; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Qy 1 KKKMADNGTIVEELKQLEQWN 25
Db 1 KKKMADNGTIVEELKQLEQWN 25

Db 314 RKKVAEKYISVEELEKAIKPYELI 338

RESULT 48

sax-3 protein - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C/Accession: T42405

R/Zaller, J.A.; Yi, B.A.; Bargmann, C.I.

Cell 92, 217-227, 1998

A/Title: The conserved immunoglobulin superfamily member SAX-3/Robo directs multiple asp

A/Reference number: 222160; MUID:98117250; PMID:9458046

A/Accession: T42405

A/Status: preliminary; translated from GB/EMBL/DDBJ

A/Molecule type: mRNA

A/Residues: 1-1273 <ZAL>

A/Cross-references: UNIPROT:O44928; EMBL:AF041053; NID:G2804779; PIDN:AAC38848.1; PID:92

C/Genetics:

A/Note: sax-3

C/Function:

A/Description: sax-3 function is required at the time of axon guidance

Query Match 37.8%; Score 48; DB 2; Length 1273;

Best Local Similarity 40.0%; Pred. No. 3.6e+02;

Matches 8; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

Db 369 RTKVSPGTLTIEEVROYDE 388

RESULT 49

A59282

nonmuscle myosin II heavy chain A - African clawed frog

C/Species: Xenopus laevis (African clawed frog)

C/Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004

C/Accession: A59282

R/BhacI, Dey, N.; Taïra, M.; Conti, M.A.; Nooruddin, H.; Adelerstein, R.S.

Mech. Dev. 78, 33-36, 1998

A/Title: Differential expression of non-muscle myosin heavy chain genes during Xenopus e

A/Reference number: A59282; MUID:98077683; PMID:9858676

A/Accession: A59282

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-1964 <BHA>

A/Cross-references: UNIPROT:O93522; GB:AF055895; NID:G3660671; PIDN:AAC83556.1; PID:9366

A/Experimental source: cell line XC

A/Superfamily: myosin heavy chain; myosin motor domain homology

F;84-764/Domain: myosin motor domain homology <MMO>

Query Match 37.8%; Score 48; DB 2; Length 1964;

Best Local Similarity 56.5%; Pred. No. 5.6e+02;

Matches 13; Conservative 6; Mismatches 2; Indels 2; Gaps 2;

Db 1370 KKKMDENVGSLTVEELKKKLOK 1392

RESULT 50

S60545

envelope polypeptide gp41 - human immunodeficiency virus type 1 (isolate CI-45-1) (fragm

C/Species: human immunodeficiency virus type 1, HIV-1

C/Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

C/Accession: S60545

R/Janssens, W.; Heyndrickx, L.; Van de Peer, Y.; Bouckaert, A.; Franssen, K.; Motte, J.;

AIDS 8, 21-26, 1994

A/Title: Molecular phylogeny of part of the env gene of HIV-1 strains isolated in Cote d

A/Reference number: S60521; MUID:94280700; PMID:8011235

A/Accession: S60545

A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-294 <JAN>

A/Cross-references: UNIPROT:O76190; EMBL:X72047; NID:G468669; PIDN:CA50930.1; PID:G4686

A/Experimental source: isolate CI-45-1

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1993

C/Genetics:

A/Gene: env

C/Superfamily: type B retrovirus env polypeptide

C/Keywords: AIDS; glycoprotein; immunodeficiency; polypeptide

Query Match

Best Local Similarity 37.4%; Score 47.5; DB 2; Length 294;

Matches 9; Conservative 6; Mismatches 4; Indels 1; Gaps 1;

Db 136 NGTITLQCKIKQIVNMOKV 155

7 NGTITVE-ELKOLLEOMNLV 25

Search completed: May 11, 2005, 21:23:16
Job time : 31 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 11, 2005, 21:15:49 ; Search time 120.745 Seconds
(without alignments)
106.025 Million cell updates/sec

Title: US-10-712-812-6

Perfect score: 127

Sequence: 1 KKKKADNGITVEELKQLEQNNLV 25

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 1000 summaries

Database :

Uniprot_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|---------------------|
| 1 | 112 | 88.2 | 143 | 2 | Q6ARI0 SARS CORONA |
| 2 | 112 | 88.2 | 143 | 2 | Q6ARI4 SARS CORONA |
| 3 | 112 | 88.2 | 143 | 2 | Q6ARI8 SARS CORONA |
| 4 | 112 | 88.2 | 143 | 2 | Q6ARI2 SARS CORONA |
| 5 | 112 | 88.2 | 143 | 2 | Q6ARI6 SARS CORONA |
| 6 | 112 | 88.2 | 143 | 2 | Q6ARI4 SARS CORONA |
| 7 | 112 | 88.2 | 143 | 2 | Q6ARI8 SARS CORONA |
| 8 | 112 | 88.2 | 143 | 2 | Q6ARI2 SARS CORONA |
| 9 | 112 | 88.2 | 143 | 2 | Q6ARI6 SARS CORONA |
| 10 | 112 | 88.2 | 143 | 2 | Q6ARI0 SARS CORONA |
| 11 | 112 | 88.2 | 143 | 2 | Q6ARI4 SARS CORONA |
| 12 | 112 | 88.2 | 143 | 2 | Q6ARI8 SARS CORONA |
| 13 | 112 | 88.2 | 143 | 2 | Q6ARI2 SARS CORONA |
| 14 | 112 | 88.2 | 143 | 2 | Q6ARI6 SARS CORONA |
| 15 | 112 | 88.2 | 143 | 2 | Q6ARI0 SARS CORONA |
| 16 | 112 | 88.2 | 143 | 2 | Q6ARI4 SARS CORONA |
| 17 | 112 | 88.2 | 143 | 2 | Q6ARI8 SARS CORONA |
| 18 | 112 | 88.2 | 221 | 1 | VME1 CVHSA |
| 19 | 112 | 88.2 | 221 | 2 | Q6GVB9 HUMAN CORONA |
| 20 | 112 | 88.2 | 221 | 2 | Q6GVB9 HUMAN CORONA |
| 21 | 112 | 88.2 | 221 | 2 | Q6GVB9 HUMAN CORONA |
| 22 | 112 | 88.2 | 221 | 2 | Q6GVB9 HUMAN CORONA |
| 23 | 112 | 88.2 | 221 | 2 | Q6GVB9 HUMAN CORONA |
| 24 | 112 | 88.2 | 221 | 2 | Q6GVB9 HUMAN CORONA |
| 25 | 112 | 88.2 | 221 | 2 | Q6GVB9 HUMAN CORONA |
| 26 | 112 | 88.2 | 221 | 2 | Q6GVB9 HUMAN CORONA |
| 27 | 112 | 88.2 | 221 | 2 | Q6GVB9 HUMAN CORONA |
| 28 | 112 | 88.2 | 221 | 2 | Q6GVB9 HUMAN CORONA |
| 29 | 112 | 88.2 | 221 | 2 | Q6GVB9 HUMAN CORONA |
| 30 | 112 | 88.2 | 221 | 2 | Q6GVB9 HUMAN CORONA |
| 31 | 112 | 88.2 | 221 | 2 | Q6GVB9 HUMAN CORONA |

| | | | | | | | | | | | | | |
|-----|------|------|-------|---|------------|---------------------|-----|------|------|------|---|------------|--------------------|
| 105 | 50.5 | 39.8 | 852 | 2 | Q9DQ10 | Q9dq10 human immun | 178 | 49 | 38.6 | 536 | 2 | Q9BE16 | Q9be16 macaca fasc |
| 106 | 50 | 39.4 | 149 | 2 | O8ENU0 | O8enu0 oceanobacil | 179 | 49 | 38.6 | 643 | 1 | SYT_HAEIN | P33014 haemophilus |
| 107 | 50 | 39.4 | 174 | 2 | O6Z2J1 | O6z2j1 ocyza sativ | 180 | 49 | 38.6 | 648 | 1 | CH6B_DROME | O9vps dirosophila |
| 108 | 50 | 39.4 | 184 | 2 | O8KUZ5 | O8kuz5 uncultured | 181 | 49 | 38.6 | 1744 | 2 | O9R0J5 | O9r0j5 rattus norv |
| 109 | 50 | 39.4 | 184 | 2 | O6BH71 | O6bh71 clostridium | 182 | 49 | 38.6 | 2788 | 2 | O7WRX9 | O7wrx9 anabaena ci |
| 110 | 50 | 39.4 | 184 | 2 | O6BH72 | O6bh72 clostridium | 183 | 49 | 38.6 | 4416 | 2 | O9J3F3 | O9j3f3 murine hepa |
| 111 | 50 | 39.4 | 264 | 1 | YE54_SCHPO | O11171 sciliosacch | 184 | 49 | 38.6 | 4416 | 2 | O9J3F8 | O9j3f8 murine hepa |
| 112 | 50 | 39.4 | 274 | 2 | OBR136 | O8i136 fusobacteri | 185 | 49 | 38.6 | 7124 | 1 | R1AB_CVM2 | O9pya3 m replicase |
| 113 | 50 | 39.4 | 294 | 2 | O94072 | O94072 caenorhabdi | 186 | 48.5 | 38.2 | 163 | 2 | O9KMW4 | O9mwv4 human immun |
| 114 | 50 | 39.4 | 300 | 2 | Q7WVC9 | Q7wvc9 actinetobac | 187 | 48.5 | 38.2 | 174 | 2 | O7OCJ8 | O7ocj8 human immun |
| 115 | 50 | 39.4 | 300 | 2 | Q9F7D7 | Q9f7d7 actinetobac | 188 | 48.5 | 38.2 | 179 | 2 | O9DVP8 | O9dvp8 human immun |
| 116 | 50 | 39.4 | 323 | 1 | PXP_HAEIN | P44828 haemophilus | 189 | 48.5 | 38.2 | 185 | 2 | O5S132 | O5s132 mus musculu |
| 117 | 50 | 39.4 | 516 | 2 | Q96KP3 | Q96kp3 homo sapien | 190 | 48.5 | 38.2 | 193 | 2 | O7ZN14 | O7zn14 human immun |
| 118 | 50 | 39.4 | 531 | 2 | O98974 | O98974 ritzobium 1 | 191 | 48.5 | 38.2 | 195 | 2 | O7OR66 | O7orc6 human immun |
| 119 | 50 | 39.4 | 536 | 1 | CN1B_HUMAN | O01064 homo sapien | 192 | 48.5 | 38.2 | 203 | 2 | O8AD00 | O8adu0 human immun |
| 120 | 50 | 39.4 | 546 | 1 | CH60_MOLSU | O7mae3 wolinnella s | 193 | 48.5 | 38.2 | 206 | 2 | Q7SUT3 | O7sut3 human immun |
| 121 | 50 | 39.4 | 549 | 1 | CH62_BRAVA | P33861 bradyrhizob | 194 | 48.5 | 38.2 | 211 | 2 | O7ZN99 | O7zn99 human immun |
| 122 | 50 | 39.4 | 673 | 2 | O9PR23 | O9pr23 ureaplasma | 195 | 48.5 | 38.2 | 212 | 2 | O7OR95 | O7orc5 human immun |
| 123 | 50 | 39.4 | 846 | 2 | O8N270 | O8n270 homo sapien | 196 | 48.5 | 38.2 | 842 | 2 | O73340 | O73340 human immun |
| 124 | 50 | 39.4 | 846 | 2 | O8I114 | P34552 caenorhabdi | 197 | 48.5 | 38.2 | 842 | 2 | O6UFC3 | O6ufc3 human immun |
| 125 | 50 | 39.4 | 861 | 1 | P058_CAEEL | P34552 caenorhabdi | 198 | 48.5 | 38.2 | 855 | 2 | O6UFC3 | O6ufc3 human immun |
| 126 | 50 | 39.4 | 868 | 2 | O6ALT6 | O6alt6 deesulfoale | 199 | 48.5 | 38.2 | 872 | 2 | O9IUZ0 | O9iuz0 human immun |
| 127 | 50 | 39.4 | 882 | 2 | O8I115 | O8i115 caenorhabdi | 200 | 48.5 | 38.2 | 872 | 2 | O9IUZ1 | O9iuz1 human immun |
| 128 | 50 | 39.4 | 1118 | 2 | O7R2P7 | O7r2p7 gliardia lam | 201 | 48 | 37.8 | 119 | 2 | O6PRV2 | O6prv2 coturnix co |
| 129 | 50 | 39.4 | 1325 | 2 | O9UG16 | O9ug16 homo sapien | 202 | 48 | 37.8 | 125 | 2 | O05614 | O05614 pseudomonas |
| 130 | 50 | 39.4 | 1458 | 1 | SPCN_MOUSE | P16546 mus musculu | 203 | 48 | 37.8 | 126 | 2 | P84137 | P84137 bacillus st |
| 131 | 50 | 39.4 | 1803 | 1 | PNO_EUGER | O94i05 euglena gra | 204 | 48 | 37.8 | 127 | 2 | O8CBJ3 | O8cbj3 mus musculu |
| 132 | 50 | 39.4 | 2443 | 2 | Q96J17 | O96j17 homo sapien | 205 | 48 | 37.8 | 159 | 1 | GNAL_YEAST | O8khe8 uncultured |
| 133 | 50 | 39.4 | 2452 | 2 | O7Z6M5 | O7z6m5 homo sapien | 206 | 48 | 37.8 | 184 | 2 | O8KHT8 | O8kht8 uncultured |
| 134 | 50 | 39.4 | 2452 | 2 | O6IRK8 | O6irk8 rattus norv | 207 | 48 | 37.8 | 184 | 2 | O8KIA7 | O8kia7 uncultured |
| 135 | 50 | 39.4 | 2472 | 1 | SPCN_HUMAN | O13813 homo sapien | 208 | 48 | 37.8 | 184 | 2 | O8KP73 | O8kpw3 uncultured |
| 136 | 50 | 39.4 | 2472 | 1 | SPCN_RAT | P16086 rattus norv | 209 | 48 | 37.8 | 184 | 2 | O8KUZ1 | O8kuz1 uncultured |
| 137 | 50 | 39.4 | 2477 | 1 | SPCN_CHICK | P07751 gallus gall | 210 | 48 | 37.8 | 184 | 2 | O8KVI0 | O8kvi0 uncultured |
| 138 | 50 | 39.4 | 4091 | 2 | Q7QAT8 | O7qa48 anophles g | 211 | 48 | 37.8 | 184 | 2 | O8KVI6 | O8kvi6 uncultured |
| 139 | 50 | 39.4 | 13536 | 2 | O8JVS0 | O8jvs0 pseudomonas | 212 | 48 | 37.8 | 184 | 2 | O8KVA2 | O8kva2 uncultured |
| 140 | 49.5 | 39.0 | 143 | 2 | O6T702 | O6t702 symbiobacte | 213 | 48 | 37.8 | 184 | 2 | O8KVA4 | O8kva4 uncultured |
| 141 | 49.5 | 39.0 | 177 | 2 | O9QRL9 | O9qrl9 human immun | 214 | 48 | 37.8 | 184 | 2 | O8KVA5 | O8kva5 uncultured |
| 142 | 49.5 | 39.0 | 201 | 2 | O8US59 | O8us59 human immun | 215 | 48 | 37.8 | 184 | 2 | O8KVB6 | O8kvb6 uncultured |
| 143 | 49.5 | 39.0 | 203 | 2 | O7O521 | O7o521 human immun | 216 | 48 | 37.8 | 184 | 2 | O8KVB8 | O8kvb8 uncultured |
| 144 | 49.5 | 39.0 | 203 | 2 | O7O528 | O7o528 human immun | 217 | 48 | 37.8 | 184 | 2 | O8KVC3 | O8kvc3 uncultured |
| 145 | 49.5 | 39.0 | 208 | 2 | O8Q7K0 | O8q7k0 human immun | 218 | 48 | 37.8 | 184 | 2 | O8KVC6 | O8kvc6 uncultured |
| 146 | 49.5 | 39.0 | 573 | 2 | O6FY31 | O6fy31 candida gla | 219 | 48 | 37.8 | 184 | 2 | O8KVS5 | O8kvs5 uncultured |
| 147 | 49.5 | 39.0 | 855 | 2 | O8UL72 | O8ul72 human immun | 220 | 48 | 37.8 | 184 | 2 | O8KVS5 | O8kvs5 uncultured |
| 148 | 49.5 | 39.0 | 897 | 2 | O99786 | O99786 cache valle | 221 | 48 | 37.8 | 184 | 2 | O8KVS5 | O8kvs5 uncultured |
| 149 | 49.5 | 39.0 | 897 | 2 | O91ZG4 | O91z94 cache valle | 222 | 48 | 37.8 | 184 | 2 | O8KVS6 | O8kvs6 uncultured |
| 150 | 49.5 | 39.0 | 897 | 2 | O791LN3 | O791ln3 strephylcoc | 223 | 48 | 37.8 | 184 | 2 | O8KVS8 | O8kvs8 uncultured |
| 151 | 49 | 38.6 | 118 | 2 | O99MNS | O99mns rattus norv | 224 | 48 | 37.8 | 184 | 2 | O8KVI6 | O8kvi6 uncultured |
| 152 | 49 | 38.6 | 123 | 2 | O9X5T5 | O9x5t5 streptomyc | 225 | 48 | 37.8 | 184 | 2 | O8KVI2 | O8kvi2 uncultured |
| 153 | 49 | 38.6 | 143 | 2 | O9X1X6 | O9x1x6 homo sapien | 226 | 48 | 37.8 | 184 | 2 | O8KVL5 | O8kvl5 uncultured |
| 154 | 49 | 38.6 | 180 | 2 | O7ONT8 | O7ont8 helicobacte | 227 | 48 | 37.8 | 184 | 2 | O8KVO4 | O8kvo4 uncultured |
| 155 | 49 | 38.6 | 183 | 2 | O6SWP2 | O6swp2 manheimia | 228 | 48 | 37.8 | 184 | 2 | O8KVO8 | O8kvo8 uncultured |
| 156 | 49 | 38.6 | 184 | 2 | O8KVI5 | O8kvi5 uncultured | 229 | 48 | 37.8 | 184 | 2 | O8KVO8 | O8kvo8 uncultured |
| 157 | 49 | 38.6 | 184 | 2 | O8KVI6 | O8kvi6 uncultured | 230 | 48 | 37.8 | 184 | 2 | O8KVS5 | O8kvs5 uncultured |
| 158 | 49 | 38.6 | 184 | 2 | O8KVI6 | O8kvi6 uncultured | 231 | 48 | 37.8 | 184 | 2 | O8KVS5 | O8kvs5 uncultured |
| 159 | 49 | 38.6 | 218 | 1 | TH01_YEAST | P40040 saccharomyc | 232 | 48 | 37.8 | 184 | 2 | O68GZ9 | O68gz9 human immun |
| 160 | 49 | 38.6 | 431 | 2 | O74KT2 | O74ky2 lactobacill | 233 | 48 | 37.8 | 184 | 2 | O68H01 | O68h01 rumiococcu |
| 161 | 49 | 38.6 | 458 | 2 | O6PDS5 | O6pds5 mus musculu | 234 | 48 | 37.8 | 184 | 2 | O68H40 | O68h40 eubacterium |
| 162 | 49 | 38.6 | 462 | 1 | TRPE_LBPPI | P24463 leptospira | 235 | 48 | 37.8 | 184 | 2 | O68H45 | O68h45 eubacterium |
| 163 | 49 | 38.6 | 473 | 1 | LCBI_HUMAN | O15269 homo sapien | 236 | 48 | 37.8 | 184 | 2 | O68H56 | O68h56 eubacterium |
| 164 | 49 | 38.6 | 475 | 2 | O14917 | O14917 homo sapien | 237 | 48 | 37.8 | 184 | 2 | O68H59 | O68h59 clostridium |
| 165 | 49 | 38.6 | 485 | 1 | SYE_CLOAB | O97kc9 clostridium | 238 | 48 | 37.8 | 184 | 2 | O68H62 | O68h62 clostridium |
| 166 | 49 | 38.6 | 495 | 2 | O9DBS6 | O9db85 mus musculu | 239 | 48 | 37.8 | 184 | 2 | O68H80 | O68h80 butyrivibri |
| 167 | 49 | 38.6 | 504 | 1 | NORR_ECOS7 | O8r854 escherichia | 240 | 48 | 37.8 | 184 | 2 | O65H00 | O65h00 bacillus li |
| 168 | 49 | 38.6 | 504 | 1 | NORR_ECOS6 | O8r854 escherichia | 241 | 48 | 37.8 | 184 | 2 | O74076 | O74076 human immun |
| 169 | 49 | 38.6 | 504 | 1 | NORR_ECOS6 | O8r854 escherichia | 242 | 48 | 37.8 | 184 | 2 | VT1A_MOUSE | O9151 rattus norv |
| 170 | 49 | 38.6 | 504 | 1 | NORR_ECOS6 | P37013 escherichia | 243 | 48 | 37.8 | 224 | 1 | VT1A_MOUSE | O9151 rattus norv |
| 171 | 49 | 38.6 | 506 | 1 | NORR_SHIFL | P59402 shigella fl | 244 | 48 | 37.8 | 226 | 2 | O37049 | O37049 porcine epi |
| 172 | 49 | 38.6 | 506 | 1 | NORR_SALTY | O8r4c6 salmonella | 245 | 48 | 37.8 | 226 | 2 | O37351 | O37351 porcine epi |
| 173 | 49 | 38.6 | 512 | 2 | O6DBR9 | O8rmj8 erwinia car | 246 | 48 | 37.8 | 226 | 2 | O72839 | O72839 porcine epi |
| 174 | 49 | 38.6 | 513 | 2 | O6WUL7 | O6wul7 erwinia car | 247 | 48 | 37.8 | 226 | 2 | O610S8 | O610s8 porcine epi |
| 175 | 49 | 38.6 | 534 | 1 | CN1B_BOVIN | O01061 bos taurus | 248 | 48 | 37.8 | 235 | 1 | O8TSC8 | O8tsc8 methanosarc |
| 176 | 49 | 38.6 | 535 | 1 | CN1B_MOUSE | O01065 mus musculu | 249 | 48 | 37.8 | 254 | 1 | WI12_CAEEL | O23306 caenorhabdi |
| 177 | 49 | 38.6 | 535 | 1 | CN1B_RAT | O01066 rattus norv | 250 | 48 | 37.8 | 294 | 2 | O6BED9 | O6bed9 caenorhabdi |

| | | | | | | | | | | | | | |
|-----|------|------|------|---|------------|--------------------|-----|------|------|------|---|------------|--------------------|
| 251 | 48 | 37.8 | 299 | 2 | Q84SQ1 | Q84sq1 oryza sativ | 324 | 47.5 | 37.4 | 294 | 2 | Q76190 | Q76190 human immun |
| 252 | 48 | 37.8 | 299 | 2 | Q9HUA1 | Q9hual pseudomonas | 325 | 47.5 | 37.4 | 342 | 2 | Q91U83 | Q91u83 human immun |
| 253 | 48 | 37.8 | 309 | 2 | Q17902 | Q17902 caenorhabdi | 326 | 47.5 | 37.4 | 405 | 2 | Q66LA6 | Q66la6 human immun |
| 254 | 48 | 37.8 | 312 | 2 | Q82KX3 | Q82kx3 salmonella | 327 | 47.5 | 37.4 | 486 | 2 | Q72MJ2 | Q72mj2 human immun |
| 255 | 48 | 37.8 | 335 | 2 | Q8YFZ4 | Q8yFz4 anabaena sp | 328 | 47.5 | 37.4 | 495 | 2 | Q748Z6 | Q748z6 human immun |
| 256 | 48 | 37.8 | 338 | 2 | Q7WZ12 | Q7wz12 haemophilus | 329 | 47.5 | 37.4 | 583 | 2 | Q8EP19 | Q8ep19 human immun |
| 257 | 48 | 37.8 | 428 | 2 | Q7XT74 | Q7xt74 oryza sativ | 330 | 47.5 | 37.4 | 846 | 2 | Q6BBR0 | Q6bbR0 human immun |
| 258 | 48 | 37.8 | 441 | 2 | Q8Y6G5 | Q8y6g5 listeria mo | 331 | 47.5 | 37.4 | 849 | 2 | Q8J9B8 | Q8j9B8 human immun |
| 259 | 48 | 37.8 | 442 | 2 | Q92AT6 | Q92at6 listeria in | 332 | 47.5 | 37.4 | 861 | 2 | Q6XJ54 | Q6xj54 human immun |
| 260 | 48 | 37.8 | 442 | 2 | Q71YU6 | Q71yu6 listeria mo | 333 | 47.5 | 37.4 | 863 | 2 | Q6UPP6 | Q6upP6 human immun |
| 261 | 48 | 37.8 | 446 | 2 | Q8D2V4 | Q8d2v4 wigglewort | 334 | 47.5 | 37.4 | 869 | 2 | Q8ULP9 | Q8ulP9 human immun |
| 262 | 48 | 37.8 | 447 | 1 | SR54_SULSO | SR54 sulfolobus | 335 | 47.5 | 37.4 | 874 | 2 | Q8UL68 | Q8ul68 human immun |
| 263 | 48 | 37.8 | 457 | 1 | Q74IW2 | Q74iw2 lactobacill | 336 | 47.5 | 37.4 | 874 | 2 | Q8UL68 | Q8ul68 human immun |
| 264 | 48 | 37.8 | 462 | 1 | UTAI_YEAST | Q1059 saccharomyc | 337 | 47.5 | 37.4 | 1119 | 2 | Q6TUP9 | Q6tup9 human immun |
| 265 | 48 | 37.8 | 517 | 2 | Q63OH3 | Q63oh3 bacillus ce | 338 | 47.5 | 37.0 | 184 | 2 | Q8KVA1 | Q8kva1 human immun |
| 266 | 48 | 37.8 | 517 | 2 | Q81JMS | Q81jms bacillus an | 339 | 47.5 | 37.0 | 184 | 2 | Q8KVE4 | Q8kve4 human immun |
| 267 | 48 | 37.8 | 517 | 2 | Q6HAK8 | Q6hak8 bacillus th | 340 | 47.5 | 37.0 | 184 | 2 | Q68G17 | Q68g17 human immun |
| 268 | 48 | 37.8 | 530 | 2 | Q72X14 | Q72x14 bacillus ce | 341 | 47.5 | 37.0 | 184 | 2 | Q68H43 | Q68h43 human immun |
| 269 | 48 | 37.8 | 536 | 2 | Q814J7 | Q814j7 bacillus ce | 342 | 47.5 | 37.0 | 184 | 2 | Q68H67 | Q68h67 human immun |
| 270 | 48 | 37.8 | 540 | 2 | Q8FP25 | Q8fp25 corynebacte | 343 | 47.5 | 37.0 | 186 | 2 | Q8KVD7 | Q8kvd7 human immun |
| 271 | 48 | 37.8 | 553 | 2 | Q9WGG2 | Q9wgg2 hyphartria | 344 | 47.5 | 37.0 | 186 | 2 | Q8KXV5 | Q8kxv5 human immun |
| 272 | 48 | 37.8 | 594 | 2 | Q8EMV1 | Q8emv1 oceanobacil | 345 | 47.5 | 37.0 | 190 | 2 | Q54564 | Q54564 human immun |
| 273 | 48 | 37.8 | 647 | 2 | Q8CA10 | Q8ca10 mus musculu | 346 | 47.5 | 37.0 | 199 | 2 | Q7MV58 | Q7mv58 porphyromon |
| 274 | 48 | 37.8 | 654 | 2 | Q97563 | Q97563 sulfolobus | 347 | 47.5 | 37.0 | 215 | 1 | AROD_METKA | AROD metka |
| 275 | 48 | 37.8 | 856 | 2 | Q6APR6 | Q6apR6 desulfotale | 348 | 47.5 | 37.0 | 281 | 2 | Q48759 | Q48759 arabidopsis |
| 276 | 48 | 37.8 | 914 | 1 | SYA_PYRAB | Q9YJ36 pyrococcus | 349 | 47.5 | 37.0 | 312 | 2 | Q8ZLM0 | Q8zlm0 human immun |
| 277 | 48 | 37.8 | 1027 | 2 | Q9WPP5 | Q9wpp5 chlamydiae | 350 | 47.5 | 37.0 | 370 | 2 | Q6MR14 | Q6mr14 human immun |
| 278 | 48 | 37.8 | 1213 | 2 | Q8IC20 | Q8ic20 plasmidium | 351 | 47.5 | 37.0 | 407 | 1 | MYC_ASTVU | MYC astvu |
| 279 | 48 | 37.8 | 1269 | 2 | Q01632 | Q01632 caenorhabdi | 352 | 47.5 | 37.0 | 453 | 2 | Q8BLJ3 | Q8blj3 human immun |
| 280 | 48 | 37.8 | 1273 | 2 | Q44928 | Q44928 caenorhabdi | 353 | 47.5 | 37.0 | 459 | 2 | Q7MEF6 | Q7mef6 human immun |
| 281 | 48 | 37.8 | 1762 | 2 | Q6A070 | Q6a070 mus musculu | 354 | 47.5 | 37.0 | 459 | 2 | Q87HY2 | Q87hy2 vibrio para |
| 282 | 48 | 37.8 | 1964 | 2 | Q93522 | Q93522 xenopus lae | 355 | 47.5 | 37.0 | 459 | 2 | Q8D7E7 | Q8d7e7 human immun |
| 283 | 48 | 37.8 | 4437 | 2 | Q8GCP3 | Q8gcp3 streptomyce | 356 | 47.5 | 37.0 | 472 | 2 | Q98OR0 | Q98or0 human immun |
| 284 | 47.5 | 37.4 | 149 | 2 | Q3YD13 | Q3yD13 drosophila | 357 | 47.5 | 37.0 | 493 | 2 | Q732A5 | Q732a5 human immun |
| 285 | 47.5 | 37.4 | 155 | 2 | Q73383 | Q73383 human immun | 358 | 47.5 | 37.0 | 493 | 2 | Q8A2P4 | Q8a2p4 human immun |
| 286 | 47.5 | 37.4 | 156 | 2 | Q91WS8 | Q91ws8 human immun | 359 | 47.5 | 37.0 | 508 | 2 | Q6HUV5 | Q6huv5 human immun |
| 287 | 47.5 | 37.4 | 168 | 2 | Q8Q2G9 | Q8q2g9 human immun | 360 | 47.5 | 37.0 | 510 | 2 | Q636N5 | Q636n5 human immun |
| 288 | 47.5 | 37.4 | 171 | 2 | Q7OR72 | Q7or72 human immun | 361 | 47.5 | 37.0 | 510 | 2 | Q8R8K4 | Q8r8k4 human immun |
| 289 | 47.5 | 37.4 | 178 | 2 | Q99FP39 | Q99f39 human immun | 362 | 47.5 | 37.0 | 510 | 2 | Q732T5 | Q732t5 human immun |
| 290 | 47.5 | 37.4 | 184 | 2 | Q8Q1U2 | Q8q1u2 human immun | 363 | 47.5 | 37.0 | 510 | 2 | Q81WP5 | Q81wp5 human immun |
| 291 | 47.5 | 37.4 | 184 | 2 | Q8Q1U3 | Q8q1u3 human immun | 364 | 47.5 | 37.0 | 510 | 2 | Q6HF24 | Q6hf24 human immun |
| 292 | 47.5 | 37.4 | 184 | 2 | Q8Q1U4 | Q8q1u4 human immun | 365 | 47.5 | 37.0 | 553 | 2 | Q7MBB4 | Q7mbb4 human immun |
| 293 | 47.5 | 37.4 | 184 | 2 | Q8Q1U5 | Q8q1u5 human immun | 366 | 47.5 | 37.0 | 577 | 2 | Q9ST62 | Q9st62 human immun |
| 294 | 47.5 | 37.4 | 184 | 2 | Q8Q1U6 | Q8q1u6 human immun | 367 | 47.5 | 37.0 | 608 | 2 | Q42620 | Q42620 magnaporthe |
| 295 | 47.5 | 37.4 | 184 | 2 | Q8Q1U7 | Q8q1u7 human immun | 368 | 47.5 | 37.0 | 627 | 2 | Q9KPY2 | Q9kpy2 human immun |
| 296 | 47.5 | 37.4 | 184 | 2 | Q8Q1U8 | Q8q1u8 human immun | 369 | 47.5 | 37.0 | 657 | 2 | Q8APU5 | Q8apu5 human immun |
| 297 | 47.5 | 37.4 | 184 | 2 | Q8Q1U9 | Q8q1u9 human immun | 370 | 47.5 | 37.0 | 659 | 1 | SPA2_SYNY3 | SPA2 syny3 |
| 298 | 47.5 | 37.4 | 184 | 2 | Q8Q1V0 | Q8q1v0 human immun | 371 | 47.5 | 37.0 | 667 | 2 | Q5462 | Q5462 human immun |
| 299 | 47.5 | 37.4 | 184 | 2 | Q8Q1V1 | Q8q1v1 human immun | 372 | 47.5 | 37.0 | 689 | 2 | Q89ZV9 | Q89zv9 human immun |
| 300 | 47.5 | 37.4 | 184 | 2 | Q90C08 | Q90c08 human immun | 373 | 47.5 | 37.0 | 749 | 2 | Q9RPM1 | Q9rpm1 human immun |
| 301 | 47.5 | 37.4 | 186 | 2 | Q7SKV1 | Q7skv1 human immun | 374 | 47.5 | 37.0 | 759 | 1 | BURL_THFAC | BURL thfac |
| 302 | 47.5 | 37.4 | 195 | 2 | Q7ORC5 | Q7orc5 human immun | 375 | 47.5 | 37.0 | 804 | 2 | Q8A7T2 | Q8a7t2 human immun |
| 303 | 47.5 | 37.4 | 196 | 2 | Q9JB55 | Q9jb55 human immun | 376 | 47.5 | 37.0 | 863 | 2 | Q76148 | Q76148 human immun |
| 304 | 47.5 | 37.4 | 197 | 2 | Q6SUT1 | Q6sut1 human immun | 377 | 47.5 | 37.0 | 867 | 2 | Q7QBJ3 | Q7qbj3 human immun |
| 305 | 47.5 | 37.4 | 199 | 2 | Q7SKT3 | Q7skt3 human immun | 378 | 47.5 | 37.0 | 999 | 2 | Q6GIM3 | Q6gim3 human immun |
| 306 | 47.5 | 37.4 | 199 | 2 | Q7ZNI0 | Q7zni0 human immun | 379 | 47.5 | 37.0 | 1066 | 2 | Q93W58 | Q93w58 human immun |
| 307 | 47.5 | 37.4 | 202 | 2 | Q6J8T0 | Q6j8t0 human immun | 380 | 47.5 | 37.0 | 1067 | 2 | Q98Z57 | Q98z57 human immun |
| 308 | 47.5 | 37.4 | 202 | 2 | Q90N01 | Q90n01 human immun | 381 | 47.5 | 37.0 | 1198 | 2 | Q04538 | Q04538 human immun |
| 309 | 47.5 | 37.4 | 202 | 2 | Q6AL44 | Q6al44 human immun | 382 | 47.5 | 37.0 | 1290 | 2 | Q9S1A7 | Q9s1a7 human immun |
| 310 | 47.5 | 37.4 | 203 | 2 | Q8J8H4 | Q8j8h4 human immun | 383 | 47.5 | 37.0 | 1291 | 2 | Q8RGT3 | Q8rgt3 human immun |
| 311 | 47.5 | 37.4 | 204 | 2 | Q6RHL9 | Q6rhl9 human immun | 384 | 47.5 | 37.0 | 1291 | 2 | Q9RNB9 | Q9rnb9 human immun |
| 312 | 47.5 | 37.4 | 205 | 2 | Q8J8I6 | Q8j8i6 human immun | 385 | 47.5 | 37.0 | 2156 | 2 | Q81DB7 | Q81db7 human immun |
| 313 | 47.5 | 37.4 | 208 | 2 | Q8QO11 | Q8qo11 human immun | 386 | 47.5 | 37.0 | 2816 | 2 | Q8G983 | Q8g983 human immun |
| 314 | 47.5 | 37.4 | 209 | 2 | Q8US45 | Q8us45 human immun | 387 | 47.5 | 37.0 | 4467 | 2 | Q9J3B9 | Q9j3b9 human immun |
| 315 | 47.5 | 37.4 | 210 | 2 | Q7OQW2 | Q7oqw2 human immun | 388 | 47.5 | 37.0 | 4470 | 2 | Q66WN5 | Q66wn5 human immun |
| 316 | 47.5 | 37.4 | 211 | 2 | Q7OQW4 | Q7oqw4 human immun | 389 | 47.5 | 37.0 | 7176 | 1 | RIAB_CVMA5 | RIAB cvma5 |
| 317 | 47.5 | 37.4 | 211 | 2 | Q8AD04 | Q8ad04 human immun | 390 | 47.5 | 37.0 | 7178 | 2 | Q66WN6 | Q66wn6 human immun |
| 318 | 47.5 | 37.4 | 216 | 2 | Q700Q1 | Q70q01 human immun | 391 | 46.5 | 36.6 | 79 | 2 | Q70493 | Q70493 human immun |
| 319 | 47.5 | 37.4 | 217 | 2 | Q700S1 | Q70qs1 human immun | 392 | 46.5 | 36.6 | 104 | 2 | Q78877 | Q78877 human immun |
| 320 | 47.5 | 37.4 | 219 | 2 | Q7ZBA3 | Q7zba3 human immun | 393 | 46.5 | 36.6 | 104 | 2 | Q78881 | Q78881 human immun |
| 321 | 47.5 | 37.4 | 221 | 2 | Q7ZP24 | Q7zpz4 human immun | 394 | 46.5 | 36.6 | 159 | 2 | Q9JBS7 | Q9jbs7 human immun |
| 322 | 47.5 | 37.4 | 224 | 2 | Q7ZME5 | Q7zmes human immun | 395 | 46.5 | 36.6 | 161 | 2 | Q70R49 | Q70r49 human immun |
| 323 | 47.5 | 37.4 | 294 | 2 | Q76168 | Q76168 human immun | 396 | 46.5 | 36.6 | 162 | 2 | Q70QK1 | Q70qk1 human immun |

| | | | | | | | | | | | | | | | | | |
|-----|------|------|-----|---|------------|------------|-------------|-------|-----|------|------|------|--------|-------------|-------------|--------------|-------|
| 397 | 46.5 | 36.6 | 168 | 2 | 06J4B0 | 06J4B0 | human | immun | 470 | 46.5 | 36.6 | 402 | 2 | 066LA3 | 066LA3 | human | immun |
| 398 | 46.5 | 36.6 | 169 | 2 | 070QZ6 | 070QZ6 | human | immun | 471 | 46.5 | 36.6 | 409 | 2 | 041635 | 041635 | human | immun |
| 399 | 46.5 | 36.6 | 169 | 2 | 070R29 | 070R29 | human | immun | 472 | 46.5 | 426 | 2 | 087QW7 | 087QW7 | vibrio | para | |
| 400 | 46.5 | 36.6 | 176 | 2 | 070R40 | 070R40 | human | immun | 473 | 46.5 | 36.6 | 428 | 2 | 061PPI | 061PPI | photobacter | |
| 401 | 46.5 | 36.6 | 183 | 2 | 09DVA1 | 09DVA1 | human | immun | 474 | 46.5 | 36.6 | 428 | 2 | 09KSZ5 | 09KSZ5 | vibrio | choi |
| 402 | 46.5 | 36.6 | 190 | 2 | 08US55 | 08US55 | human | immun | 475 | 46.5 | 36.6 | 429 | 2 | 07MLV1 | 07MLV1 | vibrio | vuln |
| 403 | 46.5 | 36.6 | 191 | 2 | 070R37 | 070R37 | human | immun | 476 | 46.5 | 36.6 | 462 | 2 | 082VU0 | 082VU0 | nitrosomona | |
| 404 | 46.5 | 36.6 | 194 | 2 | 091VV5 | 091VV5 | human | immun | 477 | 46.5 | 36.6 | 486 | 2 | 08RC59 | 08RC59 | thermoanaer | |
| 405 | 46.5 | 36.6 | 195 | 2 | 070525 | 070525 | human | immun | 478 | 46.5 | 588 | 2 | 0855G1 | 0855G1 | oryza | saliv | |
| 406 | 46.5 | 36.6 | 195 | 2 | 07ZND6 | 07ZND6 | human | immun | 479 | 46.5 | 594 | 2 | 09POM8 | 09POM8 | ureaplasma | | |
| 407 | 46.5 | 36.6 | 195 | 2 | 09QNX2 | 09QNX2 | human | immun | 480 | 46.5 | 36.6 | 801 | 2 | 09MMU9 | 09MMU9 | human | immun |
| 408 | 46.5 | 36.6 | 196 | 2 | 070R78 | 070R78 | human | immun | 481 | 46.5 | 36.6 | 847 | 2 | 09MTS1 | 09MTS1 | human | immun |
| 409 | 46.5 | 36.6 | 197 | 2 | 06SU01 | 06SU01 | human | immun | 482 | 46.5 | 36.6 | 849 | 2 | 09YKT4 | 09YKT4 | human | immun |
| 410 | 46.5 | 36.6 | 197 | 2 | 06SU08 | 06SU08 | human | immun | 483 | 46.5 | 36.6 | 849 | 2 | 09YKT7 | 09YKT7 | human | immun |
| 411 | 46.5 | 36.6 | 197 | 2 | 06SU08 | 06SU08 | human | immun | 484 | 46.5 | 36.6 | 850 | 2 | 090BY2 | 090BY2 | human | immun |
| 412 | 46.5 | 36.6 | 197 | 2 | 06SU09 | 06SU09 | human | immun | 485 | 46.5 | 36.6 | 858 | 2 | 06UPF9 | 06UPF9 | human | immun |
| 413 | 46.5 | 36.6 | 197 | 2 | 06SU09 | 06SU09 | human | immun | 486 | 46.5 | 36.6 | 858 | 2 | 073293 | 073293 | human | immun |
| 414 | 46.5 | 36.6 | 197 | 2 | 06SU02 | 06SU02 | human | immun | 487 | 46.5 | 36.6 | 1366 | 2 | 08KXN9 | 08KXN9 | streptococc | |
| 415 | 46.5 | 36.6 | 197 | 2 | 06SUW3 | 06SUW3 | human | immun | 488 | 46.5 | 36.6 | 1366 | 2 | 08P2F2 | 08P2F2 | streptococc | |
| 416 | 46.5 | 36.6 | 197 | 2 | 09DVI5 | 09DVI5 | human | immun | 489 | 46.5 | 36.6 | 1372 | 2 | 087BN3 | 087BN3 | chaetocospae | |
| 417 | 46.5 | 36.6 | 198 | 2 | 07SKS3 | 07SKS3 | human | immun | 490 | 46.5 | 36.6 | 1373 | 1 | RPC2 | CHAGL | wolfinella s | |
| 418 | 46.5 | 36.6 | 199 | 2 | 07SU41 | 07SU41 | human | immun | 491 | 46 | 36.2 | 90 | 2 | 07MS15 | 07MS15 | plasmodium | |
| 419 | 46.5 | 36.6 | 199 | 2 | 08ALM1 | 08ALM1 | human | immun | 492 | 46 | 36.2 | 100 | 2 | 07RM11 | 07RM11 | populus tre | |
| 420 | 46.5 | 36.6 | 200 | 1 | COAE_BACAN | COAE_BACAN | | | 493 | 46 | 36.2 | 114 | 2 | 08S313 | 08S313 | bulfolobus | |
| 421 | 46.5 | 36.6 | 200 | 2 | 0633I3 | 0633I3 | bacillus an | | 494 | 46 | 36.2 | 118 | 1 | Y352 | SUTSO | capetium an | |
| 422 | 46.5 | 36.6 | 200 | 2 | 06HCU7 | 06HCU7 | bacillus th | | 495 | 46 | 36.2 | 124 | 2 | 06RJZ7 | 06RJZ7 | parachlamyd | |
| 423 | 46.5 | 36.6 | 201 | 2 | 097D99 | 097D99 | clostridium | | 496 | 46 | 36.2 | 124 | 2 | 06M9J5 | 06M9J5 | pluteilla xy | |
| 424 | 46.5 | 36.6 | 201 | 2 | 0619P6 | 0619P6 | human | immun | 497 | 46 | 36.2 | 131 | 2 | 09JGU5 | 09JGU5 | uncultured | |
| 425 | 46.5 | 36.6 | 201 | 2 | 07SU31 | 07SU31 | human | immun | 498 | 46 | 36.2 | 184 | 2 | 08KH65 | 08KH65 | uncultured | |
| 426 | 46.5 | 36.6 | 201 | 2 | 07SU33 | 07SU33 | human | immun | 499 | 46 | 36.2 | 184 | 2 | 08KH00 | 08KH00 | uncultured | |
| 427 | 46.5 | 36.6 | 201 | 2 | 07SU42 | 07SU42 | human | immun | 500 | 46 | 36.2 | 184 | 2 | 08KHJ9 | 08KHJ9 | uncultured | |
| 428 | 46.5 | 36.6 | 202 | 2 | 07ZP14 | 07ZP14 | human | immun | 501 | 46 | 36.2 | 184 | 2 | 08KH184 | 08KH184 | uncultured | |
| 429 | 46.5 | 36.6 | 202 | 2 | 08AL57 | 08AL57 | human | immun | 502 | 46 | 36.2 | 184 | 2 | 08KV31 | 08KV31 | uncultured | |
| 430 | 46.5 | 36.6 | 203 | 2 | 070518 | 070518 | human | immun | 503 | 46 | 36.2 | 184 | 2 | 08KV49 | 08KV49 | uncultured | |
| 431 | 46.5 | 36.6 | 203 | 2 | 070522 | 070522 | human | immun | 504 | 46 | 36.2 | 184 | 2 | 08KV63 | 08KV63 | uncultured | |
| 432 | 46.5 | 36.6 | 203 | 2 | 070529 | 070529 | human | immun | 505 | 46 | 36.2 | 184 | 2 | 08KV65 | 08KV65 | uncultured | |
| 433 | 46.5 | 36.6 | 203 | 2 | 0705G2 | 0705G2 | human | immun | 506 | 46 | 36.2 | 184 | 2 | 08KV72 | 08KV72 | uncultured | |
| 434 | 46.5 | 36.6 | 203 | 2 | 07SU04 | 07SU04 | human | immun | 507 | 46 | 36.2 | 184 | 2 | 08KV87 | 08KV87 | uncultured | |
| 435 | 46.5 | 36.6 | 203 | 2 | 07SU09 | 07SU09 | human | immun | 508 | 46 | 36.2 | 184 | 2 | 08KV98 | 08KV98 | uncultured | |
| 436 | 46.5 | 36.6 | 203 | 2 | 08AL98 | 08AL98 | human | immun | 509 | 46 | 36.2 | 184 | 2 | 08KVA3 | 08KVA3 | uncultured | |
| 437 | 46.5 | 36.6 | 204 | 2 | 070540 | 070540 | human | immun | 510 | 46 | 36.2 | 184 | 2 | 08KV80 | 08KV80 | uncultured | |
| 438 | 46.5 | 36.6 | 205 | 2 | 07SKV0 | 07SKV0 | human | immun | 511 | 46 | 36.2 | 184 | 2 | 08KV87 | 08KV87 | uncultured | |
| 439 | 46.5 | 36.6 | 205 | 2 | 07SU35 | 07SU35 | human | immun | 512 | 46 | 36.2 | 184 | 2 | 08KV82 | 08KV82 | uncultured | |
| 440 | 46.5 | 36.6 | 206 | 2 | 07SU37 | 07SU37 | human | immun | 513 | 46 | 36.2 | 184 | 2 | 08KV61 | 08KV61 | uncultured | |
| 441 | 46.5 | 36.6 | 206 | 2 | 07SU58 | 07SU58 | human | immun | 514 | 46 | 36.2 | 184 | 2 | 08KV67 | 08KV67 | uncultured | |
| 442 | 46.5 | 36.6 | 206 | 2 | 07SU08 | 07SU08 | human | immun | 515 | 46 | 36.2 | 184 | 2 | 08KV80 | 08KV80 | uncultured | |
| 443 | 46.5 | 36.6 | 206 | 2 | 07SU12 | 07SU12 | human | immun | 516 | 46 | 36.2 | 184 | 2 | 08KV11 | 08KV11 | uncultured | |
| 444 | 46.5 | 36.6 | 207 | 2 | 06SU58 | 06SU58 | human | immun | 517 | 46 | 36.2 | 184 | 2 | 08KV11 | 08KV11 | uncultured | |
| 445 | 46.5 | 36.6 | 209 | 2 | 07SU68 | 07SU68 | human | immun | 518 | 46 | 36.2 | 184 | 2 | 08KV86 | 08KV86 | uncultured | |
| 446 | 46.5 | 36.6 | 214 | 2 | 08J9D8 | 08J9D8 | human | immun | 519 | 46 | 36.2 | 184 | 2 | 08KVNO | 08KVNO | uncultured | |
| 447 | 46.5 | 36.6 | 215 | 2 | 08J9D8 | 08J9D8 | human | immun | 520 | 46 | 36.2 | 184 | 2 | 08KVP7 | 08KVP7 | uncultured | |
| 448 | 46.5 | 36.6 | 218 | 2 | 07SU08 | 07SU08 | human | immun | 521 | 46 | 36.2 | 184 | 2 | 06BH36 | 06BH36 | lactobacilli | |
| 449 | 46.5 | 36.6 | 218 | 2 | 07SU01 | 07SU01 | human | immun | 522 | 46 | 36.2 | 184 | 2 | 06BH41 | 06BH41 | eubacterium | |
| 450 | 46.5 | 36.6 | 218 | 2 | 09WLR7 | 09WLR7 | human | immun | 523 | 46 | 36.2 | 184 | 2 | 06BH42 | 06BH42 | eubacterium | |
| 451 | 46.5 | 36.6 | 220 | 2 | 07SU04 | 07SU04 | human | immun | 524 | 46 | 36.2 | 184 | 2 | 06BH68 | 06BH68 | clostridium | |
| 452 | 46.5 | 36.6 | 220 | 2 | 07ZMF5 | 07ZMF5 | human | immun | 525 | 46 | 36.2 | 185 | 2 | 06BS72 | 06BS72 | uncultured | |
| 453 | 46.5 | 36.6 | 223 | 2 | 07SU39 | 07SU39 | human | immun | 526 | 46 | 36.2 | 185 | 2 | 06J157 | 06J157 | chlamydia p | |
| 454 | 46.5 | 36.6 | 265 | 2 | 09WTR3 | 09WTR3 | human | immun | 527 | 46 | 36.2 | 186 | 2 | 08KVQ1 | 08KVQ1 | uncultured | |
| 455 | 46.5 | 36.6 | 276 | 2 | 09WE10 | 09WE10 | human | immun | 528 | 46 | 36.2 | 216 | 2 | 08CTQ3 | 08CTQ3 | staphylococ | |
| 456 | 46.5 | 36.6 | 277 | 2 | 08D8M8 | 08D8M8 | vibrio | vuln | 529 | 46 | 36.2 | 222 | 2 | 08ECT2 | 08ECT2 | shewanella | |
| 457 | 46.5 | 36.6 | 278 | 2 | 076212 | 076212 | human | immun | 530 | 46 | 36.2 | 227 | 2 | 06LVS1 | 06LVS1 | methanococc | |
| 458 | 46.5 | 36.6 | 288 | 2 | 073316 | 073316 | human | immun | 531 | 46 | 36.2 | 227 | 2 | 06ZWT8 | 06ZWT8 | homo sapien | |
| 459 | 46.5 | 36.6 | 301 | 2 | 070212 | 070212 | human | immun | 532 | 46 | 36.2 | 292 | 2 | 07Z6A8 | 07Z6A8 | homo sapien | |
| 460 | 46.5 | 36.6 | 327 | 2 | 0871A9 | 0871A9 | vibrio | para | 533 | 46 | 36.2 | 292 | 2 | 0896D1 | 0896D1 | clostridium | |
| 461 | 46.5 | 36.6 | 328 | 2 | 091U84 | 091U84 | human | immun | 534 | 46 | 36.2 | 298 | 2 | 0892F7 | 0892F7 | clostridium | |
| 462 | 46.5 | 36.6 | 347 | 2 | 07ZP53 | 07ZP53 | human | immun | 535 | 46 | 36.2 | 306 | 2 | 08XIDS | 08XIDS | clostridium | |
| 463 | 46.5 | 36.6 | 358 | 2 | 08QB00 | 08QB00 | human | immun | 536 | 46 | 36.2 | 335 | 1 | FLIG_THEMEA | FLIG_THEMEA | thermotoga | |
| 464 | 46.5 | 36.6 | 359 | 2 | P87967 | P87967 | human | immun | 537 | 46 | 36.2 | 336 | 2 | 069F81 | 069F81 | h | |
| 465 | 46.5 | 36.6 | 359 | 2 | 08OAZ6 | 08OAZ6 | human | immun | 538 | 46 | 36.2 | 340 | 1 | YMA1_ARCFU | YMA1_ARCFU | archaeoglob | |
| 466 | 46.5 | 36.6 | 359 | 2 | 08OAZ7 | 08OAZ7 | human | immun | 539 | 46 | 36.2 | 382 | 2 | 069BD1 | 069BD1 | campylobact | |
| 467 | 46.5 | 36.6 | 359 | 2 | 08QB01 | 08QB01 | human | immun | 540 | 46 | 36.2 | 382 | 2 | 069BT1 | 069BT1 | campylobact | |
| 468 | 46.5 | 36.6 | 386 | 2 | 08Q843 | 08Q843 | human | immun | 541 | 46 | 36.2 | 401 | 2 | 08VR20 | 08VR20 | chlamydophi | |
| 469 | 46.5 | 36.6 | 386 | 2 | 08Q846 | 08Q846 | human | immun | 542 | 46 | 36.2 | 401 | 2 | 090HW7 | 090HW7 | human | immun |

| | | | | | | | | | | | | | | | | |
|-----|------|------|------|---|------------|------------|--------------|-----|------|------|-----|---|------------|------------|-------|-------|
| 543 | 46 | 36.2 | 403 | 2 | Q9BPM3 | Q9BPM3 | toxoplasma | 616 | 45.5 | 35.8 | 194 | 2 | Q6VG99 | Q6VG99 | human | immun |
| 544 | 46 | 36.2 | 408 | 2 | Q83WK4 | Q83WK4 | chlamydia | 617 | 45.5 | 35.8 | 195 | 2 | Q7ZNG0 | Q7ZNG0 | human | immun |
| 545 | 46 | 36.2 | 417 | 2 | Q59792 | Q59792 | chlamydia p | 618 | 45.5 | 35.8 | 196 | 2 | Q68ID5 | Q68ID5 | human | immun |
| 546 | 46 | 36.2 | 419 | 2 | Q972U4 | Q972U4 | sulfolobus | 619 | 45.5 | 35.8 | 196 | 2 | Q9JB10 | Q9JB10 | human | immun |
| 547 | 46 | 36.2 | 420 | 2 | Q23306 | Q23306 | arabidopsis | 620 | 45.5 | 35.8 | 196 | 2 | Q9JB11 | Q9JB11 | human | immun |
| 548 | 46 | 36.2 | 433 | 2 | Q944W2 | Q944W2 | arabidopsis | 621 | 45.5 | 35.8 | 196 | 2 | Q9JB12 | Q9JB12 | human | immun |
| 549 | 46 | 36.2 | 449 | 2 | Q63611 | Q63611 | bacillus ce | 622 | 45.5 | 35.8 | 196 | 2 | Q9JB10 | Q9JB10 | human | immun |
| 550 | 46 | 36.2 | 449 | 2 | Q732M5 | Q732M5 | bacillus ce | 623 | 45.5 | 35.8 | 196 | 2 | Q9JBK0 | Q9JBK0 | human | immun |
| 551 | 46 | 36.2 | 449 | 2 | Q819W2 | Q819W2 | bacillus ce | 624 | 45.5 | 35.8 | 197 | 2 | Q6SUT5 | Q6SUT5 | human | immun |
| 552 | 46 | 36.2 | 449 | 2 | Q81WJ2 | Q81WJ2 | bacillus an | 625 | 45.5 | 35.8 | 197 | 2 | Q6SUT4 | Q6SUT4 | human | immun |
| 553 | 46 | 36.2 | 449 | 2 | Q6HEX0 | Q6HEX0 | bacillus th | 626 | 45.5 | 35.8 | 197 | 2 | Q6SUT5 | Q6SUT5 | human | immun |
| 554 | 46 | 36.2 | 460 | 1 | IR44_HUMAN | IR44_HUMAN | Q9HWZ3 | 627 | 45.5 | 35.8 | 197 | 2 | Q6SUT6 | Q6SUT6 | human | immun |
| 555 | 46 | 36.2 | 463 | 2 | Q8BSN1 | Q8BSN1 | oceanobacill | 628 | 45.5 | 35.8 | 197 | 2 | Q9JB11 | Q9JB11 | human | immun |
| 556 | 46 | 36.2 | 473 | 2 | Q90990 | Q90990 | gallus gall | 629 | 45.5 | 35.8 | 198 | 2 | Q8J4L4 | Q8J4L4 | human | immun |
| 557 | 46 | 36.2 | 474 | 1 | GCGB_THEMA | GCGB_THEMA | Q9WY57 | 630 | 45.5 | 35.8 | 198 | 2 | Q9JBC6 | Q9JBC6 | human | immun |
| 558 | 46 | 36.2 | 475 | 2 | Q63363 | Q63363 | rattus norv | 631 | 45.5 | 35.8 | 199 | 2 | Q70543 | Q70543 | human | immun |
| 559 | 46 | 36.2 | 477 | 2 | Q68960 | Q68960 | heilcobacte | 632 | 45.5 | 35.8 | 199 | 2 | Q7ZN11 | Q7ZN11 | human | immun |
| 560 | 46 | 36.2 | 477 | 2 | Q25326 | Q25326 | heilcobacte | 633 | 45.5 | 35.8 | 199 | 2 | Q9JBD1 | Q9JBD1 | human | immun |
| 561 | 46 | 36.2 | 477 | 2 | Q92LM7 | Q92LM7 | heilcobacte | 634 | 45.5 | 35.8 | 200 | 1 | COAE_BACCI | COAE_BACCI | | |
| 562 | 46 | 36.2 | 480 | 2 | Q8G4H4 | Q8G4H4 | bifidobacte | 635 | 45.5 | 35.8 | 200 | 1 | COAE_BACCR | COAE_BACCR | | |
| 563 | 46 | 36.2 | 497 | 2 | Q986B0 | Q986B0 | chlamydia p | 636 | 45.5 | 35.8 | 200 | 2 | Q72062 | Q72062 | human | immun |
| 564 | 46 | 36.2 | 497 | 2 | Q9X4G4 | Q9X4G4 | chlamydia p | 637 | 45.5 | 35.8 | 201 | 2 | Q6J9C1 | Q6J9C1 | human | immun |
| 565 | 46 | 36.2 | 497 | 2 | Q9X4G5 | Q9X4G5 | chlamydia p | 638 | 45.5 | 35.8 | 201 | 2 | Q9JBD8 | Q9JBD8 | human | immun |
| 566 | 46 | 36.2 | 513 | 2 | Q6T1H2 | Q6T1H2 | oryza sativ | 639 | 45.5 | 35.8 | 202 | 2 | Q9JB18 | Q9JB18 | human | immun |
| 567 | 46 | 36.2 | 513 | 2 | Q7XSQ5 | Q7XSQ5 | oryza sativ | 640 | 45.5 | 35.8 | 202 | 2 | Q9JB19 | Q9JB19 | human | immun |
| 568 | 46 | 36.2 | 533 | 2 | Q6KCS3 | Q6KCS3 | nicotiana p | 641 | 45.5 | 35.8 | 202 | 2 | Q9JB12 | Q9JB12 | human | immun |
| 569 | 46 | 36.2 | 539 | 1 | CH61_BRAJA | CH61_BRAJA | bradyrhizob | 642 | 45.5 | 35.8 | 202 | 2 | Q9JB12 | Q9JB12 | human | immun |
| 570 | 46 | 36.2 | 542 | 2 | Q7VC71 | Q7VC71 | prochloroco | 643 | 45.5 | 35.8 | 203 | 2 | Q6SUN1 | Q6SUN1 | human | immun |
| 571 | 46 | 36.2 | 543 | 1 | CH60_CHLMU | CH60_CHLMU | chlamydia m | 644 | 45.5 | 35.8 | 203 | 2 | Q9JBB6 | Q9JBB6 | human | immun |
| 572 | 46 | 36.2 | 543 | 1 | CH60_CHLTR | CH60_CHLTR | chlamydia t | 645 | 45.5 | 35.8 | 203 | 2 | Q9JBB8 | Q9JBB8 | human | immun |
| 573 | 46 | 36.2 | 543 | 2 | Q6A114 | Q6A114 | chlamydia t | 646 | 45.5 | 35.8 | 203 | 2 | Q9JBB9 | Q9JBB9 | human | immun |
| 574 | 46 | 36.2 | 544 | 1 | CH60_CHLPN | CH60_CHLPN | chlamydia p | 647 | 45.5 | 35.8 | 203 | 2 | Q9JBC5 | Q9JBC5 | human | immun |
| 575 | 46 | 36.2 | 544 | 1 | CH61_CHLCV | CH61_CHLCV | chlamydia p | 648 | 45.5 | 35.8 | 203 | 2 | Q9JBC9 | Q9JBC9 | human | immun |
| 576 | 46 | 36.2 | 544 | 2 | Q6XNR4 | Q6XNR4 | chlamydia p | 649 | 45.5 | 35.8 | 203 | 2 | Q9JBD2 | Q9JBD2 | human | immun |
| 577 | 46 | 36.2 | 549 | 2 | Q8MXA4 | Q8MXA4 | schistosoma | 650 | 45.5 | 35.8 | 203 | 2 | Q9JBF3 | Q9JBF3 | human | immun |
| 578 | 46 | 36.2 | 550 | 2 | Q8DK21 | Q8DK21 | synecococc | 651 | 45.5 | 35.8 | 204 | 2 | Q6QAA6 | Q6QAA6 | human | immun |
| 579 | 46 | 36.2 | 558 | 1 | CH62_ANASP | CH62_ANASP | anabaena sp | 652 | 45.5 | 35.8 | 204 | 2 | Q6RHM5 | Q6RHM5 | human | immun |
| 580 | 46 | 36.2 | 572 | 1 | DPY4_HUMAN | DPY4_HUMAN | homo sapien | 653 | 45.5 | 35.8 | 204 | 2 | Q9JBD7 | Q9JBD7 | human | immun |
| 581 | 46 | 36.2 | 575 | 2 | Q9Y1U8 | Q9Y1U8 | toxoplasma | 654 | 45.5 | 35.8 | 204 | 2 | Q9JBF5 | Q9JBF5 | human | immun |
| 582 | 46 | 36.2 | 577 | 2 | Q27723 | Q27723 | plasmodium | 655 | 45.5 | 35.8 | 205 | 2 | Q6QAA8 | Q6QAA8 | human | immun |
| 583 | 46 | 36.2 | 579 | 2 | Q974B0 | Q974B0 | plasmodium | 656 | 45.5 | 35.8 | 205 | 2 | Q6RHM4 | Q6RHM4 | human | immun |
| 584 | 46 | 36.2 | 579 | 2 | Q7RFT8 | Q7RFT8 | plasmodium | 657 | 45.5 | 35.8 | 205 | 2 | Q6RHM4 | Q6RHM4 | human | immun |
| 585 | 46 | 36.2 | 580 | 2 | Q81JN9 | Q81JN9 | plasmodium | 658 | 45.5 | 35.8 | 205 | 2 | Q6AL66 | Q6AL66 | human | immun |
| 586 | 46 | 36.2 | 592 | 2 | Q9VAH9 | Q9VAH9 | drosophila | 659 | 45.5 | 35.8 | 206 | 1 | Y140_METJA | Y140_METJA | | |
| 587 | 46 | 36.2 | 609 | 2 | Q7SAN8 | Q7SAN8 | neurospora | 660 | 45.5 | 35.8 | 207 | 2 | Q6SUF2 | Q6SUF2 | human | immun |
| 588 | 46 | 36.2 | 643 | 1 | SYT_PASMT | SYT_PASMT | pasteurella | 661 | 45.5 | 35.8 | 207 | 2 | Q6SUF4 | Q6SUF4 | human | immun |
| 589 | 46 | 36.2 | 644 | 2 | Q9FM17 | Q9FM17 | arabidopsis | 662 | 45.5 | 35.8 | 208 | 2 | Q7SUI3 | Q7SUI3 | human | immun |
| 590 | 46 | 36.2 | 705 | 2 | Q64JY5 | Q64JY5 | plasmodium | 663 | 45.5 | 35.8 | 215 | 2 | Q9YXG5 | Q9YXG5 | human | immun |
| 591 | 46 | 36.2 | 712 | 2 | Q83P57 | Q83P57 | shigella fl | 664 | 45.5 | 35.8 | 216 | 2 | Q9OR12 | Q9OR12 | human | immun |
| 592 | 46 | 36.2 | 797 | 2 | Q8A6B8 | Q8A6B8 | bacteroides | 665 | 45.5 | 35.8 | 217 | 2 | Q73094 | Q73094 | human | immun |
| 593 | 46 | 36.2 | 867 | 2 | Q6BFO1 | Q6BFO1 | brachydanio | 666 | 45.5 | 35.8 | 217 | 2 | Q73095 | Q73095 | human | immun |
| 594 | 46 | 36.2 | 923 | 2 | Q7ZVM0 | Q7ZVM0 | brachydanio | 667 | 45.5 | 35.8 | 217 | 2 | Q73097 | Q73097 | human | immun |
| 595 | 46 | 36.2 | 959 | 2 | Q88NM8 | Q88NM8 | pseudomonas | 668 | 45.5 | 35.8 | 217 | 2 | Q73106 | Q73106 | human | immun |
| 596 | 46 | 36.2 | 963 | 2 | Q91411 | Q91411 | pseudomonas | 669 | 45.5 | 35.8 | 217 | 2 | Q73109 | Q73109 | human | immun |
| 597 | 46 | 36.2 | 970 | 2 | Q886B0 | Q886B0 | pseudomonas | 670 | 45.5 | 35.8 | 217 | 2 | Q73109 | Q73109 | human | immun |
| 598 | 46 | 36.2 | 971 | 2 | Q7RPM3 | Q7RPM3 | plasmodium | 671 | 45.5 | 35.8 | 218 | 2 | Q73099 | Q73099 | human | immun |
| 599 | 46 | 36.2 | 979 | 2 | Q6C909 | Q6C909 | yarrowia li | 672 | 45.5 | 35.8 | 219 | 2 | Q73096 | Q73096 | human | immun |
| 600 | 46 | 36.2 | 1052 | 1 | MSLP_RAT | MSLP_RAT | rattus norv | 673 | 45.5 | 35.8 | 219 | 2 | Q73098 | Q73098 | human | immun |
| 601 | 46 | 36.2 | 1057 | 2 | Q81I33 | Q81I33 | plasmodium | 674 | 45.5 | 35.8 | 219 | 2 | Q73110 | Q73110 | human | immun |
| 602 | 46 | 36.2 | 1284 | 2 | Q7WRJ5 | Q7WRJ5 | anabaena ci | 675 | 45.5 | 35.8 | 219 | 2 | Q73111 | Q73111 | human | immun |
| 603 | 46 | 36.2 | 2787 | 2 | Q961A9 | Q961A9 | microcyctis | 676 | 45.5 | 35.8 | 219 | 2 | Q73112 | Q73112 | human | immun |
| 604 | 46 | 36.2 | 2795 | 2 | Q8RTG5 | Q8RTG5 | microcyctis | 677 | 45.5 | 35.8 | 219 | 2 | Q73113 | Q73113 | human | immun |
| 605 | 46 | 36.2 | 2795 | 2 | Q9RNB1 | Q9RNB1 | microcyctis | 678 | 45.5 | 35.8 | 219 | 2 | Q73114 | Q73114 | human | immun |
| 606 | 46 | 36.2 | 7389 | 1 | BRAL_MOUSE | BRAL_MOUSE | mus muscu | 679 | 45.5 | 35.8 | 219 | 2 | Q73115 | Q73115 | human | immun |
| 607 | 45.5 | 35.8 | 70 | 1 | SLYX_AGRUS | SLYX_AGRUS | agrobacteri | 680 | 45.5 | 35.8 | 219 | 2 | Q73116 | Q73116 | human | immun |
| 608 | 45.5 | 35.8 | 70 | 1 | SLYX_RHIME | SLYX_RHIME | rhizobium m | 681 | 45.5 | 35.8 | 219 | 2 | Q73117 | Q73117 | human | immun |
| 609 | 45.5 | 35.8 | 138 | 2 | Q97UZ6 | Q97UZ6 | rhizobium m | 682 | 45.5 | 35.8 | 219 | 2 | Q73117 | Q73117 | human | immun |
| 610 | 45.5 | 35.8 | 177 | 2 | Q8JF19 | Q8JF19 | human immun | 683 | 45.5 | 35.8 | 219 | 2 | Q73117 | Q73117 | human | immun |
| 611 | 45.5 | 35.8 | 177 | 2 | Q8JF20 | Q8JF20 | human immun | 684 | 45.5 | 35.8 | 220 | 2 | Q73117 | Q73117 | human | immun |
| 612 | 45.5 | 35.8 | 177 | 2 | Q7ZPM0 | Q7ZPM0 | human immun | 685 | 45.5 | 35.8 | 221 | 2 | Q90QY4 | Q90QY4 | human | immun |
| 613 | 45.5 | 35.8 | 183 | 2 | Q7ZNA1 | Q7ZNA1 | human immun | 686 | 45.5 | 35.8 | 221 | 2 | Q730B5 | Q730B5 | human | immun |
| 614 | 45.5 | 35.8 | 183 | 2 | Q9DV55 | Q9DV55 | human immun | 687 | 45.5 | 35.8 | 225 | 2 | Q73083 | Q73083 | human | immun |
| 615 | 45.5 | 35.8 | 187 | 2 | Q6UDP2 | Q6UDP2 | human immun | 688 | 45.5 | 35.8 | 225 | 2 | Q73084 | Q73084 | human | immun |

| | | | | | | | | | | | | | |
|-----|------|------|------|---|------------|------------------------|-----|------|------|-------|---|------------|------------------------|
| 689 | 45.5 | 35.8 | 225 | 2 | Q73085 | Q73085 human immun | 762 | 45.5 | 35.8 | 1434 | 2 | Q9PX54 | Q9PX54 cache valle |
| 690 | 45.5 | 35.8 | 225 | 2 | Q73086 | Q73086 human immun | 763 | 45.5 | 35.8 | 18519 | 2 | Q8ISF6 | Q8ISF6 caenorhabdi |
| 691 | 45.5 | 35.8 | 225 | 2 | Q73087 | Q73087 human immun | 764 | 45.5 | 35.8 | 18534 | 2 | Q8ISF7 | Q8ISF7 caenorhabdi |
| 692 | 45.5 | 35.8 | 225 | 2 | Q73088 | Q73088 human immun | 765 | 45 | 35.4 | 66 | 2 | Q8ER91 | Q8ER91 oceanobacil |
| 693 | 45.5 | 35.8 | 244 | 2 | Q6TX66 | Q6TX66 human immun | 766 | 45 | 35.4 | 91 | 2 | Q8PI21 | Q8PI21 streptococc |
| 694 | 45.5 | 35.8 | 244 | 2 | Q6TXH1 | Q6TXH1 human immun | 767 | 45 | 35.4 | 91 | 2 | Q8D275 | Q8D275 streptococc |
| 695 | 45.5 | 35.8 | 248 | 2 | Q9W1T6 | Q9W1T6 human immun | 768 | 45 | 35.4 | 91 | 2 | Q8E072 | Q8E072 streptococc |
| 696 | 45.5 | 35.8 | 257 | 2 | Q8IXY3 | Q8IXY3 homo sapien | 769 | 45 | 35.4 | 91 | 2 | Q8EE68 | Q8EE68 sulfolobus |
| 697 | 45.5 | 35.8 | 258 | 2 | Q8ACR6 | Q8ACR6 human immun | 770 | 45 | 35.4 | 104 | 2 | Q980B8 | Q980B8 sulfolobus |
| 698 | 45.5 | 35.8 | 258 | 2 | Q9W2N2 | Q9W2N2 human immun | 771 | 45 | 35.4 | 106 | 2 | Q37878 | Q37878 lactobacill |
| 699 | 45.5 | 35.8 | 267 | 2 | Q6JMB2 | Q6JMB2 human immun | 772 | 45 | 35.4 | 106 | 2 | Q8K894 | Q8K894 streptococc |
| 700 | 45.5 | 35.8 | 284 | 2 | Q74IV8 | Q74IV8 lactobacill | 773 | 45 | 35.4 | 118 | 2 | Q67859 | Q67859 aquifex aeo |
| 701 | 45.5 | 35.8 | 289 | 2 | Q83CA6 | Q83CA6 coxiella bu | 774 | 45 | 35.4 | 128 | 2 | Q26723 | Q26723 methanobact |
| 702 | 45.5 | 35.8 | 293 | 2 | Q9J4P0 | Q9J4P0 human immun | 775 | 45 | 35.4 | 136 | 2 | Q842E7 | Q842E7 streptococc |
| 703 | 45.5 | 35.8 | 303 | 2 | Q9J4N0 | Q9J4N0 human immun | 776 | 45 | 35.4 | 154 | 2 | Q8GXV2 | Q8GXV2 arabidopsi |
| 704 | 45.5 | 35.8 | 311 | 2 | Q9TNU1 | Q9TNU1 haplonitriu | 777 | 45 | 35.4 | 164 | 2 | Q7VB06 | Q7VB06 prochloroco |
| 705 | 45.5 | 35.8 | 343 | 2 | Q9IU97 | Q9IU97 human immun | 778 | 45 | 35.4 | 180 | 2 | Q70NS3 | Q70NS3 helicobacte |
| 706 | 45.5 | 35.8 | 347 | 2 | Q6CX56 | Q6CX56 Kluveromyc | 779 | 45 | 35.4 | 180 | 2 | Q70NS4 | Q70NS4 helicobacte |
| 707 | 45.5 | 35.8 | 349 | 2 | Q9IUB8 | Q9IUB8 human immun | 780 | 45 | 35.4 | 180 | 2 | Q70NS6 | Q70NS6 helicobacte |
| 708 | 45.5 | 35.8 | 359 | 2 | P87965 | P87965 human immun | 781 | 45 | 35.4 | 180 | 2 | Q70NS9 | Q70NS9 helicobacte |
| 709 | 45.5 | 35.8 | 392 | 2 | Q15A74 | Q15A74 uncultured | 782 | 45 | 35.4 | 180 | 2 | Q70NT0 | Q70NT0 helicobacte |
| 710 | 45.5 | 35.8 | 397 | 2 | Q15A74 | Q15A74 human immun | 783 | 45 | 35.4 | 180 | 2 | Q70NT3 | Q70NT3 helicobacte |
| 711 | 45.5 | 35.8 | 405 | 2 | Q6GLA5 | Q6GLA5 human immun | 784 | 45 | 35.4 | 180 | 2 | Q70NT5 | Q70NT5 helicobacte |
| 712 | 45.5 | 35.8 | 410 | 2 | Q8Q2F9 | Q8Q2F9 human immun | 785 | 45 | 35.4 | 180 | 2 | Q70NT7 | Q70NT7 helicobacte |
| 713 | 45.5 | 35.8 | 422 | 2 | Q8ZGX3 | Q8ZGX3 yersinia pe | 786 | 45 | 35.4 | 180 | 2 | Q70NT9 | Q70NT9 helicobacte |
| 714 | 45.5 | 35.8 | 425 | 1 | BIOA_SERWA | BIOA_SERWA yersinia ma | 787 | 45 | 35.4 | 180 | 2 | Q70NU0 | Q70NU0 helicobacte |
| 715 | 45.5 | 35.8 | 426 | 2 | Q66D56 | Q66D56 yersinia pe | 788 | 45 | 35.4 | 180 | 2 | Q70NU1 | Q70NU1 helicobacte |
| 716 | 45.5 | 35.8 | 426 | 2 | Q8BD03 | Q8BD03 yersinia pe | 789 | 45 | 35.4 | 180 | 2 | Q70NU2 | Q70NU2 helicobacte |
| 717 | 45.5 | 35.8 | 430 | 2 | Q6W332 | Q6W332 human immun | 790 | 45 | 35.4 | 180 | 2 | Q70NU3 | Q70NU3 helicobacte |
| 718 | 45.5 | 35.8 | 438 | 2 | Q90C05 | Q90C05 human immun | 791 | 45 | 35.4 | 180 | 2 | Q70NU6 | Q70NU6 helicobacte |
| 719 | 45.5 | 35.8 | 454 | 2 | Q7ZBH6 | Q7ZBH6 simian-huma | 792 | 45 | 35.4 | 180 | 2 | Q70NU7 | Q70NU7 helicobacte |
| 720 | 45.5 | 35.8 | 455 | 2 | Q7ZB10 | Q7ZB10 simian-huma | 793 | 45 | 35.4 | 180 | 2 | Q70NU9 | Q70NU9 helicobacte |
| 721 | 45.5 | 35.8 | 456 | 2 | Q7ZBJ2 | Q7ZBJ2 simian-huma | 794 | 45 | 35.4 | 180 | 2 | Q70NV0 | Q70NV0 helicobacte |
| 722 | 45.5 | 35.8 | 490 | 2 | Q24430 | Q24430 glycine max | 795 | 45 | 35.4 | 180 | 2 | Q70NV1 | Q70NV1 helicobacte |
| 723 | 45.5 | 35.8 | 490 | 2 | Q84P28 | Q84P28 glycine max | 796 | 45 | 35.4 | 180 | 2 | Q70NV2 | Q70NV2 helicobacte |
| 724 | 45.5 | 35.8 | 501 | 2 | Q93X19 | Q93X19 solanum tub | 797 | 45 | 35.4 | 180 | 2 | Q70NV5 | Q70NV5 helicobacte |
| 725 | 45.5 | 35.8 | 506 | 2 | Q6U9B2 | Q6U9B2 bacterioph | 798 | 45 | 35.4 | 180 | 2 | Q70NV7 | Q70NV7 helicobacte |
| 726 | 45.5 | 35.8 | 582 | 1 | MSBA_VIBPA | MSBA_VIBPA vibrio para | 799 | 45 | 35.4 | 180 | 2 | Q70NV8 | Q70NV8 helicobacte |
| 727 | 45.5 | 35.8 | 603 | 2 | Q6YV77 | Q6YV77 oryza sativ | 800 | 45 | 35.4 | 184 | 2 | Q8KV27 | Q8KV27 uncultured |
| 728 | 45.5 | 35.8 | 644 | 2 | Q80814 | Q80814 arabidopsi | 801 | 45 | 35.4 | 184 | 2 | Q8KV43 | Q8KV43 uncultured |
| 729 | 45.5 | 35.8 | 759 | 2 | Q99TL6 | Q99TL6 strephyloloc | 802 | 45 | 35.4 | 184 | 2 | Q8KV69 | Q8KV69 uncultured |
| 730 | 45.5 | 35.8 | 759 | 2 | Q7A0Q5 | Q7A0Q5 strephyloloc | 803 | 45 | 35.4 | 184 | 2 | Q8KV91 | Q8KV91 uncultured |
| 731 | 45.5 | 35.8 | 759 | 2 | Q7A586 | Q7A586 strephyloloc | 804 | 45 | 35.4 | 184 | 2 | Q8KV00 | Q8KV00 uncultured |
| 732 | 45.5 | 35.8 | 759 | 2 | Q6G8T2 | Q6G8T2 strephyloloc | 805 | 45 | 35.4 | 184 | 2 | Q6BH37 | Q6BH37 lachnospira |
| 733 | 45.5 | 35.8 | 759 | 2 | Q6G6G7 | Q6G6G7 strephyloloc | 806 | 45 | 35.4 | 184 | 2 | Q68H58 | Q68H58 clostridium |
| 734 | 45.5 | 35.8 | 795 | 2 | Q99BY6 | Q99BY6 human immun | 807 | 45 | 35.4 | 185 | 2 | Q8KPC6 | Q8KPC6 flexispira |
| 735 | 45.5 | 35.8 | 799 | 2 | Q7ZGR4 | Q7ZGR4 human immun | 808 | 45 | 35.4 | 186 | 2 | Q8IG33 | Q8IG33 caenorhabdi |
| 736 | 45.5 | 35.8 | 833 | 2 | Q9QKH9 | Q9QKH9 human immun | 809 | 45 | 35.4 | 186 | 2 | Q8KVN6 | Q8KVN6 uncultured |
| 737 | 45.5 | 35.8 | 833 | 2 | Q9QKI3 | Q9QKI3 human immun | 810 | 45 | 35.4 | 186 | 2 | Q6BH18 | Q6BH18 prevotella |
| 738 | 45.5 | 35.8 | 841 | 2 | Q9DVL7 | Q9DVL7 human immun | 811 | 45 | 35.4 | 186 | 2 | Q6GJ48 | Q6GJ48 strephyloloc |
| 739 | 45.5 | 35.8 | 849 | 2 | Q6H1S7 | Q6H1S7 human immun | 812 | 45 | 35.4 | 190 | 2 | Q7X3Q5 | Q7X3Q5 strephyloloc |
| 740 | 45.5 | 35.8 | 854 | 2 | Q6S720 | Q6S720 human immun | 813 | 45 | 35.4 | 194 | 2 | Q6DKB7 | Q6DKB7 xenopus lae |
| 741 | 45.5 | 35.8 | 854 | 2 | Q9WSE4 | Q9WSE4 human immun | 814 | 45 | 35.4 | 204 | 1 | HAML_CLOPE | HAML_CLOPE clostridium |
| 742 | 45.5 | 35.8 | 855 | 2 | Q8UL67 | Q8UL67 human immun | 815 | 45 | 35.4 | 207 | 2 | Q294E5 | Q294E5 archaeoglob |
| 743 | 45.5 | 35.8 | 859 | 2 | Q902S4 | Q902S4 human immun | 816 | 45 | 35.4 | 215 | 2 | Q6XLM7 | Q6XLM7 brassica ra |
| 744 | 45.5 | 35.8 | 859 | 2 | Q6JNM4 | Q6JNM4 human immun | 817 | 45 | 35.4 | 216 | 2 | Q6XLM5 | Q6XLM5 brassica ol |
| 745 | 45.5 | 35.8 | 861 | 2 | Q6JNP2 | Q6JNP2 human immun | 818 | 45 | 35.4 | 226 | 2 | Q6XLM8 | Q6XLM8 brassica ra |
| 746 | 45.5 | 35.8 | 861 | 2 | Q80367 | Q80367 human immun | 819 | 45 | 35.4 | 226 | 1 | VMEL_PEDV7 | VMEL_PEDV7 porcine epi |
| 747 | 45.5 | 35.8 | 863 | 2 | Q6BC68 | Q6BC68 human immun | 820 | 45 | 35.4 | 226 | 1 | VMEL_PEDVB | VMEL_PEDVB porcine epi |
| 748 | 45.5 | 35.8 | 868 | 2 | Q8JCB10 | Q8JCB10 human immun | 821 | 45 | 35.4 | 226 | 2 | Q91AU9 | Q91AU9 porcine epi |
| 749 | 45.5 | 35.8 | 868 | 2 | Q8JCB35 | Q8JCB35 human immun | 822 | 45 | 35.4 | 226 | 2 | Q692M0 | Q692M0 porcine epi |
| 750 | 45.5 | 35.8 | 868 | 2 | Q6BC31 | Q6BC31 human immun | 823 | 45 | 35.4 | 230 | 2 | Q98F05 | Q98F05 thizobium l |
| 751 | 45.5 | 35.8 | 897 | 2 | Q997B5 | Q997B5 cache valle | 824 | 45 | 35.4 | 233 | 2 | Q78YQ2 | Q78YQ2 xenopus lae |
| 752 | 45.5 | 35.8 | 897 | 2 | Q997B7 | Q997B7 cache valle | 825 | 45 | 35.4 | 238 | 2 | Q662V2 | Q662V2 borellia ga |
| 753 | 45.5 | 35.8 | 897 | 2 | Q997B8 | Q997B8 cache valle | 826 | 45 | 35.4 | 258 | 2 | Q8ZU62 | Q8ZU62 pyrobaculum |
| 754 | 45.5 | 35.8 | 897 | 2 | Q91ZJ9 | Q91ZJ9 cache valle | 827 | 45 | 35.4 | 258 | 2 | Q88XH7 | Q88XH7 lactobacill |
| 755 | 45.5 | 35.8 | 897 | 2 | Q91ZK0 | Q91ZK0 cache valle | 828 | 45 | 35.4 | 260 | 1 | DCX_HUMAN | DCX_HUMAN homo sapien |
| 756 | 45.5 | 35.8 | 897 | 2 | Q91ZK1 | Q91ZK1 cache valle | 829 | 45 | 35.4 | 281 | 2 | Q8XP21 | Q8XP21 clostridium |
| 757 | 45.5 | 35.8 | 897 | 2 | Q9J6I0 | Q9J6I0 cache valle | 830 | 45 | 35.4 | 292 | 2 | Q65E39 | Q65E39 bacillus l1 |
| 758 | 45.5 | 35.8 | 1058 | 2 | Q9FLR5 | Q9FLR5 arabidopsi | 831 | 45 | 35.4 | 294 | 2 | Q48432 | Q48432 lactobacill |
| 759 | 45.5 | 35.8 | 1434 | 2 | Q9J6L5 | Q9J6L5 cache valle | 832 | 45 | 35.4 | 296 | 2 | Q73JN0 | Q73JN0 treponema d |
| 760 | 45.5 | 35.8 | 1434 | 2 | Q9J6L6 | Q9J6L6 cache valle | 833 | 45 | 35.4 | 303 | 2 | Q895V5 | Q895V5 clostridium |
| 761 | 45.5 | 35.8 | 1434 | 2 | Q9J6L7 | Q9J6L7 cache valle | 834 | 45 | 35.4 | 307 | 2 | Q9M2H8 | Q9M2H8 arabidopsi |

| | | | | | | | | | | | | | |
|-----|----|------|-----|---|-------------|---------------------|-----|------|------|------|---|------------|----------------------|
| 835 | 45 | 35.4 | 321 | 2 | Q8JB39 | Q8JB39 human immun | 908 | 45 | 35.4 | 877 | 1 | SYA_WOLPM | P61709 wolbachia p |
| 836 | 45 | 35.4 | 330 | 2 | Q7P275 | Q7P275 fusobacteri | 909 | 45 | 35.4 | 877 | 2 | Q7Z627 | Q7Z627 homo sapien |
| 837 | 45 | 35.4 | 334 | 2 | Q7MNH9 | Q7MNH9 bordetella | 910 | 45 | 35.4 | 878 | 2 | Q80K39 | Q80K39 mus musculu |
| 838 | 45 | 35.4 | 345 | 2 | Q9A0Y0 | Q9A0Y0 streptococ | 911 | 45 | 35.4 | 894 | 2 | Q9BKD2 | Q9BKD2 homo sapien |
| 839 | 45 | 35.4 | 357 | 2 | Q89ZZ9 | Q89ZZ9 bacteroides | 912 | 45 | 35.4 | 896 | 2 | Q8XZ06 | Q8XZ06 ralsstonia s |
| 840 | 45 | 35.4 | 368 | 2 | Q754L5 | Q754L5 aebhya goss | 913 | 45 | 35.4 | 897 | 2 | Q8YWP3 | Q8YWP3 anabaena sp |
| 841 | 45 | 35.4 | 376 | 1 | XYNA_BACOV | P49942 bacteroides | 914 | 45 | 35.4 | 902 | 2 | Q7PX97 | Q7PX97 anophelies g |
| 842 | 45 | 35.4 | 377 | 2 | Q9FNC6 | Q9FNC6 arabisdopsis | 915 | 45 | 35.4 | 930 | 2 | Q93IL7 | Q93IL7 colypochetrix |
| 843 | 45 | 35.4 | 386 | 2 | Q8EM80 | Q8EM80 mycoplasma | 916 | 45 | 35.4 | 974 | 2 | Q6PG37 | Q6PG37 homo sapien |
| 844 | 45 | 35.4 | 387 | 2 | Q6SE78 | Q6SE78 bacillus li | 917 | 45 | 35.4 | 1025 | 2 | Q7Z7W5 | Q7Z7W5 coprinus ci |
| 845 | 45 | 35.4 | 399 | 2 | Q8LG40 | Q8LG40 arabisdopsis | 918 | 45 | 35.4 | 1052 | 1 | MSIP_CRIGR | Q922A8 citreulius |
| 846 | 45 | 35.4 | 399 | 2 | Q67XY1 | Q67XY1 arabisdopsis | 919 | 45 | 35.4 | 1052 | 1 | MSIP_HUMAN | Q14703 homo sapien |
| 847 | 45 | 35.4 | 400 | 2 | Q8XW53 | Q8XW53 ralsstonia s | 920 | 45 | 35.4 | 1052 | 1 | MSIP_MOUSE | Q9WCT2 mus musculu |
| 848 | 45 | 35.4 | 401 | 1 | APQM_THEMEA | Q9X295 thermotoga | 921 | 45 | 35.4 | 1052 | 2 | Q6PG67 | Q6PG67 mus musculu |
| 849 | 45 | 35.4 | 402 | 2 | Q9QIM7 | Q9QIM7 human immun | 922 | 45 | 35.4 | 1055 | 2 | Q80UB0 | Q80UB0 mus musculu |
| 850 | 45 | 35.4 | 423 | 2 | Q6XS08 | Q6XS08 human immun | 923 | 45 | 35.4 | 1060 | 2 | Q9P789 | Q9P789 schizosacch |
| 851 | 45 | 35.4 | 429 | 2 | Q8DX40 | Q8DX40 streptococ | 924 | 45 | 35.4 | 1060 | 2 | Q9P789 | Q9P789 schizosacch |
| 852 | 45 | 35.4 | 444 | 2 | Q73FT9 | Q73FT9 wolbachia p | 925 | 45 | 35.4 | 1374 | 2 | Q6F1H8 | Q6F1H8 mesoplasma |
| 853 | 45 | 35.4 | 451 | 2 | Q7NRE9 | Q7NRE9 chromobacte | 926 | 45 | 35.4 | 1493 | 2 | Q6F1H8 | Q6F1H8 mesoplasma |
| 854 | 45 | 35.4 | 459 | 2 | Q9KLN6 | Q9KLN6 vibrio chol | 927 | 45 | 35.4 | 1504 | 2 | Q68D66 | Q68D66 homo sapien |
| 855 | 45 | 35.4 | 460 | 2 | Q76H22 | Q76H22 bartonella | 928 | 45 | 35.4 | 1549 | 1 | SMC4_CAEEL | Q9Y4F4 homo sapien |
| 856 | 45 | 35.4 | 466 | 2 | Q6B8C6 | Q6B8C6 drosophila | 929 | 45 | 35.4 | 1752 | 2 | Q6B7A2 | Q6B7A2 debaryomyce |
| 857 | 45 | 35.4 | 466 | 2 | Q9JWX2 | Q9JWX2 eliseeria m | 930 | 45 | 35.4 | 1946 | 2 | Q6B7A2 | Q6B7A2 apis mellif |
| 858 | 45 | 35.4 | 470 | 2 | Q93707 | Q93707 sulfolobus | 931 | 45 | 35.4 | 2471 | 2 | Q6CQ08 | Q6CQ08 Kluveromyc |
| 859 | 45 | 35.4 | 473 | 1 | LCB1_CRIGR | Q54695 citreulius | 932 | 45 | 35.4 | 2572 | 2 | Q7PRV6 | Q7PRV6 anophelies g |
| 860 | 45 | 35.4 | 473 | 1 | LCB1_MOUSE | Q35704 mus musculu | 933 | 45 | 35.4 | 2811 | 2 | Q7Q9V2 | Q7Q9V2 anophelies g |
| 861 | 45 | 35.4 | 473 | 2 | Q8BH11 | Q8BH11 m mus muscu | 934 | 45 | 35.4 | 3432 | 2 | Q87WM7 | Q87WM7 pseudomonas |
| 862 | 45 | 35.4 | 473 | 2 | Q8C295 | Q8C295 mus musculu | 935 | 45 | 35.4 | 5085 | 2 | Q7OLM4 | Q7OLM4 bacillus br |
| 863 | 45 | 35.4 | 483 | 2 | Q6V9I8 | Q6V9I8 trypanosoma | 936 | 45 | 35.4 | 7180 | 1 | RIAB_CVMJH | RIAB_CVMJH |
| 864 | 45 | 35.4 | 483 | 2 | Q94KU1 | Q94KU1 spinacia ol | 937 | 45 | 35.4 | 7756 | 2 | Q40374 | Q40374 human immun |
| 865 | 45 | 35.4 | 494 | 2 | Q9M072 | Q9M072 drosophila | 938 | 45 | 35.0 | 84 | 2 | Q40376 | Q40376 human immun |
| 866 | 45 | 35.4 | 495 | 1 | 1A1C_ARATH | Q8G9Y0 arabisdopsis | 939 | 44.5 | 35.0 | 84 | 2 | Q40382 | Q40382 human immun |
| 867 | 45 | 35.4 | 514 | 2 | Q964E9 | Q964E9 ipomoea bat | 940 | 44.5 | 35.0 | 84 | 2 | Q40382 | Q40382 human immun |
| 868 | 45 | 35.4 | 516 | 2 | Q81DB5 | Q81DB5 bacillus ce | 941 | 44.5 | 35.0 | 84 | 2 | Q40382 | Q40382 human immun |
| 869 | 45 | 35.4 | 516 | 2 | Q9CK28 | Q9CK28 pasteurella | 942 | 44.5 | 35.0 | 84 | 2 | Q40384 | Q40384 human immun |
| 870 | 45 | 35.4 | 519 | 2 | Q6PA21 | Q6PA21 xenopus lae | 943 | 44.5 | 35.0 | 84 | 2 | Q40386 | Q40386 human immun |
| 871 | 45 | 35.4 | 528 | 1 | Q6F3J9 | Q6F3J9 oryza sativ | 944 | 44.5 | 35.0 | 84 | 2 | Q40389 | Q40389 human immun |
| 872 | 45 | 35.4 | 535 | 2 | Q9MBL8 | Q9MBL8 corynebacte | 945 | 44.5 | 35.0 | 84 | 2 | Q40391 | Q40391 human immun |
| 873 | 45 | 35.4 | 538 | 2 | Q6KE85 | Q6KE85 corynebacte | 946 | 44.5 | 35.0 | 84 | 2 | Q40393 | Q40393 human immun |
| 874 | 45 | 35.4 | 539 | 1 | CH60_FUSUN | Q855X7 fusobacteri | 947 | 44.5 | 35.0 | 84 | 2 | Q40395 | Q40395 human immun |
| 875 | 45 | 35.4 | 539 | 1 | CH60_FUSNP | Q8G100 fusobacteri | 948 | 44.5 | 35.0 | 84 | 2 | Q40401 | Q40401 human immun |
| 876 | 45 | 35.4 | 543 | 1 | CH62_SYNEI | Q57002 synechococc | 949 | 44.5 | 35.0 | 84 | 2 | Q40402 | Q40402 human immun |
| 877 | 45 | 35.4 | 545 | 1 | CH60_HELHP | Q7X317 helicobacte | 950 | 44.5 | 35.0 | 84 | 2 | Q40414 | Q40414 human immun |
| 878 | 45 | 35.4 | 545 | 1 | CH60_MYCPE | Q8CXQ7 mycoplasma | 951 | 44.5 | 35.0 | 84 | 2 | Q40423 | Q40423 human immun |
| 879 | 45 | 35.4 | 546 | 1 | CH60_HELBP | Q9N5F0 helicobacte | 952 | 44.5 | 35.0 | 84 | 2 | Q40424 | Q40424 human immun |
| 880 | 45 | 35.4 | 546 | 1 | CH60_HELBP | Q43383 helicobacte | 953 | 44.5 | 35.0 | 84 | 2 | Q40425 | Q40425 human immun |
| 881 | 45 | 35.4 | 546 | 1 | Q8RNU2 | Q8RNU2 helicobacte | 954 | 44.5 | 35.0 | 84 | 2 | Q40428 | Q40428 human immun |
| 882 | 45 | 35.4 | 547 | 1 | CH61_RHOPA | Q9YJd1 drosophila | 955 | 44.5 | 35.0 | 84 | 2 | Q40430 | Q40430 human immun |
| 883 | 45 | 35.4 | 548 | 2 | Q9VJd1 | Q9YJd1 drosophila | 956 | 44.5 | 35.0 | 84 | 2 | Q40433 | Q40433 human immun |
| 884 | 45 | 35.4 | 560 | 1 | DTXN_CORBE | P00589 corynebacte | 957 | 44.5 | 35.0 | 84 | 2 | Q40435 | Q40435 human immun |
| 885 | 45 | 35.4 | 560 | 1 | DTXN_CORBE | P00587 corynebacte | 958 | 44.5 | 35.0 | 84 | 2 | Q40441 | Q40441 human immun |
| 886 | 45 | 35.4 | 560 | 2 | Q6YIX8 | Q6YIX8 corynebacte | 959 | 44.5 | 35.0 | 84 | 2 | Q40442 | Q40442 human immun |
| 887 | 45 | 35.4 | 560 | 2 | Q6YIX9 | Q6YIX9 corynebacte | 960 | 44.5 | 35.0 | 84 | 2 | Q91293 | Q91293 human immun |
| 888 | 45 | 35.4 | 560 | 2 | Q6NKL5 | Q6NKL5 corynebacte | 961 | 44.5 | 35.0 | 146 | 2 | Q9UWV7 | Q9UWV7 sulfolobus |
| 889 | 45 | 35.4 | 567 | 1 | DTX_CORBE | Q8U588 corynebacte | 962 | 44.5 | 35.0 | 149 | 1 | LRPB_BACSU | P96653 bacillus su |
| 890 | 45 | 35.4 | 582 | 2 | Q8BU59 | Q8BU59 mus musculu | 963 | 44.5 | 35.0 | 157 | 2 | Q7OR53 | Q7OR53 human immun |
| 891 | 45 | 35.4 | 593 | 2 | Q8A796 | Q8A796 bacteroides | 964 | 44.5 | 35.0 | 158 | 2 | Q9MWT3 | Q9MWT3 human immun |
| 892 | 45 | 35.4 | 595 | 2 | Q89BH2 | Q89BH2 bradyrhizob | 965 | 44.5 | 35.0 | 159 | 2 | Q9JER4 | Q9JER4 human immun |
| 893 | 45 | 35.4 | 630 | 2 | Q97J38 | Q97J38 sulfolobus | 966 | 44.5 | 35.0 | 159 | 2 | Q9JER4 | Q9JER4 human immun |
| 894 | 45 | 35.4 | 636 | 2 | Q7LATS | Q7LATS homo sapien | 967 | 44.5 | 35.0 | 168 | 2 | Q91WR3 | Q91WR3 human immun |
| 895 | 45 | 35.4 | 649 | 2 | Q7RTS4 | Q7RTS4 plasmodium | 968 | 44.5 | 35.0 | 169 | 2 | Q91WR3 | Q91WR3 human immun |
| 896 | 45 | 35.4 | 652 | 2 | Q7XRMO | Q7XRMO oryza sativ | 969 | 44.5 | 35.0 | 171 | 2 | Q7OR20 | Q7OR20 human immun |
| 897 | 45 | 35.4 | 663 | 2 | Q8DSW8 | Q8DSW8 streptococ | 970 | 44.5 | 35.0 | 175 | 2 | Q6U429 | Q6U429 human immun |
| 898 | 45 | 35.4 | 673 | 2 | Q8BDV6 | Q8BDV6 mus musculu | 971 | 44.5 | 35.0 | 175 | 2 | Q6U430 | Q6U430 human immun |
| 899 | 45 | 35.4 | 674 | 2 | Q91Y31 | Q91Y31 mus musculu | 972 | 44.5 | 35.0 | 175 | 2 | Q6U431 | Q6U431 human immun |
| 900 | 45 | 35.4 | 731 | 2 | Q7RH47 | Q7RH47 plasmodium | 973 | 44.5 | 35.0 | 175 | 2 | Q6U432 | Q6U432 human immun |
| 901 | 45 | 35.4 | 755 | 2 | Q9M122 | Q9M122 arabisdopsis | 974 | 44.5 | 35.0 | 175 | 2 | Q6U433 | Q6U433 human immun |
| 902 | 45 | 35.4 | 778 | 2 | Q6B2_HUMAN | Q15057 homo sapien | 975 | 44.5 | 35.0 | 177 | 2 | Q892D2 | Q892D2 clostridium |
| 903 | 45 | 35.4 | 778 | 2 | Q6IVG4 | Q6IVG4 oryctolagus | 976 | 44.5 | 35.0 | 177 | 2 | Q698V0 | Q698V0 human immun |
| 904 | 45 | 35.4 | 795 | 2 | Q9NEX4 | Q9NEX4 caenorhabdi | 977 | 44.5 | 35.0 | 178 | 2 | Q8UPK4 | Q8UPK4 human immun |
| 905 | 45 | 35.4 | 799 | 2 | Q7Z3K9 | Q7Z3K9 homo sapien | 978 | 44.5 | 35.0 | 178 | 2 | Q8UPK4 | Q8UPK4 human immun |
| 906 | 45 | 35.4 | 865 | 2 | Q6MCD7 | Q6MCD7 parachlamyd | 979 | 44.5 | 35.0 | 178 | 2 | Q8UPK8 | Q8UPK8 human immun |
| 907 | 45 | 35.4 | 872 | 1 | S3B2_HUMAN | Q13435 homo sapien | 980 | 44.5 | 35.0 | 178 | 2 | Q8UPK1 | Q8UPK1 human immun |

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981 44.5 35.0 179 2 Q90CM9 human immun
982 44.5 35.0 186 2 Q90RS9 human immun
983 44.5 35.0 188 2 Q92963 human immun
984 44.5 35.0 188 2 Q9DVB3 human immun
985 44.5 35.0 194 2 Q92254 human immun
986 44.5 35.0 194 2 Q92254 human immun
987 44.5 35.0 194 2 Q9DVB5 human immun
988 44.5 35.0 195 2 Q9DVB5 human immun
989 44.5 35.0 195 2 Q6V883 human immun
990 44.5 35.0 195 2 Q9DVB9 human immun
991 44.5 35.0 196 2 Q9SKV3 human immun
992 44.5 35.0 196 2 Q9JBH9 human immun
993 44.5 35.0 196 2 Q9JBH3 human immun
994 44.5 35.0 196 2 Q9JBH4 human immun
995 44.5 35.0 196 2 Q9JBH6 human immun
996 44.5 35.0 196 2 Q9JBK2 human immun
997 44.5 35.0 196 2 Q9JBK5 human immun
998 44.5 35.0 197 2 Q6SUT4 human immun
999 44.5 35.0 198 2 Q6QAA4 human immun
1000 44.5 35.0 198 2 Q6SY26 human immun
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ALIGNMENTS

RESULT 1

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Q6SR10 PRELIMINARY; PRT; 143 AA.
ID Q6SR10
AC Q6SR10;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Membrane glycoprotein M (Fragment).
OS SARS coronavirus TW-PH2.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; SARS coronavirus TW.
OX NCBI_TaxID=264388;
RN [1]
RP SEQUENCE FROM N.A.
RA Lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,
RA Yang J.-Y., Chen H.-Y., Chen Y.-M.Arthur.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY451891; AAS44759.1; -
DR GO: GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
FT NON_TER 143
SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AE971ED CRC64;
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Query Match 88.2%; Score 112; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 4 MADNGITVEELKQLLEQMNLY 25
DB 1 MADNGITVEELKQLLEQMNLY 22
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RESULT 2

```
Q6SR14 PRELIMINARY; PRT; 143 AA.
ID Q6SR14
AC Q6SR14;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Membrane glycoprotein M (Fragment).
OS SARS coronavirus TW-PH1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; SARS coronavirus TW.
OX NCBI_TaxID=264387;
RN [1]
RP SEQUENCE FROM N.A.
RA Lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,
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RA Yang J.-Y., Chen H.-Y., Chen Y.-M.Arthur.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY451890; AAS44755.1; -
DR GO: GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
FT NON_TER 143
SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AE971ED CRC64;
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```
Query Match 88.2%; Score 112; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 4 MADNGITVEELKQLLEQMNLY 25
DB 1 MADNGITVEELKQLLEQMNLY 22
```

RESULT 3

```
Q6SR18 PRELIMINARY; PRT; 143 AA.
ID Q6SR18
AC Q6SR18;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Membrane glycoprotein M (Fragment).
OS SARS coronavirus TW-YM4.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; SARS coronavirus TW.
OX NCBI_TaxID=264386;
RN [1]
RP SEQUENCE FROM N.A.
RA Lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,
RA Yang J.-Y., Chen H.-Y., Chen Y.-M.Arthur.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY451889; AAS44751.1; -
DR GO: GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
FT NON_TER 143
SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AE971ED CRC64;
```

```
Query Match 88.2%; Score 112; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 4 MADNGITVEELKQLLEQMNLY 25
DB 1 MADNGITVEELKQLLEQMNLY 22
```

RESULT 4

```
Q6SRJ2 PRELIMINARY; PRT; 143 AA.
ID Q6SRJ2
AC Q6SRJ2;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Membrane glycoprotein M (Fragment).
OS SARS coronavirus TW-YM3.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; SARS coronavirus TW.
OX NCBI_TaxID=264385;
RN [1]
RP SEQUENCE FROM N.A.
RA Lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,
RA Yang J.-Y., Chen H.-Y., Chen Y.-M.Arthur.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY451888; AAS44747.1; -
DR GO: GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
FT NON_TER 143
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SQL SEQUENCE 143 AA; 16423 MW; 1CAB09A94AB971ED CRC64;
Query Match 88.2%; Score 112; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MADNGTIVEELKQLEQMNLY 25
DB 1 MADNGTIVEELKQLEQMNLY 22

RESULT 5
Q6SRJ6 PRELIMINARY; PRT; 143 AA.
AC Q6SRJ6.
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Membrane glycoprotein M (Fragment).
OS SARS coronavirus TW-YM2.
OC Viruses; sRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; SARS coronavirus TW.
CX NCBI_TaxID=264384;
RN [1]
RP SEQUENCE FROM N.A.
RA Lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY451887; AAS44743.1; -
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
FT NON TER 143
SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AB971ED CRC64;

Query Match 88.2%; Score 112; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MADNGTIVEELKQLEQMNLY 25
DB 1 MADNGTIVEELKQLEQMNLY 22

RESULT 6
Q6SRK4 PRELIMINARY; PRT; 143 AA.
AC Q6SRK4.
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Membrane glycoprotein M (Fragment).
OS SARS coronavirus TW-GD5.
OC Viruses; sRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; SARS coronavirus TW.
CX NCBI_TaxID=264382;
RN [1]
RP SEQUENCE FROM N.A.
RA Lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY451885; AAS44735.1; -
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
FT NON TER 143
SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AB971ED CRC64;

Query Match 88.2%; Score 112; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MADNGTIVEELKQLEQMNLY 25

DB 1 MADNGTIVEELKQLEQMNLY 22

RESULT 7
Q6SRK8 PRELIMINARY; PRT; 143 AA.
AC Q6SRK8.
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Membrane glycoprotein M (Fragment).
OS SARS coronavirus TW-GD4.
OC Viruses; sRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; SARS coronavirus TW.
CX NCBI_TaxID=264381;
RN [1]
RP SEQUENCE FROM N.A.
RA Lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY451884; AAS44731.1; -
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
FT NON TER 143
SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AB971ED CRC64;

Query Match 88.2%; Score 112; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MADNGTIVEELKQLEQMNLY 25
DB 1 MADNGTIVEELKQLEQMNLY 22

RESULT 8
Q6SRL2 PRELIMINARY; PRT; 143 AA.
AC Q6SRL2.
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Membrane glycoprotein M (Fragment).
OS SARS coronavirus TW-GD3.
OC Viruses; sRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; SARS coronavirus TW.
CX NCBI_TaxID=264380;
RN [1]
RP SEQUENCE FROM N.A.
RA Lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY451883; AAS44727.1; -
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
FT NON TER 143
SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AB971ED CRC64;

Query Match 88.2%; Score 112; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MADNGTIVEELKQLEQMNLY 25
DB 1 MADNGTIVEELKQLEQMNLY 22

RESULT 9
Q6SRL6 PRELIMINARY; PRT; 143 AA.

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AC Q6SR16;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Membrane glycoprotein M (Fragment).
OS SARS coronavirus TW-GD2.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; SARS coronavirus TW.
OX NCBI_TaxId=264379;
RN [1]
RP SEQUENCE FROM N.A.
RA Ian Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,
RA Yang J.-Y., Chen H.-Y., Chen Y.-M.Arthur.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY451882; AAS44723.1; -.
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
FT NON TER 143
SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AE971ED CRC64;

Query Match 88.2%; Score 112; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 MADNGITVEELKQLEQNMNV 25
DB 1 MADNGITVEELKQLEQNMNV 22

RESULT 10
Q6SRM0
ID Q6SRM0 PRELIMINARY; PRT; 143 AA.
AC Q6SRM0;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Membrane glycoprotein M (Fragment).
OS SARS coronavirus TW-GD1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; SARS coronavirus TW.
OX NCBI_TaxId=264378;
RN [1]
RP SEQUENCE FROM N.A.
RA Ian Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,
RA Yang J.-Y., Chen H.-Y., Chen Y.-M.Arthur.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY451881; AAS44719.1; -.
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
FT NON TER 143
SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AE971ED CRC64;

Query Match 88.2%; Score 112; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 MADNGITVEELKQLEQNMNV 25
DB 1 MADNGITVEELKQLEQNMNV 22

RESULT 11
Q6SRM4
ID Q6SRM4 PRELIMINARY; PRT; 143 AA.
AC Q6SRM4;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Membrane glycoprotein M (Fragment).
OS SARS coronavirus TW-KC3.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;

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OC Coronaviridae; Coronavirus; SARS coronavirus TW.
OX NCBI_TaxId=264377;
RN [1]
RP SEQUENCE FROM N.A.
RA Ian Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,
RA Yang J.-Y., Chen H.-Y., Chen Y.-M.Arthur.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY451880; AAS44715.1; -.
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
FT NON TER 143
SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AE971ED CRC64;

Query Match 88.2%; Score 112; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 MADNGITVEELKQLEQNMNV 25
DB 1 MADNGITVEELKQLEQNMNV 22

RESULT 12
Q6SRM8
ID Q6SRM8 PRELIMINARY; PRT; 143 AA.
AC Q6SRM8;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Membrane glycoprotein M (Fragment).
OS SARS coronavirus TW-KC1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; SARS coronavirus TW.
OX NCBI_TaxId=264376;
RN [1]
RP SEQUENCE FROM N.A.
RA Ian Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,
RA Yang J.-Y., Chen H.-Y., Chen Y.-M.Arthur.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY451879; AAS44711.1; -.
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
FT NON TER 143
SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AE971ED CRC64;

Query Match 88.2%; Score 112; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 MADNGITVEELKQLEQNMNV 25
DB 1 MADNGITVEELKQLEQNMNV 22

RESULT 13
Q6SRN2
ID Q6SRN2 PRELIMINARY; PRT; 143 AA.
AC Q6SRN2;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Membrane glycoprotein M (Fragment).
OS SARS coronavirus TW-JC2.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; SARS coronavirus TW.
OX NCBI_TaxId=264375;
RN [1]
RP SEQUENCE FROM N.A.
RA Ian Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,
RA Yang J.-Y., Chen H.-Y., Chen Y.-M.Arthur.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AY451878; AAS44707.1; -.
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M.1.
FT NON_TER 143
SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AB971ED CRC64;

Query Match 88.2%; Score 112; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MADNGITVEELKQLEQNMNV 25
Db 1 MADNGITVEELKQLEQNMNV 22

RESULT 14

Q6SRN6 PRELIMINARY; PRT; 143 AA.
AC Q6SRN6;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Membrane glycoprotein M (Fragment).
OS SARS coronavirus TW-Hp2.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; SARS coronavirus TW.
OX NCBI_TaxId=264374;

RN [1]
RP SEQUENCE FROM N.A.
RA Ian Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,
Yang J.-Y., Chen H.-Y., Chen Y.-M, Arthur.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY451877; AAS44703.1; -.
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M.1.
FT NON_TER 143
SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AB971ED CRC64;

Query Match 88.2%; Score 112; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MADNGITVEELKQLEQNMNV 25
Db 1 MADNGITVEELKQLEQNMNV 22

RESULT 15

Q6SRP0 PRELIMINARY; PRT; 143 AA.
AC Q6SRP0;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Membrane glycoprotein M (Fragment).
OS SARS coronavirus TW-Hp3.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; SARS coronavirus TW.
OX NCBI_TaxId=264373;

RN [1]
RP SEQUENCE FROM N.A.
RA Ian Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,
Yang J.-Y., Chen H.-Y., Chen Y.-M, Arthur.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY451876; AAS44699.1; -.
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M.1.
FT NON_TER 143
SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AB971ED CRC64;

Query Match 88.2%; Score 112; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MADNGITVEELKQLEQNMNV 25
Db 1 MADNGITVEELKQLEQNMNV 22

RESULT 16

Q6SRP4 PRELIMINARY; PRT; 143 AA.
AC Q6SRP4;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Membrane glycoprotein M (Fragment).
OS SARS coronavirus TW-Hp2.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; SARS coronavirus TW.
OX NCBI_TaxId=264372;

RN [1]
RP SEQUENCE FROM N.A.
RA Ian Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,
Yang J.-Y., Chen H.-Y., Chen Y.-M, Arthur.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY451875; AAS44695.1; -.
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M.1.
FT NON_TER 143
SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AB971ED CRC64;

Query Match 88.2%; Score 112; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MADNGITVEELKQLEQNMNV 25
Db 1 MADNGITVEELKQLEQNMNV 22

RESULT 17

Q6SRP8 PRELIMINARY; PRT; 143 AA.
AC Q6SRP8;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Membrane glycoprotein M (Fragment).
OS SARS coronavirus TW-Hp1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; SARS coronavirus TW.
OX NCBI_TaxId=264371;

RN [1]
RP SEQUENCE FROM N.A.
RA Ian Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,
Yang J.-Y., Chen H.-Y., Chen Y.-M, Arthur.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY451874; AAS44691.1; -.
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M.1.
FT NON_TER 143
SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AB971ED CRC64;

Query Match 88.2%; Score 112; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MADNGITVEELKQLEQNMNV 25
Db 1 MADNGITVEELKQLEQNMNV 22

RESULT 18
ID VME1_CVHSA STANDARD; PRT; 221 AA.
AC P59596; Q65885; Q7608; Q776R1; Q776R5; Q776S0; Q776S3; Q77726;
AC Q777P6; Q777S6; Q777S12;
DT 10-OCT-2003 (Ref. 42, Created)
DT 10-OCT-2003 (Ref. 42, Last sequence update)
DT 25-OCT-2004 (Ref. 45, Last annotation update)
DE E1 glycoprotein (Matrix glycoprotein) (Membrane glycoprotein).
GN Name=M;
OS Human coronavirus (strain SARS) (HCoV-SARS) (SARS-CoV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=227859;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate Urbani;
RX MEDLINE=22660724; PubMed=12730500; DOI=10.1126/science.1085952;
RA Roca P.A., Oberste M.S., Monroe S.S., Nix W.A., Campagnoli R.,
RA Iacono J.P., Penaranda S., Bankamp B., Maher K., Chen M.-H.,
RA Tong S., Tamn A., Lowe L., Frace M., Derlet J.L., Chen Q., Wang D.,
RA Ericman D.D., Perez T.C.T., Burns C., Kaszalek T.G., Rollin P.E.,
RA Sanchez A., Liffick S., Hollway B., Limor J., McCaustland K.,
RA Olsen-Rasmussen M., Fouchier R., Guenther S., Osterhaus A.D.M.E.,
RA Drost C., Pallansch M.A., Anderson L.J., Bellini W.J.;
RT "Characterization of a novel coronavirus associated with severe acute
RT respiratory syndrome";
RL Science 300:1394-1399(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate Tor2;
RX MEDLINE=22660725; PubMed=12730501; DOI=10.1126/science.1085953;
RA Marra M.A., Jones S.J., Astell C.R., Holt R.A., Brooks-Wilson A.,
RA Butlerfield Y.S.N., Khattar J., Asano J.K., Barber S.A., Chan S.Y.,
RA Cloutier A., Coughlin S.M., Freeman D., Glin N., Griffith O.L.,
RA Leach S.R., Mayo M., McDonald H., Montgomery S.B., Pandolfi P.K.,
RA Perreault A.S., Robertson A.G., Schein J.E., Siddiqui A., Smailus D.E.,
RA Stott J.M., Yang G.S., Plummer F., Andonov A., Artsob H., Bastien N.,
RA Bernard K., Booth T.F., Bowness D., Czud M., Drebot M., Fernandez L.,
RA Flick R., Garbutt M., Gray M., Groila A., Jones S., Feldman H.,
RA Meyers A., Kabani A., Li Y., Normand S., Stroher U., Tipples G.A.,
RA Tyler S., Vogrig R., Ward D., Watson B., Brunham R.C., Kraiden M.,
RA Petric M., Skowronski D.M., Upton C., Roper R.L.;
RT "The genome sequence of the SARS-associated coronavirus";
RL Science 300:1399-1404(2003).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate CUHK-Su10, and Isolate CUHK-W1;
RX MEDLINE=22737955; PubMed=12853594; DOI=10.1056/NEJM200307103490216;
RA Tsui S.K.W., Chin S.-S.C., Lo Y.M.D.;
RT "Coronavirus genomic-sequence variations and the epidemiology of the
RT severe acute respiratory syndrome";
RL N. Engl. J. Med. 349:187-188(2003).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate GZ50, and Isolate HKU-36871;
RX MEDLINE=22913660; PubMed=12958366; DOI=10.1126/science.1087139;
RA Guan Y., Zheng B.J., He Y.Q., Liu X.L., Zhuang Z.X., Cheng C.L.,
RA Luo S.W., Li P.H., Zhang L.J., Guan Y.J., Butt K.M., Wong K.L.,
RA Chan K.W., Lam W., Shortridge K.F., Yuen K.Y., Peiris J.S.M.,
RA Poon L.L.M.;
RT "Isolation and characterization of viruses related to the SARS
RT coronavirus from animals in southern China";
RL Science 302:276-278(2003).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate HKU-39849;
RX MEDLINE=22738472; PubMed=12876307;
RA Zeng F.Y., Chan C.W., Chan M.N., Chen J.D., Chow K.Y.C., Hon C.C.C.,
RA Hui R.K.H., Li J., Li V.Y., Wang C.Y., Wang P.Y., Guan Y., Zheng B.,
RA Poon L.L.M., Chan K.H., Yuen K.Y., Peiris J.S.M., Leung F.C.;

RT "The complete genome sequence of severe acute respiratory syndrome
RT coronavirus strain HKU-39849 (HK-39).";
RL Exp. Biol. Med. 228:866-873(2003).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate Sin2500, Isolate Sin2677, Isolate Sin2679,
RC Isolate Sin2748, and Isolate Sin2774;
RX MEDLINE=22660704; PubMed=12781537; DOI=10.1016/S0140-6736(03)13414-9;
RA Ruan Y., Wei C.L., Ling A.E., Vega V.B., Thoreau H., Se Thoe S.Y.,
RA Chia J.-M., Ng P., Chiu K.P., Lim L., Zhang T., Chan K.P., Oon L.E.L.,
RA Ng M.L., Leo S.Y., Ng L.F.P., Ren E.C., Stanton L.W., Long P.M.,
RA Liu E.T.;
RT "Comparative full-length genome sequence analysis of 14 SARS
RT coronavirus isolates and common mutations associated with putative
RT origins of infection";
RL Lancet 361:1779-1785(2003).
RN [7]
RP ERRATUM.
RX PubMed=12781581;
RA Ruan Y., Wei C.L., Ling A.E., Vega V.B., Thoreau H., Se Thoe S.Y.,
RA Chia J.-M., Ng P., Chiu K.P., Lim L., Zhang T., Chan K.P., Oon L.E.L.,
RA Ng M.L., Leo S.Y., Ng L.F.P., Ren E.C., Stanton L.W., Long P.M.,
RA Liu E.T.;
RL Lancet 361:1832-1832(2003).
RN [8]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate BJ01, Isolate BJ02, Isolate BJ03, Isolate BJ04, and
RC Isolate GD01;
RA Qin E., Zhu Q., Yu M., Fan B., Chang G., Si B., Yang B., Peng W.,
RA Jiang T., Liu B., Deng Y., Liu H., Zhang Y., Wang C., Li Y., Gan Y.,
RA Li X., Lu F., Tan G., Yang R., Cao W.S., Wang J., Chen W., Cong L.,
RA Deng Y., Dong W., Han Y., Hu W., Lei W., Li C., Li G., Li H.,
RA Li S., Li S., Li W., Lin W., Liu J., Liu Z., Lu H., Ni P.,
RA Qi Q., Sun Y., Tang L., Tong Z., Wang J., Wang X., Wu Q., Xi Y.,
RA Xu Z., Yang L., Ye C., Ye J., Zhang B., Zhang F., Zhang J., Zhang X.,
RA Zhou J., Yang H.;
RT Submitted (Apr-2003) to the EMBL/GenBank/DBJ databases.
RN [9]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate TW1;
RA Yen S.-H., Kao C.-L., Tsai C.-Y., Liu C.-J., Chen D.-S., Chen P.-J.;
RT "The complete genome of SARS coronavirus clone TW1";
RL Submitted (May-2003) to the EMBL/GenBank/DBJ databases.
RN [10]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate FRA;
RA Rickmann M., Becker S., Klenk H.-D., Doerr H.W., Stadler K.,
RA Censini S., Guidotti S., Maignani V., Scarselli M., Mora M.,
RA Donati C., Han J., Song H.C., Abriani S., Covacci A., Rappelli R.;
RT "SARS virus is a close relative of type II coronaviruses";
RL Submitted (May-2003) to the EMBL/GenBank/DBJ databases.
RN [11]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate Frankfurt 1;
RA Thiel V., Hertzog T., Putics A., Ivanov K.A., Schelle B., Bayer S.,
RA Scheiner B., Weisbach B., Ziebur J.;
RL Submitted (May-2003) to the EMBL/GenBank/DBJ databases.
RN [12]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate Shanghai QX1;
RA Yuan Z., Zhang X., Hu Y., Lan S., Wang H., Zhou Z., Wen Y.;
RT "Analysis of SARS coronavirus genome in Shanghai isolates";
RL Submitted (Jan-2004) to the EMBL/GenBank/DBJ databases.
RN [13]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate Z01;
RA Cong L.-M., Ding G.-Q., Lu Y.-Y., Yan J.-Q., Weng J.-Q., Cheng S.-Y.,
RA Zhang Y.-J., Mei L.-L., Wang Z.-G., Hu N., Wo J., Yao J., Zhu H.-P.,
RA Lu Q.-Y., Li M.-H., Gong L.-M., Shi W.;
RL Submitted (Jun-2003) to the EMBL/GenBank/DBJ databases.
RN [14]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate TWC;


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RA Yang J.-Y., Lin J.-H., Chiu S.-C., Wang S.-F., Lee S.-C., Lin Y.-C.,
RA Hsu C.-K., Chen H.-Y., Chang J.-G., Chen P.-J., Su I.-J.;
RT "Genomic sequence of SARS isolate from the first fatal case in
RT Taiwan.";
RL Submitted (JUN-2003) to the EMBL/Genbank/DBJ databases.
RN [15]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate Taiwan TC1, Isolate Taiwan TC2, and Isolate Taiwan TC3;
RA Chang J.-G.C., Lin T.-H., Chen C.-M., Lin C.-S., Chan W.-L.,
RA Shih M.-C.;
RL Submitted (JUL-2003) to the EMBL/Genbank/DBJ databases.
RN [16]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate TW1, Isolate TW2, Isolate TW3, and
RC Isolate TW4;
RA Shu H.-Y., Wu K.-M., Tsai S.-F.;
RL Submitted (JUL-2003) to the EMBL/Genbank/DBJ databases.
RN [17]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate HSR 1;
RA Canducci F., Clementi M., Poli G., Vicenzi E.;
RL Submitted (JUL-2003) to the EMBL/Genbank/DBJ databases.
RN [18]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate TW2, and Isolate TW3;
RA Yang J.-Y., Lin J.-H., Chiu S.-C., Wang S.-F., Lee H.-C., Lin Y.-C.,
RA Yao C.-W., Chiu T.-S., Lu J.-J., Chen A., Hsu C.-K., Chen H.-Y.,
RA Chen P.-J., Su I.-J.;
RL Submitted (AUG-2003) to the EMBL/Genbank/DBJ databases.
RN [19]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate AS;
RA Balotta C., Corvase S., Violin M., Galli M., Moroni M.,
RA Vigeant G.M., Ruan Y.-J., Salemi M.;
RL Submitted (OCT-2003) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: Component of the viral envelope that plays a central
CC role in virus morphogenesis and assembly via its interactions with
CC other viral proteins (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: Belongs to the coronavirus M protein family.
CC -----
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CC -----
DR EMBL; AY278741; AAP13444.1; -
DR EMBL; AY274119; AAP1041.1; -
DR EMBL; AY278554; AAP13571.1; -
DR EMBL; AY282752; -; NOT_ANNOTATED_CDS.
DR EMBL; AY304492; -; NOT_ANNOTATED_CDS.
DR EMBL; AY304495; -; NOT_ANNOTATED_CDS.
DR EMBL; AY278491; -; NOT_ANNOTATED_CDS.
DR EMBL; AY283794; -; NOT_ANNOTATED_CDS.
DR EMBL; AY283795; -; NOT_ANNOTATED_CDS.

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Query Match 88.2%; Score 112; DB 1; Length 221;
Best Local Similarity 100.0%; Pred. No. 2,4e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 4 MADNGITVEBLKQLEQMNLY 25
DB 1 MADNGITVEBLKQLEQMNLY 22

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RESULT 19

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ID 066VB9 PRELIMINARY; PRT; 221 AA.
AC 066VB9;
DT 25-OCT-2004 (TREMBLrel. 28, Created)

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DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE M protein.
OS SARS coronavirus GD322.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=291613;
RN [1]
RP SEQUENCE FROM N.A.
RA Hu Z., Zhao W., Yan H.;
RT "The analyses on M genes' variation rules of SARS-CoV and their
RT influence upon the possible B cell epitopes of M genes.";
RL Submitted (JUL-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY702026; AAU07933.1; -
DR InterPro: IPR002574; Corona_M.
DR Pfam: PF01635; Corona_M.1.
SQ SEQUENCE 221 AA; 25060 MW; 275C37085A0215A8 CRC64;

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Query Match 88.2%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 2,4e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 4 MADNGITVEBLKQLEQMNLY 25
DB 1 MADNGITVEBLKQLEQMNLY 22

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RESULT 20

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ID 06GYQ7 PRELIMINARY; PRT; 221 AA.
AC 06GYQ7;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein M.
GN ORFNames=SARS-CoVp08;
OS SARS coronavirus L147-2004.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=273522;
RN [1]
RP SEQUENCE FROM N.A.
RA Li J., Wei W., Xiao W., Wang M., Wang J., Zhao J., Sun Z., Pei Y.,
RA Chen Y.;
RL Submitted (APR-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY595412; AAT52332.1; -
DR GO: GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro: IPR002574; Corona_M.
DR Pfam: PF01635; Corona_M.1.
KW Hypothetical protein.
SQ SEQUENCE 221 AA; 25060 MW; 275C37085A0215A8 CRC64;

```

Query Match 88.2%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 2,4e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 4 MADNGITVEBLKQLEQMNLY 25
DB 1 MADNGITVEBLKQLEQMNLY 22

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RESULT 21

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ID 06JH34 PRELIMINARY; PRT; 221 AA.
AC 06JH34;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Membrane protein.
OS SARS coronavirus Sin03-11.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=255729;

```

```

RN [1]
  SEQUENCE FROM N.A.
RC STRAIN=Shno3-11;
RA Jin W.W., Feng J.D., Du Z.L., Hu L.X., Liu Y.X., Liu Y.F., Zhang X.M.,
RA Gao H., Ning Y., Zhang J.S., Li N., Yin W.D.;
RL Submitted (NOV-2003) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY485278; AAR23256.1;
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M.1.
SQ SEQUENCE 221 AA; 25016 MW; 6658652E2927478E CRC64;

Query Match
  88.2%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MADNGTITVEELKQLEQNMNV 25
  |||||
  1 MADNGTITVEELKQLEQNMNV 22

RESULT 22
Q6UH42 PRELIMINARY; PRT; 221 AA.
AC Q6UH42;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Membrane protein.
OS SARS coronavirus Shno1-11.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=255730;
RN [1]
  SEQUENCE FROM N.A.
RC STRAIN=Shno1-11;
RA Jin W.W., Feng J.D., Du Z.L., Hu L.X., Liu Y.X., Liu Y.F., Zhang X.M.,
RA Gao H., Ning Y., Zhang J.S., Li N., Yin W.D.;
RL Submitted (NOV-2003) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY485277; AAR23248.1;
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M.1.
SQ SEQUENCE 221 AA; 25016 MW; 6658652E2927478E CRC64;

Query Match
  88.2%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MADNGTITVEELKQLEQNMNV 25
  |||||
  1 MADNGTITVEELKQLEQNMNV 22

Db 1 MADNGTITVEELKQLEQNMNV 22

RESULT 23
Q6R7Y2 PRELIMINARY; PRT; 221 AA.
AC Q6R7Y2;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Membrane protein M.
OS SARS coronavirus NS-1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=260743;
RN [1]
  SEQUENCE FROM N.A.
RC STRAIN=NS-1;
RA Zhang H., Wei C., Ding R., Wang W., Li W., Wang J., Tao W., Yu X.,
RA Guo H., Chen J., Wei W., Li J., Zhang Y., Wang X., Sun Y., Jiao J.,
RA Wang Y., Zhou C.;
RL Submitted (DEC-2003) to the EMBL/Genbank/DBJ databases.

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DR EMBL; AY508724; AAR91590.1;
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M.1.
SQ SEQUENCE 221 AA; 25060 MW; 275C37085A0215A8 CRC64;

Query Match
  88.2%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MADNGTITVEELKQLEQNMNV 25
  |||||
  1 MADNGTITVEELKQLEQNMNV 22

Db 1 MADNGTITVEELKQLEQNMNV 22

RESULT 24
Q6RCW1 PRELIMINARY; PRT; 221 AA.
AC Q6RCW1;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Putative envelope protein M.
OS SARS coronavirus TW9.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=258972;
RN [1]
  SEQUENCE FROM N.A.
RC PubMed=14983045; DOI=10.1073/pnas.0307904100;
RG National Taiwan University SARS Research Team;
RA Yeh S.-H., Wang H.-Y., Tsai C.-Y., Kao C.-L., Yang J.-Y., Liu H.-W.,
RA Su I.-J., Tsai S.-F., Chen D.-S., Chen P.-J.;
RT "Characterization of severe acute respiratory syndrome coronavirus
  genomes in Taiwan: molecular epidemiology and genome evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:2542-2547(2004).
DR EMBL; AY502932; AAR87604.1;
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M.1.
RW Envelope protein.
SQ SEQUENCE 221 AA; 25016 MW; 6658652E2927478E CRC64;

Query Match
  88.2%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MADNGTITVEELKQLEQNMNV 25
  |||||
  1 MADNGTITVEELKQLEQNMNV 22

Db 1 MADNGTITVEELKQLEQNMNV 22

RESULT 25
Q6RCX2 PRELIMINARY; PRT; 221 AA.
AC Q6RCX2;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Putative envelope protein M.
OS SARS coronavirus TW8.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=258971;
RN [1]
  SEQUENCE FROM N.A.
RC PubMed=14983045; DOI=10.1073/pnas.0307904100;
RG National Taiwan University SARS Research Team;
RA Yeh S.-H., Wang H.-Y., Tsai C.-Y., Kao C.-L., Yang J.-Y., Liu H.-W.,
RA Su I.-J., Tsai S.-F., Chen D.-S., Chen P.-J.;
RT "Characterization of severe acute respiratory syndrome coronavirus
  genomes in Taiwan: molecular epidemiology and genome evolution.";

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RL Proc. Natl. Acad. Sci. U.S.A. 101:2542-2547(2004).
DR EMBL; AY502931; AAR87593.1; -.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
KW Envelope protein.
SQ SEQUENCE 221 AA; 25016 MW; 6658652E2927478E CRC64;

Query Match      88.2%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 2,4e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MADNGITVEELKQLEQNMIV 25
   |||||
Db 1 MADNGITVEELKQLEQNMIV 22

RESULT 26
Q6RCY3 PRELIMINARY; PRT; 221 AA.
ID Q6RCY3;
AC Q6RCY3;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Putative envelope protein M.
OS SARS coronavirus TW7.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_Taxid=258970;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14983045; DOI=10.1073/pnas.0307904100;
RG National Taiwan University SARS Research Team;
RA Yeh S.-H., Wang H.-Y., Tsai C.-Y., Kao C.-L., Yang J.-Y., Liu H.-W.,
   Su I.-J., Tsai S.-F., Chen D.-S., Chen P.-J.;
RT "Characterization of severe acute respiratory syndrome coronavirus
   genomes in Taiwan: molecular epidemiology and genome evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:2542-2547(2004).
DR EMBL; AY502930; AAR87582.1; -.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
KW Envelope protein.
SQ SEQUENCE 221 AA; 25016 MW; 6658652E2927478E CRC64;

Query Match      88.2%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 2,4e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MADNGITVEELKQLEQNMIV 25
   |||||
Db 1 MADNGITVEELKQLEQNMIV 22

RESULT 27
Q6RCZ4 PRELIMINARY; PRT; 221 AA.
ID Q6RCZ4;
AC Q6RCZ4;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Putative envelope protein M.
OS SARS coronavirus TW6.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_Taxid=258969;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14983045; DOI=10.1073/pnas.0307904100;
RG National Taiwan University SARS Research Team;
RA Yeh S.-H., Wang H.-Y., Tsai C.-Y., Kao C.-L., Yang J.-Y., Liu H.-W.,
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RA Su I.-J., Tsai S.-F., Chen D.-S., Chen P.-J.;
RT "Characterization of severe acute respiratory syndrome coronavirus
   genomes in Taiwan: molecular epidemiology and genome evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:2542-2547(2004).
DR EMBL; AY502929; AAR87571.1; -.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
KW Envelope protein.
SQ SEQUENCE 221 AA; 25016 MW; 6658652E2927478E CRC64;

Query Match      88.2%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 2,4e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MADNGITVEELKQLEQNMIV 25
   |||||
Db 1 MADNGITVEELKQLEQNMIV 22

RESULT 28
Q6RD05 PRELIMINARY; PRT; 221 AA.
ID Q6RD05;
AC Q6RD05;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Putative envelope protein M.
OS SARS coronavirus TW5.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_Taxid=258968;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14983045; DOI=10.1073/pnas.0307904100;
RG National Taiwan University SARS Research Team;
RA Yeh S.-H., Wang H.-Y., Tsai C.-Y., Kao C.-L., Yang J.-Y., Liu H.-W.,
   Su I.-J., Tsai S.-F., Chen D.-S., Chen P.-J.;
RT "Characterization of severe acute respiratory syndrome coronavirus
   genomes in Taiwan: molecular epidemiology and genome evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:2542-2547(2004).
DR EMBL; AY502928; AAR87560.1; -.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
KW Envelope protein.
SQ SEQUENCE 221 AA; 25016 MW; 6658652E2927478E CRC64;

Query Match      88.2%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 2,4e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MADNGITVEELKQLEQNMIV 25
   |||||
Db 1 MADNGITVEELKQLEQNMIV 22

RESULT 29
Q6RD16 PRELIMINARY; PRT; 221 AA.
ID Q6RD16;
AC Q6RD16;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Putative envelope protein M.
OS SARS coronavirus TW4.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_Taxid=258967;
RN [1]
RP SEQUENCE FROM N.A.
```



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OS SARS coronavirus TW10.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxId=258963;
RN
  [1]
  SEQUENCE FROM N.A.
  PubMed:14983045; DOI=10.1073/pnas.0307904100;
  National Taiwan University SARS Research Team;
  RA Yeh S.-H., Wang H.-Y., Tsai C.-Y., Kao C.-L., Yang J.-Y., Liu H.-W.,
  RA Su I.-J., Tsai S.-P., Chen D.-S., Chen P.-J.;
  RT "Characterization of severe acute respiratory syndrome coronavirus
  RT genomes in Taiwan: molecular epidemiology and genome evolution.";
  RL Proc. Natl. Acad. Sci. U.S.A. 101:2542-2547(2004).
  DR EMBL: AY502923; AAR87505.1; -;
  DR GO: GO:0019031; C:Viral envelope; IEA.
  DR GO: GO:0019058; P:Viral infectious cycle; IEA.
  DR InterPro: IPR002574; Corona_M.
  DR Pfam: PF01635; Corona_M; 1.
  KM Envelope protein.
  SQ SEQUENCE 221 AA; 25016 MW; 6658652E2927478E CRC64;

Query Match      88.2%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 MADNGITVEELKQLEQNLV 25
DB 1 MADNGITVEELKQLEQNLV 22

RESULT 34
O698D3
ID O698D3 PRELIMINARY; PRT; 221 AA.
AC O698D3
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE , complete genome.
OS SARS coronavirus Shanghai/CX2.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxId=258508;
RN
  [1]
  SEQUENCE FROM N.A.
  RC STRAIN=Shanghai/CX2;
  RA Yuan Z., Zhang X., Hu Y., Lan S., Zhou Z., Wang H., Wen Y.;
  RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
  DR EMBL: AY463060; AAR86779.1; -;
  DR GO: GO:0019058; P:Viral infectious cycle; IEA.
  DR InterPro: IPR002574; Corona_M.
  DR Pfam: PF01635; Corona_M; 1.
  SQ SEQUENCE 221 AA; 25044 MW; 51875ABE9BAE04FC CRC64;

Query Match      88.2%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 MADNGITVEELKQLEQNLV 25
DB 1 MADNGITVEELKQLEQNLV 22

RESULT 35
O6T1D8
ID O6T1D8 PRELIMINARY; PRT; 221 AA.
AC O6T1D8
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Membrane glycoprotein M.
OS SARS coronavirus CHN-12.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.

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OX NCBI_TaxId=260550;
RN
  [1]
  SEQUENCE FROM N.A.
  RP PubMed:14709660;
  RA Chim S.S.C., Tong Y.K., Hung E.C.W., Chiu R.W.K., Lo Y.M.D.;
  RT "Genomic sequencing of a SARS coronavirus isolate that predated the
  RT Metropole Hotel case cluster in Hong Kong.";
  RL Clin. Chem. 50:231-233(2004).
  DR EMBL: AY443095; AAS01068.1; -;
  DR GO: GO:0019058; P:Viral infectious cycle; IEA.
  DR InterPro: IPR002574; Corona_M.
  DR Pfam: PF01635; Corona_M; 1.
  SQ SEQUENCE 221 AA; 25060 MW; 275C37085A0215A8 CRC64;

Query Match      88.2%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 MADNGITVEELKQLEQNLV 25
DB 1 MADNGITVEELKQLEQNLV 22

RESULT 36
O6TPE4
ID O6TPE4 PRELIMINARY; PRT; 221 AA.
AC O6TPE4
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Matrix protein.
OS SARS coronavirus GZ02.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxId=256753;
RN
  [1]
  SEQUENCE FROM N.A.
  RA Zhou X., Hou J., He M., Ding Y., Wang Z., Li J., Liu Z., Ma S.;
  RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
  DR EMBL: AY390556; AAS0007.1; -;
  DR GO: GO:0005198; F:Structural molecule activity; IEA.
  DR GO: GO:0019058; P:Viral infectious cycle; IEA.
  DR InterPro: IPR002574; Corona_M.
  DR Pfam: PF01635; Corona_M; 1.
  KM Matrix protein.
  SQ SEQUENCE 221 AA; 25060 MW; 275C37085A0215A8 CRC64;

Query Match      88.2%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 MADNGITVEELKQLEQNLV 25
DB 1 MADNGITVEELKQLEQNLV 22

RESULT 37
O6UZE9
ID O6UZE9 PRELIMINARY; PRT; 221 AA.
AC O6UZE9
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Putative M protein.
OS SARS coronavirus PUMCO3.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxId=253435;
RN
  [1]
  SEQUENCE FROM N.A.
  RP Zou K., Zhu H., Ding K., Wang Z., Liu Y., Wang T., Yang J., Wei G.,
  RA Zhou X., Zhang W., Yu Z., Qin C., Liu X., Shen Y., Ni A., Qiang B.;

```

RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY357076; ARI14812.1; -
DR GO: GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro: IPR002574; Corona_M.
DR Pfam: PF01635; Corona_M; 1.
SQ SEQUENCE 221 AA; 25016 MW; 6658652E2927478E CRC64;

Query Match 88.2%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MADNGTITVEELKQLEQNNLV 25
Db 1 MADNGTITVEELKQLEQNNLV 22

RESULT 38

Q6UZF3 PRELIMINARY; PRT; 221 AA.
AC Q6UZF3;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DE Putative M protein.
OS SARS coronavirus PUMC02.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=253434;
RN [1]
RP SEQUENCE FROM N.A.
RA Zou K., Zhu H., Ding K., Wang Z., Liu Y., Wang T., Yang J., Wei G.,
RA Zhou X., Zhang W., Yu Z., Qin C., Liu X., Shen Y., Ni A., Qiang B.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY357075; ARI14808.1; -
DR GO: GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro: IPR002574; Corona_M.
DR Pfam: PF01635; Corona_M; 1.
SQ SEQUENCE 221 AA; 25016 MW; 6658652E2927478E CRC64;

Query Match 88.2%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MADNGTITVEELKQLEQNNLV 25
Db 1 MADNGTITVEELKQLEQNNLV 22

RESULT 39

Q6V584 PRELIMINARY; PRT; 221 AA.
AC Q6V584;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DE Putative M protein.
OS SARS coronavirus PUMC01.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=253433;
RN [1]
RP SEQUENCE FROM N.A.
RA Zou K., Zhu H., Ding K., Wang Z., Liu Y., Wang T., Yang J., Wei G.,
RA Zhou X., Zhang W., Yu Z., Fan Z., Peng X., Qin C., Liu X., Shen Y.,
RA Ni A., Qiang B.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY350750; ARI14804.1; -
DR GO: GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro: IPR002574; Corona_M.
DR Pfam: PF01635; Corona_M; 1.
SQ SEQUENCE 221 AA; 25016 MW; 6658652E2927478E CRC64;

Query Match 88.2%; Score 112; DB 2; Length 221;

Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MADNGTITVEELKQLEQNNLV 25
Db 1 MADNGTITVEELKQLEQNNLV 22

RESULT 40

Q6VA74 PRELIMINARY; PRT; 221 AA.
AC Q6VA74;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DE Putative M protein.
OS SARS coronavirus CUHK-AG03.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=239243;
RN [1]
RP SEQUENCE FROM N.A.
RA Chim S.S.C., Tsui S.K.W., Chan K.C.A., Au T.C.C., Hung E.C.M.,
RA Tong Y.K., Chiu R.W.K., Ng E.K.O., Chan P.K.S., Chu C.M., Sung J.J.Y.,
RA Tam J.S., Fung K.P., Waye M.M.Y., Lee C.Y., Yuen K.Y., Chung S.,
RA Au-Yang C., Au K.K.A., Chan A.H., Chan C.W., Kou C.Y.C., Lam W.Y.,
RA Lau S.K., Lau Y.M., Law S.L., Law P.T.W., Li M.L.Y., Wan A.W.K.,
RA Wong C.H., Yiu W.H., Lee N., Wu A., Tse C.H., Chan L.Y.S., Lo Y.M.D.;
RT Genomic characterisation of the SARS-coronavirus of the Amoy Gardens
outbreak in Hong Kong";
RL Lancet 362:1807-1808 (2003).
DR EMBL: AY345988; AAP94763.1; -
DR GO: GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro: IPR002574; Corona_M.
DR Pfam: PF01635; Corona_M; 1.
SQ SEQUENCE 221 AA; 25016 MW; 6658652E2927478E CRC64;

Query Match 88.2%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MADNGTITVEELKQLEQNNLV 25
Db 1 MADNGTITVEELKQLEQNNLV 22

RESULT 41

Q6VA85 PRELIMINARY; PRT; 221 AA.
AC Q6VA85;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DE Putative M protein.
OS SARS coronavirus CUHK-AG02.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=239242;
RN [1]
RP SEQUENCE FROM N.A.
RA Chim S.S.C., Tsui S.K.W., Chan K.C.A., Au T.C.C., Hung E.C.M.,
RA Tong Y.K., Chiu R.W.K., Ng E.K.O., Chan P.K.S., Chu C.M., Sung J.J.Y.,
RA Tam J.S., Fung K.P., Waye M.M.Y., Lee C.Y., Yuen K.Y., Chung S.,
RA Au-Yang C., Au K.K.A., Chan A.H., Chan C.W., Kou C.Y.C., Lam W.Y.,
RA Lau S.K., Lau Y.M., Law S.L., Law P.T.W., Li M.L.Y., Wan A.W.K.,
RA Wong C.H., Yiu W.H., Lee N., Wu A., Tse C.H., Chan L.Y.S., Lo Y.M.D.;
RT Genomic characterisation of the SARS-coronavirus of the Amoy Gardens
outbreak in Hong Kong";
RL Lancet 362:1807-1808 (2003).
DR EMBL: AY345987; AAP94752.1; -
DR GO: GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro: IPR002574; Corona_M.
DR Pfam: PF01635; Corona_M; 1.

SQ SEQUENCE 221 AA; 25016 MW; 6658652E2927478B CRC64;
Query Match 88.2%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 MADNGITVEELKQLEQNMNV 25
DB 1 MADNGITVEELKQLEQNMNV 22

RESULT 42
O6VA96 PRELIMINARY; PRT; 221 AA.
AC O6VA96; 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Putative M protein.
OS SARS coronavirus CUHK-AG01.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronaviruses.
OX NCBI_TaxID=239241;
RN [1]
RP SEQUENCE FROM N.A.
RA Chiu S.S.C., Tsui S.K.W., Chan K.C.A., Au T.C.C., Hung B.C.W.,
RA Tong Y.K., Chiu R.W.K., Ng E.K.O., Chan P.K.S., Chu C.M., Sung J.J.Y.,
RA Tam J.S., Fung K.P., Waye M.M.Y., Lee C.Y., Yuen K.Y., Chung S.,
RA Au-Yang C., Au K.K.A., Chan A.H., Chan C.W., Kou C.Y.C., Lam W.Y.,
RA Lau S.K., Lau Y.M., Law S.L., Law P.T.W., Li M.L.Y., Wan A.W.K.,
RA Wong C.H., Yau W.H., Lee N., Wu A., Tse C.H., Chan L.Y.S., Lo Y.M.D.;
RT "Genomic characterisation of the SARS-coronavirus of the Amoy Gardens
RT outbreak in Hong Kong";
RL Lancet 362:1807-1808(2003).
DR EMBL; AY345986; AAP94741.1;
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
SQ SEQUENCE 221 AA; 25016 MW; 6658652E2927478B CRC64;

Query Match 88.2%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 MADNGITVEELKQLEQNMNV 25
DB 1 MADNGITVEELKQLEQNMNV 22

RESULT 43
O692E0 PRELIMINARY; PRT; 221 AA.
AC O692E0; 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DE Membrane glycoprotein.
OS SARS coronavirus TGF.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronaviruses.
OX NCBI_TaxID=284672;
RN [1]
RP SEQUENCE FROM N.A.
RA Chen W., Yan W., Liu M.,
RT "Isolation and identification of viruses related to the SARS
RT Coronavirus from swines in China."
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY546624; AAT76152.1;
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
SQ SEQUENCE 221 AA; 25059 MW; 439CD30C104CBFAC CRC64;

Query Match 85.0%; Score 108; DB 2; Length 221;
Best Local Similarity 95.5%; Pred. No. 7.9e-06;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 MADNGITVEELKQLEQNMNV 25
DB 1 MADNGITVEELKQLEQNMNV 22

RESULT 44
O6QJ38 PRELIMINARY; PRT; 221 AA.
AC O6QJ38; 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Membrane protein.
OS SARS coronavirus BJ01.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronaviruses.
OX NCBI_TaxID=228407;
RN [1]
RP SEQUENCE FROM N.A.
RA Li T., Li X., Chang Z., Liu L.,
RT "Identification of SARS-CoV RNA leader sequence."
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY536759; AAS48455.1;
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
SQ SEQUENCE 221 AA; 25059 MW; 439CD30C104CBFAC CRC64;

Query Match 85.0%; Score 108; DB 2; Length 221;
Best Local Similarity 95.5%; Pred. No. 7.9e-06;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 MADNGITVEELKQLEQNMNV 25
DB 1 MADNGITVEELKQLEQNMNV 22

RESULT 45
O6SRK0 PRELIMINARY; PRT; 143 AA.
AC O6SRK0; 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Membrane glycoprotein M (Fragment).
OS SARS coronavirus TW-YM1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronaviruses; SARS coronavirus TW.
OX NCBI_TaxID=264383;
RN [1]
RP SEQUENCE FROM N.A.
RA Lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,
RA Yang J.-Y., Chen H.-Y., Chen Y.-M., Artinur.,
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY451886; AAS44739.1;
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
FT NON_TER 143
SQ SEQUENCE 143 AA; 16435 MW; 2694FA8363B971F7 CRC64;

Query Match 83.5%; Score 106; DB 2; Length 143;
Best Local Similarity 95.5%; Pred. No. 9.5e-06;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 MADNGITVEELKQLEQNMNV 25
DB 1 MADNGITVEELKQLEQNMNV 22

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RESULT 46
HOSC_THET2
ID HOSC_THET2 STANDARD; PRT; 376 AA.
AC 087136;
DT 30-MAY-2000 (Rel. 39, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Homocitrate synthase (NC 2.3.3.14).
GN Name-lys20; Ordered locus Names=TrtC1550;
OS Thermus thermophilus (strain HB27 / ATCC BAA-163 / DSM 7039).
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
NCBI_TaxID=262724;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=99085673; PubMed=9868782;
RA Kosuge T., Hoshino T.;
RT "lysine is synthesized through the alpha-aminoadipate pathway in
RT Thermus thermophilus."
RL FEWS Microbiol. Lett. 169:361-367 (1998).
RN 1;
RP SEQUENCE FROM N.A.
RX PubMed=15064768; DOI=10.1038/hb1956;
RA Henne A., Brueggemann H., Raasch C., Wlezer A., Hartech T.,
RA Liesegang H., Johann A., Lienard T., Gohl O., Martinez-Arias R.,
RA Jacob C., Starkviene V., Schlenczek S., Dencker S., Huber R.,
RA Klenk H.-P., Kramer W., Merkl R., Gottschalk G., Fritz H.-J.;
RT "The genome sequence of the extreme thermophile Thermus
RT thermophilus."
RL Nat. Biotechnol. 22:547-553 (2004).
CC -1- CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + 2-oxoglutarate = 2-
CC hydroxybutane-1,2,4-tricarboxylate + COA.
CC -1- PATHWAY: lysine biosynthesis; alpha-aminoadipic acid pathway;
CC first step.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (potential).
CC -1- SIMILARITY: Belongs to the alpha-IPM synthetase / homocitrate
CC synthase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
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CC -----
DR EMBL; AB018379; BAA3785.1; -
DR EMBL; AB017306; AAS81892.1; -
DR PIR; T51170; T51170.
DR InterPro: IPR002034; AIPM/Hcit_synth.
DR InterPro: IPR000891; HMG_L-like.
DR Pfam; PF00662; HMG_L-like; 1.
DR PROSITE; PS00815; AIPM_HOMOCIT_SYNTH_1; 1.
DR PROSITE; PS00816; AIPM_HOMOCIT_SYNTH_2; 1.
DR PROSITE; PS50991; PYR_CT; 1.
KM Complete proteome; lysine biosynthesis; Transferrase.
PT CONFLICT 104 104 A -> P (in Ref. 1).
SQ SEQUENCE 376 AA; 42159 MW; 1B8EBA63C82FCF06 CRC64;

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AC 068H54;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE 60 kDa chaperonin (Fragment).
GN Name-cpn60;
OS Clostridium xyloxyticum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OC Clostridium.
OX NCBI_TaxID=29375;
RN 1;
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 49623;
RX PubMed=15289485; DOI=10.1101/gr.2649204;
RA Hill J.E., Penny S.L., Crowell K.G., Goh S.H., Hemmingsen S.M.;
RT "cpn60: a chaperonin sequence database."
RL Genome Res. 14:1669-1675 (2004).
DR EMBL; AY691242; AAT96592.1; -
DR InterPro: IPR008950; GroEL-ATPase.
PT NON TER 1 184
FT NON TER 184 184
SQ SEQUENCE 184 AA; 19763 MW; 16302D37B6F8508E CRC64;

Query Match 44.9%; Score 57; DB 2; Length 184;
Best Local Similarity 41.7%; Pred. No. 23;
Matches 10; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

Qy 2 KKMADNGTIVEBELKQLEQNLV 25
Db 75 EKVSNNGVITIEBSKTMTELDLV 98

RESULT 48
08PLJ9
ID 08PLJ9 PRELIMINARY; PRT; 409 AA.
AC 08PLJ9;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Two-component system sensor protein.
GN Name=regS; Ordered locus Names=XAC1798;
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92829;
RN 1;
RP SEQUENCE FROM N.A.
RX STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
RA da Silva A.C.R., Ferriz J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaglini R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Camavar F., Cardozo J., Chambergro F., Clapina L.P.,
RA Ciccarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spindola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RT "comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities."
RL Nature 417:459-463 (2002).
CC -1- SIMILARITY: Contains 1 histidine kinase domain.
DR EMBL; AB011812; AAM36661.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0016301; P:kinase activity; IEA.
DR GO; GO:0000155; P:two-component sensor molecule activity; IEA.

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DR GO:0007165; P:signal transduction; IEA.
 DR InterPro: IPR003594; AP01nd; APase.
 DR InterPro: IPR004358; Bact_sens_pr_C.
 DR InterPro: IPR005467; His_Kinase.
 DR InterPro: IPR003661; His_Kin_N.
 DR InterPro: IPR009082; His_Kin_homodm.
 DR Pfam: PF02518; HATPase_c1.1.
 DR Pfam: PF00512; HisKA; 1.
 DR PRINTS: PR00344; BCTRSNSOR.
 DR SMART: SM00387; HATPase_c1.1.
 DR SMART: SM00388; HisKA; 1.
 DR POSITIVE: PSS0109; HIS_KIN; 1.
 KM Complete proteome; Kinase; Phosphorylation; Sensory transduction;
 KM Transference.
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 Oy 5 ADNGITVE-ELKQLEQNMV 25
 Db 258 ADNGHLSREVAKVEVLEQMRLV 279
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 ID RALA_HUMAN STANDARD; PRT; 206 AA.
 AC P11233;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Ras-related protein Ral-A.
 GN Name=RALA; Synonyms=RAL;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89296492; PubMed=2662142;
 RA Chardin P., Tavittian A.;
 RT "Coding sequences of human rala and ralB cDNAs";
 RL Nucleic Acids Res. 17:4380-4380(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Platelet;
 RX MEDLINE=89380251; PubMed=2550440;
 RA Polakis P.G., Weber R.F., Neville B., Didsbury J.R., Evans T.,
 RT "Identification of the ral and rac1 gene products, low molecular mass
 RT GTP-binding proteins from human platelets";
 RL J. Biol. Chem. 264:16383-16389(1989).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Pohl H.L., Iikeda S.R., Aronstam R.S.;
 RT "cDNA clones of human proteins involved in signal transduction
 RT sequenced by the Guthrie cDNA resource center (www.cdna.org)";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Ryan E., Wilson C.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RX MEDLINE=2368257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge D.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bernaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uddin T.B., Toehiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McKean P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.D., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6]
 RP ISOPRENOLD.
 RX MEDLINE=91236758; PubMed=1903399;
 RA Kinsella B.T., Erdman R.A., Maltese W.A.;
 RT "Carboxyl-terminal isoprenylation of ras-related GTP-binding proteins
 RT encoded by rac1, rac2 and rala";
 RL J. Biol. Chem. 266:9786-9794(1991).
 RN [7]
 RP INTERACTION WITH RALBP1.
 RX MEDLINE=95403450; PubMed=7673236; DOI=10.1074/jbc.270.38.22473;
 RA Julien-Plores V., Dorseuil O., Romero F., Letourneur F.,
 RA Saragosti S., Berger R., Tavittian A., Gacon G., Camonis J.H.,
 RT "Bringing Ral GTPase to Rho pathways. RLR76, a Ral effector with
 RT CDC42/Rac GTPase-activating protein activity";
 RL J. Biol. Chem. 270:22473-22477(1995).
 CC -1- SUBUNIT: Interacts with RALBP1 via its effector domain.
 CC -1- SIMILARITY: Belongs to the small GTPase superfamily. Ras family.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch).
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 DR EMBL: X15014; CAA3118.1; -;
 DR EMBL: M29893; AAA36542.1; -;
 DR EMBL: AF493910; AAM12624.1; -;
 DR EMBL: AC004837; -; NOT ANNOTATED_CDS.
 DR EMBL: BC039858; AAH39658.1; -;
 DR PIR: S04596; TVH0UA.
 DR PDB: 1UAD; X-ray; A/B=9-183.
 DR Genew: HGNC:9839; RALA.
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 DR GO:0006935; P:chemotaxis; TAS.
 DR GO:0007165; P:signal transduction; TAS.
 DR InterPro: IPR001806; Ras trnsfrmg.
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 DR Pfam: PF00071; Ras; 1.
 DR PRINTS: PR00449; RASTRNSFRMG.
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 FT NP_BIND 68 72 GTP (By similarity).
 FT NP_BIND 127 130 GTP (By similarity).
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 FT LIPID 203 203 S-geranylgeranyl cysteine.
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DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Arabidopsis thaliana genomic DNA, chromosome 3, pl clone:MU8.

OS Arabidopsis thaliana (mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;

RN [1] SEQUENCE FROM N.A.

RP MEDLINE=20277480; PubMed=10819329;

RX RA Nakamura Y.;

RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence

RT features of the regions of 4,504,864 bp covered by sixty pl and TAC

RT clones.";

RL DNA Res. 7:131-135(2000).

RN [2]

RP SEQUENCE FROM N.A.

RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;

RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB028621; BAB01352.1; -.

DR HSSP; P06787; 1F55.

DR GO; GO:0005509; F:calcium ion binding; IEA.

DR InterPro; IPR002048; EF-hand.

DR InterPro; IPR010983; EF_Hand_like.

DR Pfam; PF00036; ehand; 4.

DR PRODOM; PD000012; EF-hand; 1.

DR SMART; SM00054; EFh; 2.

DR PROSITE; PS00018; EF_HAND; UNKNOWN 1.

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Query Match

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Db 70 NGTIDIEELKKCLELKL 87

Search completed: May 11, 2005, 21:27:14

Job time : 131.745 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 11, 2005, 21:16:44 ; Search time 32.4468 Seconds
(without alignments)
57.516 Million cell updates/sec

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Perfect score: 127
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Scoring table: BLOSUM62
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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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| 3 | 55 | 43.3 | 206 3 US-09-078-317-15 | Sequence 15, Appl |
| 4 | 55 | 43.3 | 206 3 US-09-454-818-15 | Sequence 15, Appl |
| 5 | 55 | 43.3 | 206 4 US-09-709-103-48 | Sequence 48, Appl |
| 6 | 55 | 43.3 | 206 4 US-09-439-410A-48 | Sequence 48, Appl |
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| 8 | 51.5 | 40.6 | 855 4 US-09-206-551-11 | Sequence 11, Appl |
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| 11 | 50 | 39.4 | 100 4 US-09-513-999C-6125 | Sequence 6125, Ap |
| 12 | 50 | 39.4 | 300 4 US-09-648-004-26 | Sequence 26, Appl |
| 13 | 50 | 39.4 | 300 4 US-10-872-419-26 | Sequence 26, Appl |
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| 15 | 50 | 39.4 | 537 4 US-09-543-681A-4729 | Sequence 4729, Ap |
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| 50 | 46 | 36.2 | 544 4 US-09-198-452A-153 | Sequence 153, App |
| 51 | 46 | 36.2 | 544 4 US-09-809-745-3 | Sequence 3, Appl1 |
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| 95 | 44 | 34.6 | 1577 2 US-08-793-824-2 | Sequence 2, Appl1 |
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| 111 | 43 | 33.9 | 229 | 4 | US-09-270-767-41871 | Sequence 41871, A | 184 | 42 | 33.1 | 835 | 4 | US-09-947-199A-2 | Sequence 2, Appl1 |
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| 119 | 43 | 33.9 | 543 | 1 | US-08-775-709-17 | Sequence 17, Appl1 | 192 | 42 | 33.1 | 1857 | 4 | US-09-917-25A-91 | Sequence 91, Appl1 |
| 120 | 43 | 33.9 | 543 | 1 | US-08-752-929-17 | Sequence 17, Appl1 | 193 | 42 | 33.1 | 1972 | 4 | US-08-875-435B-3 | Sequence 3, Appl1 |
| 121 | 43 | 33.9 | 543 | 3 | US-09-090-793-10 | Sequence 10, Appl1 | 194 | 42 | 33.1 | 1972 | 4 | US-08-875-435B-4 | Sequence 4, Appl1 |
| 122 | 43 | 33.9 | 543 | 3 | US-09-231-899-10 | Sequence 10, Appl1 | 195 | 42 | 33.1 | 1972 | 4 | US-09-538-092-1084 | Sequence 1084, Ap |
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| 125 | 43 | 33.9 | 1086 | 4 | US-09-543-681A-7696 | Sequence 7696, Ap | 198 | 42 | 33.1 | 1984 | 4 | US-09-949-016-7113 | Sequence 7113, Ap |
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| 133 | 42.5 | 33.5 | 429 | 3 | US-08-411-768B-4 | Sequence 4, Appl1 | 206 | 41.5 | 32.7 | 463 | 1 | US-07-951-715A-25 | Sequence 25, Appl1 |
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| 135 | 42.5 | 33.5 | 431 | 2 | US-08-401-068-4 | Sequence 4, Appl1 | 208 | 41.5 | 32.7 | 463 | 3 | US-08-459-595A-25 | Sequence 25, Appl1 |
| 136 | 42.5 | 33.5 | 431 | 2 | US-08-846-338-4 | Sequence 4, Appl1 | 209 | 41.5 | 32.7 | 463 | 3 | US-08-459-504B-25 | Sequence 25, Appl1 |
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| 141 | 42 | 33.1 | 60 | 3 | US-09-400-742-10 | Sequence 10, Appl1 | 214 | 41.5 | 32.7 | 577 | 4 | US-09-248-796A-19304 | Sequence 19304, A |
| 142 | 42 | 33.1 | 60 | 3 | US-08-618-651A-10 | Sequence 10, Appl1 | 215 | 41.5 | 32.7 | 639 | 3 | US-09-347-801-17 | Sequence 17, Appl1 |
| 143 | 42 | 33.1 | 60 | 3 | US-09-915-252-23 | Sequence 23, Appl1 | 216 | 41.5 | 32.7 | 639 | 3 | US-09-854-731-17 | Sequence 17, Appl1 |
| 144 | 42 | 33.1 | 60 | 4 | US-09-970-989A-23 | Sequence 23, Appl1 | 217 | 41 | 32.3 | 71 | 1 | US-08-606-789-6 | Sequence 6, Appl1 |
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| 148 | 42 | 33.1 | 200 | 2 | US-08-531-525-33 | Sequence 33, Appl1 | 221 | 41 | 32.3 | 84 | 4 | US-09-621-976-6554 | Sequence 6554, Ap |
| 149 | 42 | 33.1 | 200 | 2 | US-08-718-270A-33 | Sequence 33, Appl1 | 222 | 41 | 32.3 | 87 | 4 | US-09-621-976-4000 | Sequence 4000, Ap |
| 150 | 42 | 33.1 | 211 | 4 | US-09-248-796A-22054 | Sequence 22054, A | 223 | 41 | 32.3 | 106 | 4 | US-09-543-681A-7810 | Sequence 7810, Ap |
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| 152 | 42 | 33.1 | 268 | 4 | US-09-328-352-8118 | Sequence 8118, Ap | 225 | 41 | 32.3 | 113 | 4 | US-09-270-767-61866 | Sequence 61866, A |
| 153 | 42 | 33.1 | 275 | 4 | US-09-902-540-12895 | Sequence 12895, A | 226 | 41 | 32.3 | 123 | 4 | US-09-248-796A-23998 | Sequence 23998, A |
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| 155 | 42 | 33.1 | 278 | 3 | US-08-618-651A-8 | Sequence 8, Appl1 | 228 | 41 | 32.3 | 164 | 3 | US-08-765-381-2 | Sequence 2, Appl1 |
| 156 | 42 | 33.1 | 278 | 3 | US-09-215-252-7 | Sequence 7, Appl1 | 229 | 41 | 32.3 | 164 | 4 | US-09-443-218-2 | Sequence 2, Appl1 |
| 157 | 42 | 33.1 | 278 | 4 | US-09-970-989A-7 | Sequence 7, Appl1 | 230 | 41 | 32.3 | 164 | 4 | US-09-443-218-5 | Sequence 5, Appl1 |
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| 168 | 42 | 33.1 | 435 | 4 | US-09-762-194-8 | Sequence 8, Appl1 | 241 | 41 | 32.3 | 319 | 4 | US-09-107-532A-5542 | Sequence 5542, Ap |
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| 171 | 42 | 33.1 | 440 | 4 | US-09-762-194-4 | Sequence 4, Appl1 | 244 | 41 | 32.3 | 390 | 4 | US-09-107-532A-6668 | Sequence 6668, Ap |
| 172 | 42 | 33.1 | 504 | 4 | US-09-270-767-46764 | Sequence 46764, Ap | 245 | 41 | 32.3 | 397 | 4 | US-09-252-991A-22719 | Sequence 22719, A |
| 173 | 42 | 33.1 | 540 | 4 | US-09-902-540-9824 | Sequence 9824, Ap | 246 | 41 | 32.3 | 455 | 3 | US-09-035-382-2 | Sequence 2, Appl1 |

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| 248 | 41 | 32.3 | 469 | 4 | US-09-252-991A-27869 | Sequence 27869, A | 321 | 40.5 | 1813 | 4 | US-09-949-016-8284 | Sequence 8285, Ap |
| 249 | 41 | 32.3 | 490 | 3 | US-09-252-149B-26 | Sequence 26, App1 | 322 | 40.5 | 1813 | 4 | US-09-949-016-8285 | Sequence 8285, Ap |
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| 252 | 41 | 32.3 | 510 | 5 | PCT-US95-06556-3 | Sequence 3, App1 | 325 | 40.5 | 31.9 | 2 | US-08-222-617A-2 | Sequence 2, App1 |
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| 256 | 41 | 32.3 | 544 | 3 | US-09-124-491-10 | Sequence 10, App1 | 329 | 40 | 72 | 4 | US-09-107-433-2938 | Sequence 2938, Ap |
| 257 | 41 | 32.3 | 544 | 3 | US-09-383-912-10 | Sequence 10, App1 | 330 | 40 | 95 | 4 | US-09-489-039A-7564 | Sequence 7564, Ap |
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| 260 | 41 | 32.3 | 699 | 2 | US-08-694-865-16 | Sequence 16, App1 | 333 | 40 | 206 | 4 | US-09-134-000C-3442 | Sequence 3442, Ap |
| 261 | 41 | 32.3 | 699 | 3 | US-09-124-491-16 | Sequence 16, App1 | 334 | 40 | 207 | 2 | US-09-022-940-1 | Sequence 1, App1 |
| 262 | 41 | 32.3 | 699 | 4 | US-09-383-912-16 | Sequence 16, App1 | 335 | 40 | 207 | 3 | US-09-216-386-1 | Sequence 1, App1 |
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| 272 | 41 | 32.3 | 926 | 1 | US-08-387-156-6 | Sequence 6, App1 | 345 | 40 | 248 | 4 | US-09-902-540-16288 | Sequence 16288, A |
| 273 | 41 | 32.3 | 926 | 2 | US-08-694-865-6 | Sequence 6, App1 | 346 | 40 | 252 | 4 | US-09-252-991A-30813 | Sequence 30813, A |
| 274 | 41 | 32.3 | 926 | 2 | US-08-878-748-6 | Sequence 6, App1 | 347 | 40 | 265 | 3 | US-09-199-637A-31 | Sequence 31, App1 |
| 275 | 41 | 32.3 | 926 | 2 | US-08-535-837-2 | Sequence 6, App1 | 348 | 40 | 291 | 4 | US-09-107-532A-4763 | Sequence 4763, Ap |
| 276 | 41 | 32.3 | 926 | 2 | US-09-124-491-6 | Sequence 6, App1 | 349 | 40 | 298 | 4 | US-09-270-767-46126 | Sequence 46126, Ap |
| 277 | 41 | 32.3 | 926 | 4 | US-09-383-912-6 | Sequence 6, App1 | 350 | 40 | 320 | 2 | US-09-027-013-1 | Sequence 1, App1 |
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| 282 | 41 | 32.3 | 936 | 4 | US-08-976-566-12 | Sequence 12, App1 | 355 | 40 | 352 | 4 | US-09-949-016-6302 | Sequence 6302, Ap |
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| 284 | 41 | 32.3 | 943 | 4 | US-08-976-566-10 | Sequence 10, App1 | 357 | 40 | 367 | 4 | US-09-949-016-9627 | Sequence 9627, Ap |
| 285 | 41 | 32.3 | 951 | 1 | US-08-455-970A-14 | Sequence 14, App1 | 358 | 40 | 377 | 2 | US-08-839-581A-31 | Sequence 31, App1 |
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| 288 | 41 | 32.3 | 977 | 2 | US-08-694-865-8 | Sequence 8, App1 | 361 | 40 | 391 | 4 | US-09-438-185A-855 | Sequence 855, App |
| 289 | 41 | 32.3 | 977 | 2 | US-08-878-748-8 | Sequence 8, App1 | 362 | 40 | 401 | 3 | US-09-005-299-17 | Sequence 17, App1 |
| 290 | 41 | 32.3 | 977 | 3 | US-09-124-491-8 | Sequence 8, App1 | 363 | 40 | 401 | 4 | US-08-768-619-17 | Sequence 17, App1 |
| 291 | 41 | 32.3 | 977 | 4 | US-09-383-912-8 | Sequence 8, App1 | 364 | 40 | 401 | 5 | PCT-US96-09848-31 | Sequence 31, App1 |
| 292 | 41 | 32.3 | 1069 | 1 | US-07-777-713-9 | Sequence 9, App1 | 365 | 40 | 403 | 4 | US-09-248-796A-14239 | Sequence 14239, A |
| 293 | 41 | 32.3 | 1069 | 1 | US-08-170-126-4 | Sequence 4, App1 | 366 | 40 | 406 | 4 | US-09-134-000C-3752 | Sequence 3752, Ap |
| 294 | 41 | 32.3 | 1069 | 3 | US-08-954-418-4 | Sequence 4, App1 | 367 | 40 | 407 | 3 | US-09-005-298-15 | Sequence 15, App1 |
| 295 | 41 | 32.3 | 1098 | 1 | US-07-777-715-7 | Sequence 7, App1 | 368 | 40 | 407 | 4 | US-08-768-619-15 | Sequence 15, App1 |
| 296 | 41 | 32.3 | 1098 | 1 | US-08-170-126-2 | Sequence 2, App1 | 369 | 40 | 407 | 5 | PCT-US96-09848-15 | Sequence 15, App1 |
| 297 | 41 | 32.3 | 1098 | 3 | US-08-954-418-2 | Sequence 2, App1 | 370 | 40 | 411 | 4 | US-09-107-532A-442 | Sequence 442, Ap |
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| 299 | 41 | 32.3 | 1132 | 2 | US-08-446-010B-18 | Sequence 18, App1 | 372 | 40 | 442 | 3 | US-09-134-001C-3033 | Sequence 3033, Ap |
| 300 | 41 | 32.3 | 1132 | 2 | US-08-805-445-18 | Sequence 18, App1 | 373 | 40 | 462 | 3 | US-09-189-527-13 | Sequence 13, App1 |
| 301 | 41 | 32.3 | 1132 | 2 | US-08-064-067D-18 | Sequence 18, App1 | 374 | 40 | 553 | 4 | US-09-902-540-9807 | Sequence 9807, Ap |
| 302 | 41 | 32.3 | 1132 | 2 | US-09-066-208-18 | Sequence 18, App1 | 375 | 40 | 572 | 4 | US-09-702-705-1815 | Sequence 1815, Ap |
| 303 | 41 | 32.3 | 1142 | 1 | US-08-097-997A-11 | Sequence 11, App1 | 376 | 40 | 572 | 4 | US-09-736-457-1815 | Sequence 1815, Ap |
| 304 | 41 | 32.3 | 1142 | 3 | US-08-665-574C-11 | Sequence 11, App1 | 377 | 40 | 611 | 4 | US-09-671-325-1815 | Sequence 1815, Ap |
| 305 | 41 | 32.3 | 1142 | 3 | US-08-946-994-11 | Sequence 11, App1 | 378 | 40 | 622 | 4 | US-09-339-947A-1 | Sequence 1, App1 |
| 306 | 41 | 32.3 | 1154 | 1 | US-08-357-598-7 | Sequence 7, App1 | 379 | 40 | 631 | 4 | US-09-949-016-10606 | Sequence 10606, A |
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| 311 | 40.5 | 31.9 | 100 | 4 | US-09-134-000C-3989 | Sequence 3989, Ap | 384 | 40 | 774 | 2 | US-07-731-157A-7 | Sequence 7, App1 |
| 312 | 40.5 | 31.9 | 166 | 4 | US-09-252-991A-24467 | Sequence 24467, A | 385 | 40 | 774 | 2 | US-08-541-780-7 | Sequence 7, App1 |
| 313 | 40.5 | 31.9 | 602 | 4 | US-09-540-236-3263 | Sequence 3263, Ap | 386 | 40 | 812 | 4 | US-09-166-350-12 | Sequence 12, App1 |
| 314 | 40.5 | 31.9 | 840 | 4 | US-09-252-991A-19561 | Sequence 19561, A | 387 | 40 | 825 | 4 | US-09-438-185A-29 | Sequence 29, App1 |
| 315 | 40.5 | 31.9 | 1769 | 4 | US-09-949-016-8280 | Sequence 8280, Ap | 388 | 40 | 868 | 4 | US-09-538-092-787 | Sequence 787, App |
| 316 | 40.5 | 31.9 | 1769 | 4 | US-09-949-016-8281 | Sequence 8281, Ap | 389 | 40 | 913 | 3 | US-08-871-089-4 | Sequence 4, App1 |
| 317 | 40.5 | 31.9 | 1769 | 4 | US-09-949-016-8282 | Sequence 8282, Ap | 390 | 40 | 919 | 4 | US-09-248-796A-19408 | Sequence 19408, A |
| 318 | 40.5 | 31.9 | 1784 | 3 | US-09-040-738-2 | Sequence 2, App1 | 391 | 40 | 983 | 3 | US-09-412-554A-2 | Sequence 2, App1 |
| 319 | 40.5 | 31.9 | 1784 | 3 | US-08-652-426A-2 | Sequence 2, App1 | 392 | 40 | 1007 | 4 | US-09-538-092-736 | Sequence 736, App |

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|-----|------|------|------|---|----------------------|--------------------|-----|----|------|-----|---|----------------------|--------------------|
| 393 | 40 | 31.5 | 1024 | 4 | US-09-562-737-41 | Sequence 41, Appl | 466 | 39 | 30.7 | 275 | 4 | US-09-107-532A-6200 | Sequence 6200, Ap |
| 394 | 40 | 31.5 | 1024 | 4 | US-09-562-737-44 | Sequence 44, Appl | 467 | 39 | 30.7 | 281 | 4 | US-09-949-016-8397 | Sequence 8397, Ap |
| 395 | 40 | 31.5 | 1052 | 4 | US-09-949-016-11508 | Sequence 11508, A | 468 | 39 | 30.7 | 289 | 4 | US-09-198-452A-128 | Sequence 728, Appl |
| 396 | 40 | 31.5 | 1154 | 4 | US-09-963-137-203 | Sequence 203, Appl | 469 | 39 | 30.7 | 298 | 1 | US-08-393-988-10 | Sequence 10, Appl |
| 397 | 40 | 31.5 | 1231 | 4 | US-09-107-532A-5150 | Sequence 5150, Ap | 470 | 39 | 30.7 | 301 | 1 | US-08-393-988-12 | Sequence 12, Appl |
| 398 | 40 | 31.5 | 1735 | 4 | US-09-902-540-14547 | Sequence 14547, A | 471 | 39 | 30.7 | 301 | 4 | US-09-248-796A-36282 | Sequence 26282, A |
| 399 | 40 | 31.5 | 1788 | 2 | US-08-962-284-2 | Sequence 2, Appl1 | 472 | 39 | 30.7 | 301 | 4 | US-09-589-092-1302 | Sequence 1302, Ap |
| 400 | 40 | 31.5 | 2509 | 4 | US-09-452-991A-16642 | Sequence 16642, A | 473 | 39 | 30.7 | 308 | 4 | US-09-489-035A-8249 | Sequence 9249, Ap |
| 401 | 40 | 31.5 | 2636 | 4 | US-09-252-991A-25753 | Sequence 25753, A | 474 | 39 | 30.7 | 321 | 4 | US-09-328-352-4883 | Sequence 4883, Ap |
| 402 | 39.5 | 31.1 | 63 | 4 | US-09-448-796A-21270 | Sequence 21270, A | 475 | 39 | 30.7 | 326 | 4 | US-09-489-032A-7348 | Sequence 7348, Ap |
| 403 | 39.5 | 31.1 | 78 | 4 | US-09-621-976-7280 | Sequence 7280, Ap | 476 | 39 | 30.7 | 358 | 4 | US-09-248-796A-19081 | Sequence 19081, A |
| 404 | 39.5 | 31.1 | 112 | 4 | US-09-603-208A-38 | Sequence 38, Appl | 477 | 39 | 30.7 | 360 | 4 | US-09-710-279-2150 | Sequence 2150, A |
| 405 | 39.5 | 31.1 | 139 | 4 | US-09-538-092-693 | Sequence 693, Appl | 478 | 39 | 30.7 | 363 | 4 | US-09-107-532A-7017 | Sequence 7017, Ap |
| 406 | 39.5 | 31.1 | 247 | 4 | US-09-328-352-5648 | Sequence 5648, Ap | 479 | 39 | 30.7 | 367 | 3 | US-08-630-915A-3678 | Sequence 3678, Ap |
| 407 | 39.5 | 31.1 | 290 | 3 | US-08-936-165A-462 | Sequence 462, Appl | 480 | 39 | 30.7 | 368 | 4 | US-09-879-957-20 | Sequence 20, Appl |
| 408 | 39.5 | 31.1 | 329 | 3 | US-09-308-003-14 | Sequence 14, Appl1 | 481 | 39 | 30.7 | 368 | 4 | US-09-879-957-20 | Sequence 6301, Ap |
| 409 | 39.5 | 31.1 | 339 | 4 | US-09-107-532A-4033 | Sequence 4033, Ap | 482 | 39 | 30.7 | 373 | 4 | US-09-949-016-6301 | Sequence 6301, Ap |
| 410 | 39.5 | 31.1 | 406 | 4 | US-09-543-681A-6072 | Sequence 6072, Ap | 483 | 39 | 30.7 | 374 | 4 | US-09-949-016-7535 | Sequence 7535, Ap |
| 411 | 39.5 | 31.1 | 426 | 1 | US-08-197-792-41 | Sequence 41, Appl | 484 | 39 | 30.7 | 376 | 4 | US-09-710-279-2106 | Sequence 2106, Ap |
| 412 | 39.5 | 31.1 | 426 | 1 | US-08-459-850-41 | Sequence 41, Appl | 485 | 39 | 30.7 | 390 | 3 | US-09-108-020-36 | Sequence 36, Appl |
| 413 | 39.5 | 31.1 | 426 | 1 | US-08-459-214-41 | Sequence 41, Appl | 486 | 39 | 30.7 | 390 | 4 | US-09-901-151-5 | Sequence 5, Appl1 |
| 414 | 39.5 | 31.1 | 455 | 4 | US-09-949-016-11525 | Sequence 11525, A | 487 | 39 | 30.7 | 390 | 4 | US-09-901-151-6 | Sequence 6, Appl1 |
| 415 | 39.5 | 31.1 | 491 | 4 | US-09-489-039A-9206 | Sequence 9206, Ap | 488 | 39 | 30.7 | 390 | 4 | US-09-685-296-36 | Sequence 36, Appl |
| 416 | 39.5 | 31.1 | 511 | 4 | US-09-134-000C-5413 | Sequence 5413, Ap | 489 | 39 | 30.7 | 397 | 4 | US-09-901-151-2 | Sequence 2, Appl1 |
| 417 | 39.5 | 31.1 | 528 | 3 | US-08-889-841B-44 | Sequence 44, Appl | 490 | 39 | 30.7 | 407 | 4 | US-09-438-185A-691 | Sequence 691, App |
| 418 | 39.5 | 31.1 | 528 | 4 | US-09-419-362-44 | Sequence 44, Appl | 491 | 39 | 30.7 | 408 | 1 | US-07-951-715A-21 | Sequence 21, Appl |
| 419 | 39.5 | 31.1 | 575 | 4 | US-09-248-796A-17643 | Sequence 17643, A | 492 | 39 | 30.7 | 408 | 2 | US-08-459-448A-21 | Sequence 21, Appl |
| 420 | 39.5 | 31.1 | 587 | 4 | US-09-646-028-50 | Sequence 50, Appl | 493 | 39 | 30.7 | 408 | 3 | US-08-459-595A-21 | Sequence 21, Appl |
| 421 | 39.5 | 31.1 | 595 | 4 | US-09-646-028-56 | Sequence 56, Appl | 494 | 39 | 30.7 | 408 | 3 | US-08-459-595A-21 | Sequence 21, Appl |
| 422 | 39.5 | 31.1 | 601 | 4 | US-09-646-028-52 | Sequence 52, Appl | 495 | 39 | 30.7 | 408 | 3 | US-08-459-444-21 | Sequence 21, Appl |
| 423 | 39.5 | 31.1 | 608 | 4 | US-09-603-208A-36 | Sequence 36, Appl | 496 | 39 | 30.7 | 408 | 3 | US-09-547-422-21 | Sequence 21, Appl |
| 424 | 39.5 | 31.1 | 844 | 4 | US-09-991-258-19 | Sequence 19, Appl | 497 | 39 | 30.7 | 408 | 4 | US-09-988-462-21 | Sequence 21, Appl |
| 425 | 39.5 | 31.1 | 855 | 1 | US-08-022-835-6 | Sequence 6, Appl1 | 498 | 39 | 30.7 | 414 | 4 | US-09-901-151-4 | Sequence 40, Appl |
| 426 | 39.5 | 31.1 | 855 | 1 | US-08-388-809-6 | Sequence 6, Appl1 | 499 | 39 | 30.7 | 426 | 3 | US-08-676-444-40 | Sequence 40, Appl |
| 427 | 39.5 | 31.1 | 855 | 2 | US-08-647-714-6 | Sequence 6, Appl1 | 500 | 39 | 30.7 | 430 | 4 | US-09-328-352-5453 | Sequence 5453, Ap |
| 428 | 39.5 | 31.1 | 884 | 4 | US-09-328-352-4598 | Sequence 4598, Ap | 501 | 39 | 30.7 | 453 | 4 | US-09-543-681A-7700 | Sequence 7700, Ap |
| 429 | 39.5 | 31.1 | 1044 | 4 | US-09-107-532A-5229 | Sequence 5229, Ap | 502 | 39 | 30.7 | 457 | 4 | US-09-248-796A-32325 | Sequence 32325, A |
| 430 | 39.5 | 31.1 | 2296 | 1 | US-08-157-005-2 | Sequence 2, Appl1 | 503 | 39 | 30.7 | 464 | 1 | US-07-951-715A-22 | Sequence 22, Appl |
| 431 | 39.5 | 31.1 | 2396 | 3 | US-08-747-863-2 | Sequence 2, Appl1 | 504 | 39 | 30.7 | 464 | 2 | US-08-459-448A-22 | Sequence 22, Appl |
| 432 | 39.5 | 31.1 | 2396 | 4 | US-09-565-864-2 | Sequence 2, Appl1 | 505 | 39 | 30.7 | 464 | 3 | US-08-459-595A-22 | Sequence 22, Appl |
| 433 | 39.5 | 31.1 | 2396 | 4 | US-10-226-065-2 | Sequence 2, Appl1 | 506 | 39 | 30.7 | 464 | 3 | US-08-459-595A-22 | Sequence 22, Appl |
| 434 | 39 | 30.7 | 14 | 1 | US-07-872-644-28 | Sequence 28, Appl | 507 | 39 | 30.7 | 464 | 3 | US-08-459-444-22 | Sequence 0, Appl |
| 435 | 39 | 30.7 | 14 | 1 | US-08-297-494-28 | Sequence 28, Appl | 508 | 39 | 30.7 | 464 | 3 | US-09-547-422-22 | Sequence 0, Appl |
| 436 | 39 | 30.7 | 14 | 1 | US-08-297-510-28 | Sequence 28, Appl | 509 | 39 | 30.7 | 464 | 4 | US-09-988-462-22 | Sequence 22, Appl |
| 437 | 39 | 30.7 | 14 | 1 | US-08-479-532-28 | Sequence 28, Appl | 510 | 39 | 30.7 | 493 | 4 | US-09-949-016-7399 | Sequence 7399, Ap |
| 438 | 39 | 30.7 | 14 | 1 | US-08-455-526-28 | Sequence 28, Appl | 511 | 39 | 30.7 | 494 | 4 | US-09-248-796A-15974 | Sequence 15974, A |
| 439 | 39 | 30.7 | 14 | 1 | US-08-455-525-28 | Sequence 28, Appl | 512 | 39 | 30.7 | 539 | 2 | US-08-978-182-3 | Sequence 3, Appl1 |
| 440 | 39 | 30.7 | 14 | 3 | US-09-139-491-28 | Sequence 28, Appl | 513 | 39 | 30.7 | 539 | 2 | US-09-205-681-3 | Sequence 3, Appl1 |
| 441 | 39 | 30.7 | 14 | 4 | US-09-883-825-28 | Sequence 28, Appl | 514 | 39 | 30.7 | 541 | 4 | US-08-828-199A-2 | Sequence 2, Appl1 |
| 442 | 39 | 30.7 | 14 | 5 | PCT-US92-03222-28 | Sequence 28, Appl | 515 | 39 | 30.7 | 545 | 4 | US-09-604-957-4 | Sequence 4, Appl1 |
| 443 | 39 | 30.7 | 75 | 2 | US-08-715-527-4 | Sequence 4, Appl1 | 516 | 39 | 30.7 | 547 | 2 | US-08-467-822-35 | Sequence 35, Appl |
| 444 | 39 | 30.7 | 75 | 5 | PCT-US95-06406A-4 | Sequence 4, Appl1 | 517 | 39 | 30.7 | 547 | 3 | US-08-432-697-35 | Sequence 35, Appl |
| 445 | 39 | 30.7 | 83 | 3 | US-09-134-001C-5335 | Sequence 5335, Ap | 518 | 39 | 30.7 | 547 | 3 | US-08-466-248-35 | Sequence 35, Appl |
| 446 | 39 | 30.7 | 95 | 4 | US-09-107-433-3132 | Sequence 3132, Ap | 519 | 39 | 30.7 | 561 | 1 | US-09-640-305-2 | Sequence 2, Appl1 |
| 447 | 39 | 30.7 | 95 | 1 | US-07-987-272A-9 | Sequence 9, Appl1 | 520 | 39 | 30.7 | 561 | 1 | US-08-360-672-2 | Sequence 2, Appl1 |
| 448 | 39 | 30.7 | 97 | 4 | US-09-461-912A-48 | Sequence 48, Appl | 521 | 39 | 30.7 | 573 | 2 | US-08-706-209-1 | Sequence 1, Appl1 |
| 449 | 39 | 30.7 | 104 | 1 | US-08-052-681-2 | Sequence 2, Appl1 | 522 | 39 | 30.7 | 573 | 3 | US-08-981-787-1 | Sequence 1, Appl1 |
| 450 | 39 | 30.7 | 134 | 4 | US-10-000-489-2 | Sequence 2, Appl1 | 523 | 39 | 30.7 | 573 | 3 | US-08-461-722-1 | Sequence 1, Appl1 |
| 451 | 39 | 30.7 | 136 | 4 | US-09-248-796A-18002 | Sequence 18002, A | 524 | 39 | 30.7 | 573 | 3 | US-08-336-251-1 | Sequence 1, Appl1 |
| 452 | 39 | 30.7 | 156 | 4 | US-09-393-627B-26 | Sequence 26, Appl | 525 | 39 | 30.7 | 573 | 4 | US-09-468-041-1 | Sequence 1, Appl1 |
| 453 | 39 | 30.7 | 170 | 4 | US-09-134-000C-4756 | Sequence 4756, Ap | 526 | 39 | 30.7 | 573 | 4 | US-08-981-861-1 | Sequence 1, Appl1 |
| 454 | 39 | 30.7 | 170 | 4 | US-09-348-796A-19501 | Sequence 19501, A | 527 | 39 | 30.7 | 573 | 4 | US-09-613-743A-1 | Sequence 1, Appl1 |
| 455 | 39 | 30.7 | 171 | 4 | US-09-328-352-4783 | Sequence 4783, Ap | 528 | 39 | 30.7 | 573 | 4 | US-09-847-637B-7 | Sequence 7, Appl1 |
| 456 | 39 | 30.7 | 198 | 4 | US-09-328-352-6068 | Sequence 6068, Ap | 529 | 39 | 30.7 | 573 | 4 | US-09-847-637B-8 | Sequence 8, Appl1 |
| 457 | 39 | 30.7 | 223 | 4 | US-09-543-681A-5667 | Sequence 5667, Ap | 530 | 39 | 30.7 | 573 | 4 | US-09-809-745-2 | Sequence 2, Appl1 |
| 458 | 39 | 30.7 | 224 | 4 | US-09-540-236-3782 | Sequence 3782, Ap | 531 | 39 | 30.7 | 573 | 5 | PCT-US94-06362-1 | Sequence 1, Appl1 |
| 459 | 39 | 30.7 | 229 | 4 | US-09-270-767-32090 | Sequence 32090, A | 532 | 39 | 30.7 | 573 | 5 | PCT-US96-11373-1 | Sequence 1, Appl1 |
| 460 | 39 | 30.7 | 229 | 4 | US-09-270-767-47307 | Sequence 47307, A | 533 | 39 | 30.7 | 573 | 5 | PCT-US96-11373-1 | Sequence 1, Appl1 |
| 461 | 39 | 30.7 | 237 | 4 | US-09-107-532A-6583 | Sequence 6583, Ap | 534 | 39 | 30.7 | 604 | 4 | US-09-949-016-6585 | Sequence 6585, Ap |
| 462 | 39 | 30.7 | 241 | 3 | US-08-896-933-32 | Sequence 32, Appl | 535 | 39 | 30.7 | 604 | 4 | US-09-949-016-10250 | Sequence 10250, A |
| 463 | 39 | 30.7 | 241 | 3 | US-09-114-235-32 | Sequence 32, Appl | 536 | 39 | 30.7 | 637 | 4 | US-09-949-016-10426 | Sequence 10426, A |
| 464 | 39 | 30.7 | 241 | 4 | US-09-108-008B-32 | Sequence 32, Appl | 537 | 39 | 30.7 | 657 | 4 | US-09-949-016-6174 | Sequence 6174, Ap |
| 465 | 39 | 30.7 | 244 | 4 | US-09-710-279-994 | Sequence 994, Appl | 538 | 39 | 30.7 | 678 | 4 | US-09-949-016-10001 | Sequence 10001, A |

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|-----|------|------|------|---|----------------------|--------------------|-----|------|------|------|---|----------------------|-------------------|
| 539 | 39 | 30.7 | 691 | 4 | US-09-830-217-12 | Sequence 12, Appl | 612 | 38.5 | 30.3 | 450 | 4 | US-09-252-991A-24440 | Sequence 24440, A |
| 540 | 39 | 30.7 | 691 | 4 | US-10-278-946-12 | Sequence 12, Appl | 613 | 38.5 | 30.3 | 476 | 4 | US-09-536-977-74 | Sequence 74, Appl |
| 541 | 39 | 30.7 | 703 | 3 | US-08-910-925-4 | Sequence 4, Appl | 614 | 38.5 | 30.3 | 494 | 4 | US-09-252-991A-28022 | Sequence 28022, A |
| 542 | 39 | 30.7 | 717 | 3 | US-08-910-925-1 | Sequence 1, Appl | 615 | 38.5 | 30.3 | 536 | 4 | US-09-595-857B-31 | Sequence 31, Appl |
| 543 | 39 | 30.7 | 743 | 3 | US-08-910-925-3 | Sequence 3, Appl | 616 | 38.5 | 30.3 | 602 | 4 | US-09-248-796A-19204 | Sequence 19204, A |
| 544 | 39 | 30.7 | 743 | 4 | US-09-949-016-6261 | Sequence 6261, Ap | 617 | 38.5 | 30.3 | 635 | 4 | US-09-536-977-68 | Sequence 68, Appl |
| 545 | 39 | 30.7 | 748 | 4 | US-09-585-858-25 | Sequence 25, Appl | 618 | 38.5 | 30.3 | 657 | 3 | US-09-256-194-2 | Sequence 2, Appl |
| 546 | 39 | 30.7 | 748 | 4 | US-10-270-878-25 | Sequence 25, Appl | 619 | 38.5 | 30.3 | 665 | 2 | US-08-448-603A-32 | Sequence 32, Appl |
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| 551 | 39 | 30.7 | 972 | 4 | US-09-710-092-2 | Sequence 2, Appl | 624 | 38.5 | 30.3 | 687 | 4 | US-09-536-977-70 | Sequence 70, Appl |
| 552 | 39 | 30.7 | 973 | 4 | US-09-392-714A-24 | Sequence 24, Appl | 625 | 38.5 | 30.3 | 715 | 4 | US-09-328-352-6830 | Sequence 6830, Ap |
| 553 | 39 | 30.7 | 976 | 3 | US-09-104-324B-4 | Sequence 4, Appl | 626 | 38.5 | 30.3 | 732 | 4 | US-08-671-757A-8 | Sequence 7, Appl |
| 554 | 39 | 30.7 | 976 | 4 | US-09-538-092-1339 | Sequence 1339, Ap | 627 | 38.5 | 30.3 | 732 | 4 | US-08-671-757A-8 | Sequence 8, Appl |
| 555 | 39 | 30.7 | 989 | 4 | US-09-902-540-15948 | Sequence 15948, A | 628 | 38.5 | 30.3 | 732 | 4 | US-09-015-078-7 | Sequence 7, Appl |
| 556 | 39 | 30.7 | 1018 | 4 | US-10-101-664A-909 | Sequence 909, Ap | 629 | 38.5 | 30.3 | 732 | 4 | US-09-015-078-8 | Sequence 8, Appl |
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| 558 | 39 | 30.7 | 1130 | 2 | US-08-460-309-2 | Sequence 2, Appl | 631 | 38.5 | 30.3 | 837 | 1 | US-07-923-976-2 | Sequence 2, Appl |
| 559 | 39 | 30.7 | 1130 | 2 | US-08-125-077-2 | Sequence 2, Appl | 632 | 38.5 | 30.3 | 857 | 2 | US-08-448-603A-30 | Sequence 30, Appl |
| 560 | 39 | 30.7 | 1130 | 6 | 5444158-2 | Sequence 2, Appl | 633 | 38.5 | 30.3 | 857 | 3 | US-09-134-075-30 | Sequence 30, Appl |
| 561 | 39 | 30.7 | 1130 | 6 | 5444158-2 | Patent No. 5444158 | 634 | 38.5 | 30.3 | 857 | 3 | US-09-492-739-30 | Sequence 30, Appl |
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| 563 | 39 | 30.7 | 1237 | 1 | US-08-241-853-2 | Sequence 2, Appl | 636 | 38.5 | 30.3 | 1019 | 4 | US-09-252-991A-24417 | Sequence 24417, A |
| 564 | 39 | 30.7 | 1237 | 2 | US-08-850-917-2 | Sequence 2, Appl | 637 | 38.5 | 30.3 | 1048 | 4 | US-08-887-534A-85 | Sequence 85, Appl |
| 565 | 39 | 30.7 | 1240 | 3 | US-08-930-996A-4 | Sequence 4, Appl | 638 | 38.5 | 30.3 | 1048 | 4 | US-09-527-431-85 | Sequence 85, Appl |
| 566 | 39 | 30.7 | 1270 | 4 | US-09-710-092-10 | Sequence 10, Appl | 639 | 38.5 | 30.3 | 1048 | 4 | US-09-446-861-85 | Sequence 85, Appl |
| 567 | 39 | 30.7 | 1354 | 3 | US-08-685-871-2 | Sequence 2, Appl | 640 | 38 | 29.9 | 37 | 3 | US-08-974-549A-68 | Sequence 68, Appl |
| 568 | 39 | 30.7 | 1426 | 4 | US-09-710-092-14 | Sequence 14, Appl | 641 | 38 | 29.9 | 37 | 3 | US-08-974-549A-210 | Sequence 210, Ap |
| 569 | 39 | 30.7 | 1430 | 3 | US-09-008-172-2 | Sequence 2, Appl | 642 | 38 | 29.9 | 37 | 4 | US-08-912-951-68 | Sequence 68, Appl |
| 570 | 39 | 30.7 | 1430 | 3 | US-09-210-361-6 | Sequence 6, Appl | 643 | 38 | 29.9 | 37 | 4 | US-09-402-181B-68 | Sequence 68, Appl |
| 571 | 39 | 30.7 | 1430 | 4 | US-09-740-374-6 | Sequence 6, Appl | 644 | 38 | 29.9 | 37 | 4 | US-09-402-181B-210 | Sequence 210, Ap |
| 572 | 39 | 30.7 | 1630 | 4 | US-09-902-540-15551 | Sequence 15551, A | 645 | 38 | 29.9 | 37 | 4 | US-09-721-456-68 | Sequence 68, Appl |
| 573 | 39 | 30.7 | 1630 | 4 | US-09-538-092-1077 | Sequence 1077, Ap | 646 | 38 | 29.9 | 37 | 4 | US-09-721-456-210 | Sequence 210, Ap |
| 574 | 39 | 30.7 | 1960 | 4 | US-09-949-016-10872 | Sequence 10872, A | 647 | 38 | 29.9 | 42 | 1 | US-08-444-005-27 | Sequence 27, Appl |
| 575 | 39 | 30.7 | 3070 | 4 | US-09-961-403-7 | Sequence 7, Appl | 648 | 38 | 29.9 | 42 | 4 | US-09-614-847-134 | Sequence 134, Ap |
| 576 | 39 | 30.7 | 3084 | 4 | US-09-562-702A-12 | Sequence 12, Appl | 649 | 38 | 29.9 | 44 | 4 | US-09-614-847-149 | Sequence 149, Ap |
| 577 | 39 | 30.7 | 3088 | 4 | US-09-562-702A-8 | Sequence 8, Appl | 650 | 38 | 29.9 | 45 | 2 | US-08-219-237B-10 | Sequence 10, Appl |
| 578 | 39 | 30.7 | 3089 | 4 | US-09-562-702A-4 | Sequence 4, Appl | 651 | 38 | 29.9 | 48 | 4 | US-09-614-847-135 | Sequence 135, Ap |
| 579 | 39 | 30.7 | 3106 | 4 | US-09-562-702A-10 | Sequence 10, Appl | 652 | 38 | 29.9 | 50 | 4 | US-09-614-847-150 | Sequence 150, Ap |
| 580 | 39 | 30.7 | 3110 | 4 | US-09-562-702A-2 | Sequence 2, Appl | 653 | 38 | 29.9 | 54 | 3 | US-08-851-843A-21 | Sequence 21, Appl |
| 581 | 39 | 30.7 | 3110 | 4 | US-09-562-702A-6 | Sequence 6, Appl | 654 | 38 | 29.9 | 54 | 3 | US-08-854-050-21 | Sequence 21, Appl |
| 582 | 39 | 30.7 | 3110 | 4 | US-09-561-709B-7 | Sequence 7, Appl | 655 | 38 | 29.9 | 54 | 3 | US-09-430-323-21 | Sequence 21, Appl |
| 583 | 39 | 30.7 | 3110 | 4 | US-09-917-254-86 | Sequence 86, Appl | 656 | 38 | 29.9 | 54 | 4 | US-09-766-253-21 | Sequence 21, Appl |
| 584 | 39 | 30.7 | 3110 | 4 | US-09-949-016-5937 | Sequence 5937, Ap | 657 | 38 | 29.9 | 63 | 3 | US-08-894-626-1 | Sequence 1, Appl |
| 585 | 39 | 30.7 | 3111 | 2 | US-08-460-309-4 | Sequence 4, Appl | 658 | 38 | 29.9 | 64 | 4 | US-09-248-796A-24105 | Sequence 24105, A |
| 586 | 39 | 30.7 | 3111 | 2 | US-08-125-077-4 | Sequence 4, Appl | 659 | 38 | 29.9 | 65 | 2 | US-08-667-087B-31 | Sequence 31, Appl |
| 587 | 39 | 30.3 | 54 | 4 | US-09-536-977-16 | Sequence 16, Appl | 660 | 38 | 29.9 | 68 | 4 | US-09-527-236A-22 | Sequence 22, Appl |
| 588 | 38.5 | 30.3 | 121 | 4 | US-09-248-796A-19888 | Sequence 19888, A | 661 | 38 | 29.9 | 70 | 4 | US-09-756-854-22 | Sequence 22, Appl |
| 589 | 38.5 | 30.3 | 124 | 4 | US-09-536-977-44 | Sequence 44, Appl | 662 | 38 | 29.9 | 70 | 4 | US-09-159-277A-5 | Sequence 5, Appl |
| 590 | 38.5 | 30.3 | 129 | 4 | US-09-583-110-3496 | Sequence 3496, Ap | 663 | 38 | 29.9 | 70 | 4 | US-08-844-691A-5 | Sequence 5, Appl |
| 591 | 38.5 | 30.3 | 134 | 4 | US-09-107-433-4837 | Sequence 4837, Ap | 664 | 38 | 29.9 | 77 | 4 | US-08-828-683A-24 | Sequence 24, Appl |
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| 593 | 38.5 | 30.3 | 192 | 4 | US-09-248-796A-21994 | Sequence 21994, A | 666 | 38 | 29.9 | 84 | 4 | US-09-069-827B-119 | Sequence 119, Ap |
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| 900 | 38 | 29.9 | 841 | 4 | US-09-861-451A-30 | Sequence 54, Appl1 | 974 | 38 | 29.9 | 312 | 4 | US-09-270-767-47024 | Sequence 47024, A |
| 901 | 38 | 29.9 | 843 | 4 | US-10-164-595-54 | Sequence 2, Appl1 | 975 | 38 | 29.9 | 317 | 3 | US-09-327-984A-37 | Sequence 37, Appl |
| 902 | 38 | 29.9 | 850 | 4 | US-09-952-060-2 | | 976 | 38 | 29.9 | | | | |

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| 977 | 37.5 | 29.5 | 324 | 4 | US-09-2248-7966A-16963 | Sequence 16963, A |
| 978 | 37.5 | 29.5 | 375 | 4 | US-09-533-0292-12 | Sequence 12, Appl |
| 979 | 37.5 | 29.5 | 389 | 4 | US-09-800-170-18 | Sequence 18, Appl |
| 980 | 37.5 | 29.5 | 420 | 4 | US-09-252-9914A-19117 | Sequence 19117, A |
| 981 | 37.5 | 29.5 | 420 | 4 | US-09-591-2979A-29 | Sequence 29, Appl |
| 982 | 37.5 | 29.5 | 424 | 1 | US-08-197-7922-11 | Sequence 31, Appl |
| 983 | 37.5 | 29.5 | 424 | 1 | US-08-445-850-21 | Sequence 31, Appl |
| 984 | 37.5 | 29.5 | 424 | 1 | US-08-459-214-31 | Sequence 31, Appl |
| 985 | 37.5 | 29.5 | 427 | 4 | US-09-328-352-4720 | Sequence 4720, Appl |
| 986 | 37.5 | 29.5 | 495 | 3 | US-08-889-8418B-25 | Sequence 25, Appl |
| 987 | 37.5 | 29.5 | 495 | 3 | US-08-888-8418B-28 | Sequence 28, Appl |
| 988 | 37.5 | 29.5 | 495 | 4 | US-09-419-362-25 | Sequence 25, Appl |
| 989 | 37.5 | 29.5 | 495 | 4 | US-09-419-362-28 | Sequence 28, Appl |
| 990 | 37.5 | 29.5 | 501 | 2 | US-08-448-603A-2 | Sequence 2, Appl |
| 991 | 37.5 | 29.5 | 501 | 3 | US-09-134-075-2 | Sequence 2, Appl |
| 992 | 37.5 | 29.5 | 501 | 3 | US-09-492-739-2 | Sequence 2, Appl |
| 993 | 37.5 | 29.5 | 501 | 4 | US-09-966-931A-2 | Sequence 2, Appl |
| 994 | 37.5 | 29.5 | 511 | 3 | US-08-448-603A-1 | Sequence 1, Appl |
| 995 | 37.5 | 29.5 | 511 | 3 | US-09-134-075-1 | Sequence 1, Appl |
| 996 | 37.5 | 29.5 | 511 | 3 | US-08-889-8418B-41 | Sequence 41, Appl |
| 997 | 37.5 | 29.5 | 511 | 3 | US-09-482-739-1 | Sequence 1, Appl |
| 998 | 37.5 | 29.5 | 511 | 4 | US-09-419-362-41 | Sequence 41, Appl |
| 999 | 37.5 | 29.5 | 511 | 4 | US-09-966-931A-1 | Sequence 1, Appl |
| 1000 | 37.5 | 29.5 | 534 | 4 | US-09-057-936-6 | Sequence 6, Appl |

ALIGNMENTS

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ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-531-525-31

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| Query Match | 43.3%; | Score 55; | DB 2; | Length 205 |
| Best Local Similarity | 41.7%; | Pred. No. 2.8; | | |
| Matches 10; | Conservative 4; | Mismatches 10; | Indels | |

QY 1 KKKMADNGTITVEELKQLLQWNL 24
| : ||| | ||| :
Db 128 KSPLEDKRQVSVEAKNRAEQWNV 151

RESULT 2
 US-08-718-270A-31
 Sequence 31, Application US/08718270A
 Patent No. 5910478
 GENERAL INFORMATION:
 APPLICANT: Hlavka, Joseph J.
 APPLICANT: Pincus, Matthew R.
 APPLICANT: No. 59104781e, John F.
 APPLICANT: Abajian, Henry B.
 APPLICANT: Kende, Andrew S.
 TITLE OF INVENTION: Peptidomimetics inhibiting
 the Oncogenic Action of P21 Ras

```

1 ADDRESS: Greenlee, Winner and Sullivan, P.C.
2 STREET: 5370 Manhattan Circle, Suite 201
3 CITY: Boulder
4 STATE: Colorado
5 COUNTRY: US
6 ZIP: 80303
7
8 COMPUTER READABLE FORM:
9 MEDIUM TYPE: Floppy disk
10 COMPUTER: IBM PC compatible
11 OPERATING SYSTEM: PC-DOS/MS-DOS
12 SOFTWARE: PatentIn Release #1.0, Version #1.30
13
14 CURRENT APPLICATION DATA:
15 APPLICATION NUMBER: US/08/718,270A
16 FILING DATE: 20-SEP-1996
17 CLASSIFICATION: 514
18
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER: US 08/531,525
21 FILING DATE: 21-SEP-1995
22
23 PRIOR APPLICATION DATA:
24 APPLICATION NUMBER: US 60/004,091
25 FILING DATE: 21-SEP-1995
26
27 ATTORNEY/AGENT INFORMATION:
28 NAME: Felder, Donna M.
29 REGISTRATION NUMBER: 33,878
30 REFERENCE/DOCKET NUMBER: 78-95
31 TELECOMMUNICATION INFORMATION:
32 TELEPHONE: (303) 499-8080
33 TELEFAX: (303) 499-8089
34
35 INFORMATION FOR SEQ ID NO: 31:
36 SEQUENCE CHARACTERISTICS:
37 LENGTH: 205 amino acids
38 TYPE: amino acid
39 STRANDEDNESS: single
40 TOPOLOGY: linear
41 MOLECULE TYPE: protein
42 HYPOTHETICAL: NO
43 ORIGINAL SOURCE:
44 ORGANISM: Homo sapiens
45
46 US-08-718-270A-31
47
48 Query Match 43.3% Score 55; DB 2; Length 205;
49 Best Local Similarity 41.7% Pred. No. 2.8;
50 Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
51
52 1 KKKKADNGITVEELKQLLEQNNL 24
53 | | | | | | | | | |
54 ::::: | | | | |

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Db 128 KSDLEDKQVSVBEAKRABQNMV 151

RESULT 3

US-09-078-317-15
; Sequence 15, Application US/09078317
; Patent No. 6017710
; GENERAL INFORMATION:
; APPLICANT: Allen, Maxine J.
; APPLICANT: Rutter, Marc
; APPLICANT: Buckler, Alan J.
; TITLE OF INVENTION: RAO Genes and Their Uses
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bozicevic & Reed, LLP
; STREET: 285 Hamilton Ave, Suite 200
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; APPLICATION NUMBER: US/09/078.317
; FILING DATE: 13-MAY-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Francis, Carol L.
; REGISTRATION NUMBER: 36,513
; REFERENCE/DOCKET NUMBER: SEQ-18P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-327-3400
; TELEFAX: 650-327-3231
; TELEX:
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 206 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6017710e
; US-09-078-317-15

Query Match 43.3%; Score 55; DB 3; Length 206;
Best Local Similarity 41.7%; Pred. No. 2.9;
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 KKKMADNGITVVELKQLEQNMV 24
Db 128 KSDLEDKQVSVBEAKRABQNMV 151

RESULT 4

US-09-454-818-15
; Sequence 15, Application US/09454818
; Patent No. 6383792
; GENERAL INFORMATION:
; APPLICANT: Allen, Maxine J.
; APPLICANT: Rutter, Marc
; APPLICANT: Buckler, Alan J.
; TITLE OF INVENTION: RAO Genes and Their Uses
; FILE REFERENCE: AYS-018DIV
; CURRENT APPLICATION NUMBER: US/09/454.818
; CURRENT FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 09/078.317
; PRIOR FILING DATE: 1998-05-13
; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-454-818-15

Query Match 43.3%; Score 55; DB 3; Length 206;
Best Local Similarity 41.7%; Pred. No. 2.9;
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 KKKMADNGITVVELKQLEQNMV 24
Db 128 KSDLEDKQVSVBEAKRABQNMV 151

RESULT 5

US-09-709-103-48
; Sequence 48, Application US/09709103
; Patent No. 6733991
; GENERAL INFORMATION:
; APPLICANT: Ciemowski, Mary
; APPLICANT: Duzic, Emir
; TITLE OF INVENTION: AGS Proteins and Nucleic Acid Molecules and Uses Therefor
; FILE REFERENCE: 60388-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/709.103
; CURRENT FILING DATE: 2000-11-08
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-09-709-103-48

Query Match 43.3%; Score 55; DB 4; Length 206;
Best Local Similarity 41.7%; Pred. No. 2.9;
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

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RESULT 6

US-09-439-410A-48
; Sequence 48, Application US/09439410A
; Patent No. 6746852
; GENERAL INFORMATION:
; APPLICANT: Ciemowski, Mary
; APPLICANT: Duzic, Emir
; TITLE OF INVENTION: AGS PROTEIN AND NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: 1919/60388-B
; CURRENT APPLICATION NUMBER: US/09/439.410A
; CURRENT FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-439-410A-48

Query Match 43.3%; Score 55; DB 4; Length 206;
Best Local Similarity 41.7%; Pred. No. 2.9;
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 KKKMADNGITVVELKQLEQNMV 24
Db 128 KSDLEDKQVSVBEAKRABQNMV 151

RESULT 7

US-09-543-681A-7926
; Sequence 7926, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 7926
; LENGTH: 300
; TYPE: PRF
; ORGANISM: Proteus mirabilis
US-09-543-681A-7926

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Best Local Similarity 47.6%; Pred. No. 8.5;
Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 3 KXADNGTIVEELKQLEQNLV 23
DB 59 KLTDDGAILYEHAKQITLQAFN 79

RESULT 8
US-09-206-551-11
; Sequence 11, Application US/09206551B

; Patent No. 6521739
; GENERAL INFORMATION:
; APPLICANT: Hahn, Beatrice H.
; APPLICANT: Gao, Feng
; APPLICANT: Marx, Preston A.
; APPLICANT: Shaw, George M.
; APPLICANT: Smith, Stephen M.
; APPLICANT: Georges-Courbot, Marie Claude
; APPLICANT: Lu, Chang Yong
; TITLE OF INVENTION: Complete Genome Sequences of a Simian
; TITLE OF INVENTION: Immunodeficiency Virus from a Red-Capped
; FILE REFERENCE: D6286
; CURRENT APPLICATION NUMBER: US/09/206,551B
; CURRENT FILING DATE: 1998-12-07
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 11
; LENGTH: 855
; TYPE: PRF
; ORGANISM: Simian immunodeficiency virus
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of homologous region of
; OTHER INFORMATION: A_U455 lentiviral env protein
US-09-206-551-11

Query Match 40.6%; Score 51.5; DB 4; Length 855;
Best Local Similarity 43.5%; Pred. No. 45;
Matches 10; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

QY 4 MADNGTIVE-ELKQLEQNLV 25
DB 401 MGPNGTITLQCRITKQINNMQRV 423

RESULT 9
US-09-206-551-12
; Sequence 12, Application US/09206551B
; Patent No. 6521739
; GENERAL INFORMATION:
; APPLICANT: Hahn, Beatrice H.
; APPLICANT: Gao, Feng
; APPLICANT: Marx, Preston A.

; APPLICANT: Shaw, George M.
; APPLICANT: Smith, Stephen M.
; APPLICANT: Georges-Courbot, Marie Claude
; APPLICANT: Lu, Chang Yong
; TITLE OF INVENTION: Complete Genome Sequences of a Simian
; TITLE OF INVENTION: Immunodeficiency Virus from a Red-Capped
; FILE REFERENCE: D6286
; CURRENT APPLICATION NUMBER: US/09/206,551B
; CURRENT FILING DATE: 1998-12-07
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 12
; LENGTH: 855
; TYPE: PRF
; ORGANISM: Simian immunodeficiency virus
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of homologous region of
; OTHER INFORMATION: B_HXB2R lentiviral env protein
US-09-206-551-12

Query Match 40.6%; Score 51.5; DB 4; Length 855;
Best Local Similarity 43.5%; Pred. No. 45;
Matches 10; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

QY 4 MADNGTIVE-ELKQLEQNLV 25
DB 401 MGPNGTITLQCRITKQINNMQRV 423

RESULT 10
US-09-248-796A-17215
; Sequence 17215, Application US/09248796A

; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 17215
; LENGTH: 770
; TYPE: PRF
; ORGANISM: Candida albicans
US-09-248-796A-17215

Query Match 39.8%; Score 50.5; DB 4; Length 770;
Best Local Similarity 34.6%; Pred. No. 56;
Matches 9; Conservative 9; Mismatches 7; Indels 1; Gaps 1;

QY 1 KKKMADNGTIVEELKQLE-QMNLV 25
DB 524 EKQIDEGFTADIDKEHKQWNNIL 549

RESULT 11
US-09-513-999C-6125
; Sequence 6125, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclet, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59_US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 3681
SOFTWARE: Patent.pm
SEQ ID NO: 6125
LENGTH: 100
TYPE: PRF
ORGANISM: Homo sapiens
US-09-513-999C-6125

Query Match 39.4%; Score 50; DB 4; Length 100;
Best Local Similarity 55.6%; Pred. No. 6.6;
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXADNGTIVBELKQLEQW 20
DB 44 KOLENGEINIEBLKQLE 61

RESULT 12
US-09-648-004-26
Sequence 26, Application US/09648004
Patent No. 6498242
GENERAL INFORMATION:
APPLICANT: CHEN, QIONG
APPLICANT: THOMAS, STUART
TITLE OF INVENTION: BIOLOGICAL METHOD FOR THE PRODUCTION OF ADIPIC ACID AND
FILE REFERENCE: CL-1341-A
CURRENT APPLICATION NUMBER: US/09/648,004
CURRENT FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/252,553
PRIOR FILING DATE: 1999-02-19
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Microsoft Office 97
SEQ ID NO: 26
LENGTH: 300
TYPE: PRF
ORGANISM: Acinetobacter sp.
US-09-648-004-26

Query Match 39.4%; Score 50; DB 4; Length 300;
Best Local Similarity 22.7%; Pred. No. 23;
Matches 5; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY 2 KXADNGTIVBELKQLEQW 23
DB 20 RMOENPNMTIEDFRSMFDEWH 41

RESULT 13
US-10-272-419-26
Sequence 26, Application US/10272419
Patent No. 6794165
GENERAL INFORMATION:
APPLICANT: CHEN, QIONG
APPLICANT: THOMAS, STUART
APPLICANT: NAGARAJAN, VASANTHA
TITLE OF INVENTION: BIOLOGICAL METHOD FOR THE PRODUCTION OF ADIPIC ACID AND
FILE REFERENCE: CL1341-A
CURRENT APPLICATION NUMBER: US/10/272,419
CURRENT FILING DATE: 2002-10-16
PRIOR APPLICATION NUMBER: 09/252,553
PRIOR FILING DATE: 1999-02-19
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Microsoft Office 97
SEQ ID NO: 26
LENGTH: 300
TYPE: PRF
ORGANISM: Acinetobacter sp.
US-10-272-419-26

Query Match 39.4%; Score 50; DB 4; Length 300;
Best Local Similarity 22.7%; Pred. No. 23;
Matches 5; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY 2 KXADNGTIVBELKQLEQW 23
DB 20 RMOENPNMTIEDFRSMFDEWH 41

RESULT 14
US-08-940-332-2
Sequence 2, Application US/08940332
Patent No. 5885834
GENERAL INFORMATION:
APPLICANT: Epstein, Paul M.
TITLE OF INVENTION: SYNTHESIS OF ANTISENSE
TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE OF PHOSPHODIESTERASE AND
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSER: ALIX, YALE & RISTAS, LLP
STREET: 750 MAIN STREET
CITY: HARTFORD
STATE: CT
COUNTRY: USA
ZIP: 06103-2721
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,332
FILING DATE: 30-SEP-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/027,207
FILING DATE: 30-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Alix, James E.
REGISTRATION NUMBER: 20,736
REFERENCE/DOCKET NUMBER: UCON/137/US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (860)527-9211
TELEFAX: (860)527-5029
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 536 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-940-332-2

Query Match 39.4%; Score 50; DB 2; Length 536;
Best Local Similarity 55.6%; Pred. No. 44;
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXADNGTIVBELKQLE 20
DB 44 KOLENGEINIEBLKQLE 61

RESULT 15
US-09-543-681A-4729
Sequence 4729, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05

PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 4729
LENGTH: 537
TYPE: PRT
ORGANISM: Proteus mirabilis
US-09-543-681A-4729

Query Match 39.4%; Score 50; DB 4; Length 537;
Best Local Similarity 36.4%; Pred. No. 44;
Matches 8; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 3 KXADNGTIVVEELKQLEQNL 24
DB 111 KXVDNGSASLEDEPPELLEDMKHL 132

RESULT 16
US-09-949-016-7536
Sequence 7536, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7536
LENGTH: 542
TYPE: PRT
ORGANISM: Human
US-09-949-016-7536

Query Match 39.4%; Score 50; DB 4; Length 542;
Best Local Similarity 55.6%; Pred. No. 44;
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXADNGTIVVEELKQLE 20
DB 50 KOLENGEINIEELKKNLE 67

RESULT 17
US-09-544-683-2
Sequence 2, Application US/09544683
Patent No. 6787137
GENERAL INFORMATION:
APPLICANT: JACOBS, ANTONIUS A. C.
APPLICANT: VAN DEN BOSCH, JOHANNES F.
TITLE OF INVENTION: CAMPYLOBACTER VACCINE
FILE REFERENCE: JACOBS
CURRENT APPLICATION NUMBER: US/09/544,683
CURRENT FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: EP99201086.8
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 545
TYPE: PRT
ORGANISM: Campylobacter jejuni
US-09-544-683-2

Query Match 39.4%; Score 50; DB 4; Length 545;
Best Local Similarity 41.7%; Pred. No. 45;
Matches 10; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 2 KXADNGTIVVEELKQLEQNLV 25
DB 166 EKVGKDGIVVEEPSINDELNVV 189

RESULT 18
US-10-192-419-2
Sequence 2, Application US/10192419
Patent No. 6790446
GENERAL INFORMATION:
APPLICANT: JACOBS, ANTONIUS A. C.
APPLICANT: VAN DEN BOSCH, JOHANNES F.
TITLE OF INVENTION: CAMPYLOBACTER VACCINE
FILE REFERENCE: JACOBS
CURRENT APPLICATION NUMBER: US/10/192,419
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/09/544,683
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: EP99201086.8
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 545
TYPE: PRT
ORGANISM: Campylobacter jejuni
US-10-192-419-2

Query Match 39.4%; Score 50; DB 4; Length 545;
Best Local Similarity 41.7%; Pred. No. 45;
Matches 10; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 2 KXADNGTIVVEELKQLEQNLV 25
DB 166 EKVGKDGIVVEEPSINDELNVV 189

RESULT 19
US-09-538-092-1312
Sequence 1312, Application US/09538092
Patent No. 6753314
GENERAL INFORMATION:
APPLICANT: Glaxo, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuratPatSegFormatter Version 0.9
SEQ ID NO 1312
LENGTH: 2472
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number Q13813
US-09-538-092-1312

Query Match 39.4%; Score 50; DB 4; Length 2472;
Best Local Similarity 47.6%; Pred. No. 2.5e+02;
Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

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QY      2 KKGADNGTITVEBELKQLLEQM 22
        ||::|| ||::||:
Db      1828 KKLSDNTTIGKEIQLRLAQF 1848

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RESULT 20
US-09-266-965-1132
Sequence 132, Application US/09266965
Patent No. 6495348
GENERAL INFORMATION:
APPLICANT: Sherman, D
APPLICANT: Mao, Y
APPLICANT: Varoglu, M
APPLICANT: He, M
APPLICANT: Sheldon, P
TITLE OF INVENTION: Micomycin biosynthetic gene cluster
FILE REFERENCE: 600.456US1
CURRENT APPLICATION NUMBER: US/09/266,965
CURRENT FILING DATE: 1999-03-12
EARLIER APPLICATION NUMBER: US 08/624,447
EARLIER FILING DATE: 1996-08-19
EARLIER APPLICATION NUMBER: PCT/US94/11279
EARLIER FILING DATE: 1994-10-06
EARLIER APPLICATION NUMBER: US 08/133,963
EARLIER FILING DATE: 1993-10-07
NUMBER OF SEQ ID NOS: 145
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 132
LENGTH: 123
TYPE: PRT
ORGANISM: Streptomyces lavendulae
US-09-266-965-1132

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| | | | | |
|-----------------------|--------|---------------|-------|---------------|
| Query Match | 38.6% | Score 49; | DB 4; | Length 123; |
| Best Local Similarity | 57.1%; | Pred. No. 12; | | |
| Matches | 8; | Conservative | 5; | Mismatches 1; |
| | | | | Indels 0; |
| | | | | Gaps 0; |

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QY      7 NGTITVEELKÖLLE 20
        |||: ||||:::|
Db      86 NGTVPVEELREME 99
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RESULT 21
US-09-538-092-241
: Sequence 241. Application US/09538092
: Patent No. 6753314
: GENERAL INFORMATION:
: APPLICANT: Gluc, Loic
: APPLICANT: Mansfield, Traci A.
: TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
: FILE REFERENCE: 15966-542
: CURRENT APPLICATION NUMBER: US/09/538, 092
: CURRENT FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: 60/127,352
: PRIOR FILING DATE: 1999-04-01
: PRIOR APPLICATION NUMBER: 60/178,965
: PRIOR FILING DATE: 2000-02-01
: NUMBER OF SEQ ID NOS: 1387
: SOFTWARE: CuratSeqFormatter Version 0.9
: SEQ ID NO 241
: LENGTH: 218
: TYPE: PRT
: ORGANISM: Saccharomyces cerevisiae
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (0)...(0)
: OTHER INFORMATION: Polypeptide Accession Number YER063W
US-09-538-092-241

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| | | | | |
|-----------------------|-------|---------------|-------|--------------------------------|
| Query Match | 38.6% | Score 49; | DB 4; | Length 218; |
| Best Local Similarity | 52.4% | Pred. No. 22; | | |
| Matches | 11; | Conservative | 4; | Mismatches 6; Indels 0; Gaps 0 |

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QY 4 MADNGTITVEELKÖLLEQNNL 24
    ||| :|| :||| :||
Db 1 MADYSSLTVQKLKDLTKRNL 21
```

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RESULT 22
US-09-949-016-9820
: Sequence 9820, Application US/09949016
: Patent No. 6812339
: GENERAL INFORMATION:
: APPLICANT: VENTER, J. Craig et al.
: TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: CLO010107
: CURRENT APPLICATION NUMBER: US/09/949,016
: CURRENT FILING DATE: 2000-04-14
: PRIOR APPLICATION NUMBER: 60/241,755
: PRIOR FILING DATE: 2000-10-20
: PRIOR APPLICATION NUMBER: 60/237,768
: PRIOR FILING DATE: 2000-10-03
: PRIOR APPLICATION NUMBER: 60/231,498
: PRIOR FILING DATE: 2000-09-08
: NUMBER OF SEQ ID NOS: 207012
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 9820
: LENGTH: 473
: TYPE: PRT
: ORGANISM: Human
US-09-949-016-9820

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| | | | | |
|-----------------------|-------|--------------|------|--------------------------------|
| Query Match | 38.6% | Score 49 | DB 4 | Length 473 |
| Best Local Similarity | 35.0% | Pred. No. 53 | | |
| Matches | 7 | Conservative | 8 | Mismatches 5; Indels 0; Gaps 0 |

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0Y      3 KMADNGTITVEELKQLEQW 22
        | : : : | : : | : |
Db      45 KLQERSDLTVEKEKELIEEW 64

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RESULT 23
US-09-489-039A-10011
: Sequence 10011, Application US/09489039A
: Patent No. 6610836
: GENERAL INFORMATION:
: APPLICANT: Gary Breton et. al
: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
: TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
: FILE REFERENCE: 2709.2004001
: CURRENT APPLICATION NUMBER: US/09/489,039A
: PRIOR APPLICATION NUMBER: US 60/117,747
: PRIOR FILING DATE: 1999-01-29
: NUMBER OF SEQ ID NOS: 14342
: SEQ ID NO 10011
: LENGTH: 532
: TYPE: prt
: ORGANISM: Klebsiella pneumoniae
US-09-489-039A-10011

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|-----------------------|----------------|--------------|----------|------------|
| Query Match | 38.6% | Score 49 | DB 4 | Length 532 |
| Best Local Similarity | 50.0% | Pred. No. 60 | | |
| Matches 9 | Conservative 6 | Mismatches 3 | Indels 0 | Gaps 0 |

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0Y .      1 KKKMADNGTITVEELKÖL 18
      | :|||||: ::|: :|
Db      290 KFKMADNGTFLDEIGEL 307

```

RESULT 24
US-07-872-644-27
; Sequence 27, Application US/07872644
; Patent No. 5389527


```

: NAME: No. 5602019and, Greta E.
: REGISTRATION NUMBER: 35,302
: REFERENCE/DOCKET NUMBER: 27866/30822
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (312) 346-5750
: TELEFAX: (312) 984-9740
:
: TELE: 25-3856
:
: INFORMATION FOR SEQ ID NO: 27:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 534 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
:
US-08-297-510-27

```

| | | | | |
|-----------------------|--------|---------------|-------|---------------|
| Query Match | 38.6% | Score 49; | DB 1; | Length 534; |
| Best Local Similarity | 50.0%; | Pred. No. 61; | | |
| Matches | 9; | Conservative | 4; | Mismatches 5; |
| | | | | Indels 0; |
| | | | | Gaps 0; |

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QY      3 KMADNGTITVEELKQLE 20
      | :|| : :|||: ||
Db      43 KQLENGEVNIEELKNLE 60
```

RESULT 27
US-08-479-532-27

GENERAL INFORMATION:
APPLICANT: Beavo, Joseph A.
APPLICANT: Bentley, Kelley
APPLICANT: Charbonneau, Harry
APPLICANT: Sonnenburg, William K.
TITLE OF INVENTION: DNA Encoding Mammalian
TITLE OF INVENTION: Phosphodiesterases
NUMBER OF SEQUENCES: 58

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark

```

? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:

```

APPLICATION NUMBER: 08/297,494
FILING DATE:
APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991

```

; INFORMATION FOR SEQ ID NO: 27
;
; SEQUENCE CHARACTERISTICS:
;     LENGTH: 534 amino acids
;     TYPE: amino acid
;     TOPOLOGY: 1linear
;
; MOLECULE TYPE: protein

```

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US-08-479-532-27

Query Match      38.6%; Score 49; DB 1; Length 534;
Best Local Similarity 50.0%; Pred. No. 61;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

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| Qy | 3 | KMADNGTITVEELKÖLLE | 20 |
| | | : : : | |
| Db | 43 | KÖLENGEVNIEELKNLE | 60 |

RESULT 28
US-08-455-526-27
; Sequence 27, Application US/08455526
; Patent No. 5789553

1 GENERAL INFORMATION:
2 APPLICANT: Beavo, Joseph A.
3 APPLICANT: Bentley, Kelley
4 APPLICANT: Charbonneau, Harry
5 APPLICANT: Sonnenburg, William K.
6 TITLE OF INVENTION: DNA Encoding Mammalian
7 TITLE OF INVENTION: Phosphodiesterases
8 NUMBER OF SEQUENCES: 58
9 CORRESPONDENCE ADDRESS:

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? FILING DATE: 04-ADR-1991
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: No. 578953and, Greta E. .
 ? REGISTRATION NUMBER: 35,302
 ? REFERENCE/DOCKET NUMBER: 27866/30822
 ? TELECOMMUNICATION INFORMATION:

```

; INFORMATION FOR SEQ ID NO: 27
;
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 534 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;
; MOLECULE TYPE: protein

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|-------------------------|-------|--------------|------------|------------|
| Query Match | 38.6% | Score 49 | DB 1 | Length 534 |
| Best Local Similarity | 50.0% | Pred. No. 61 | | |
| Matches 9, Conservative | | 4 | Mismatches | 0 |
| | | | Indels | 0 |
| | | | Gaps | 0 |

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| QY | 3 | KMADNGTITVEELKQJLE | 20 |
| | | : : : : | |
| Db | 43 | KQLENGEVNIEELKNLE | 60 |

RESULT 29
US-08-455-525-27

; Sequence 27, Application US/08455525
; Patent No. 5800987
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; TITLE OF INVENTION: Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 04-APR-1991
; APPLICATION NUMBER: US/08/455,525
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/297,494
; FILING DATE:
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5800987and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 534 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-455-525-27

Query Match 38.6%; Score 49; DB 1; Length 534;
Best Local Similarity 50.0%; Pred. No. 61;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXADNGTIVVEIKKOLE 20
DB 43 KOLENGEVNIEIKKMLE 60

RESULT 30
US-09-139-491-27
; Sequence 27, Application US/09139491
; Patent No. 6015677
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; TITLE OF INVENTION: Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25

; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/139,491
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,525
; FILING DATE: 31-MAY-1995
; APPLICATION NUMBER: 08/297,494
; FILING DATE:
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6015677and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 534 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-139-491-27

Query Match 38.6%; Score 49; DB 3; Length 534;
Best Local Similarity 50.0%; Pred. No. 61;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXADNGTIVVEIKKOLE 20
DB 43 KOLENGEVNIEIKKMLE 60

RESULT 31
US-09-883-825-27
; Sequence 27, Application US/09883825
; Patent No. 6642040
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; TITLE OF INVENTION: Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25

Best Local Similarity 30.6%; Pred. No. 57;
Matches 11; Conservative 5; Mismatches 7; Indels 13; Gaps 1;

Qy 3 KXADNGTIV-----EELKQLEQWNL 25
Db 189 KXKENDLTALITQIKKGLPLPESLNLQRLSRQWNL 224

RESULT 34

US-09-538-092-266
; Sequence 266, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Glot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 266
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number YFL017C
US-09-538-092-266

Query Match 37.8%; Score 48; DB 4; Length 159;
Best Local Similarity 40.9%; Pred. No. 21;

Matches 9; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 2 KXADNGTIVTELKQLEQWNL 23
Db 25 KVLTVGTTPSFSLIKKYN 46

RESULT 35

US-09-489-039A-7411
; Sequence 7411, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709,2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 7411
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7411

Query Match 37.8%; Score 48; DB 4; Length 208;
Best Local Similarity 37.5%; Pred. No. 29;

Matches 9; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

Qy 1 KXADNGTIVTELKQLEQWNL 24
Db 29 KDFAPSGAIRVNSQKLDIWSI 52

RESULT 36
US-09-252-991A-32836
; Sequence 32836, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 32836
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32836

Query Match 37.8%; Score 48; DB 4; Length 313;
Best Local Similarity 81.8%; Pred. No. 46;

Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KXADNGTIV 12
Db 44 KXADNGTIVL 54

RESULT 37

US-09-538-092-769
; Sequence 769, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Glot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 769
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number YPL003W
US-09-538-092-769

Query Match 37.8%; Score 48; DB 4; Length 462;
Best Local Similarity 43.8%; Pred. No. 72;

Matches 7; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

Qy 6 DNGTIVTELKQLEQ 21
Db 213 NNGRTIDQMKVLDQ 228

RESULT 38

US-09-540-245A-17
; Sequence 17, Application US/09540245A
; Patent No. 6270984
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey

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; APPLICANT: Kid, Thomas
; APPLICANT: Brose, Katja
; APPLICANT: Tessier-Lavigne, Marc
; TITLE OF INVENTION: Modulating Rbdo: Ligand Interactions
; FILE REFERENCE: 898-031-3
; CURRENT APPLICATION NUMBER: US/09/540,245A
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 60/065,544
; PRIOR FILING DATE: 1997-11-14
; PRIOR APPLICATION NUMBER: 60/081,057
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 17
; LENGTH: 1297
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
; US-09-540-245A-17

Query Match
Best Local Similarity 40.0%; Score 48; DB 3; Length 1297;
Pred. No. 2.3e+02;
Matches 8; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 KKKMADNGTIVBELKOLLEQ 20
DB 368 RTKVSPGTGLTIEVRQVDE 387

RESULT 39
US-09-270-767-45884
; Sequence 45884, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 45884
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; US-09-270-767-45884

Query Match
Best Local Similarity 37.4%; Score 47.5; DB 4; Length 149;
Pred. No. 24;
Matches 10; Conservative 4; Mismatches 6; Indels 3; Gaps 1;

QY 3 KQAD---NGTIVBELKOLLEQ 22
DB 86 KAADPQNGTISARQLRLQNW 108

RESULT 40
US-09-621-976-4009
; Sequence 4009, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4009
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
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; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -58...-1
; US-09-621-976-4009

Query Match
Best Local Similarity 36.2%; Score 46; DB 4; Length 93;
Pred. No. 23;
Matches 9; Conservative 8; Mismatches 6; Indels 2; Gaps 1;

QY 3 KQADNGTIVBELKOLLEQ 25
DB 8 RLSDGTTFEDVAVKTEQEWML 32

RESULT 41
US-09-710-279-2624
; Sequence 2624, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2624
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
; US-09-710-279-2624

Query Match
Best Local Similarity 36.2%; Score 46; DB 4; Length 216;
Pred. No. 59;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 7 NGTIVBELKOLLEQ 21
DB 59 NGTMTLEBAKYLEE 73

RESULT 42
US-09-134-001C-5279
; Sequence 5279, Application US/09134001C
; Patent No. 6180370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5279
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
; US-09-134-001C-5279

Query Match
Best Local Similarity 36.2%; Score 46; DB 3; Length 274;
Pred. No. 77;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 7 NGTIVBELKOLLEQ 21
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Db 117 NGMTLEAKYQLE 131

RESULT 43

US-09-270-767-58705
; Sequence 58705; Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 58705
; LENGTH: 365
; TYPE: PRT
; ORGANISM: *Drosophila melanogaster*
US-09-270-767-58705

Query Match 36.2%; Score 46; DB 4; Length 365;
Best Local Similarity 52.2%; Pred. No. 1.1e+02;
Matches 12; Conservative 3; Mismatches 6; Indels 2; Gaps 1;

QY 1 KKKMADNGTI--TVEELKQLEQ 21

Db 284 KVMDSGPVIRSEIKTLLE 306

RESULT 44

US-09-270-767-43356
; Sequence 43356; Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 43356
; LENGTH: 397
; TYPE: PRT
; ORGANISM: *Drosophila melanogaster*
US-09-270-767-43356

Query Match 36.2%; Score 46; DB 4; Length 397;
Best Local Similarity 52.2%; Pred. No. 1.2e+02;
Matches 12; Conservative 3; Mismatches 6; Indels 2; Gaps 1;

QY 1 KKKMADNGTI--TVEELKQLEQ 21

Db 316 KVMDSGPVIRSEIKTLLE 338

RESULT 45

US-09-248-796A-14232
; Sequence 14232; Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13

; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 14232
; LENGTH: 415
; TYPE: PRT
; ORGANISM: *Candida albicans*
US-09-248-796A-14232

Query Match 36.2%; Score 46; DB 4; Length 415;
Best Local Similarity 46.7%; Pred. No. 1.2e+02;
Matches 7; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 10 ITVEELKQLEQNL 24

Db 106 ITPKRLKRAIDQNI 120

RESULT 46

US-09-759-595-1
; Sequence 1; Application US/09759595
; Patent No. 6818419
; GENERAL INFORMATION:
; APPLICANT: Mesche, Holger
; APPLICANT: Li, Shyun
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: IRAK-4: Compositions and Methods of Use
; FILE REFERENCE: 018781-003910US
; CURRENT APPLICATION NUMBER: US/09/759,595
; CURRENT FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 60/176,395
; PRIOR FILING DATE: 2000-01-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 460
; TYPE: PRT
; ORGANISM: *Homo sapiens*
US-09-759-595-1

Query Match 36.2%; Score 46; DB 4; Length 460;
Best Local Similarity 55.0%; Pred. No. 1.4e+02;
Matches 11; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 2 KKKMADNGTITVEELKQLEQ 21

Db 213 KKLAMVDITTEELKQFPQ 232

RESULT 47

US-08-467-822-33
; Sequence 33; Application US/08467822
; Patent No. 5843460
; GENERAL INFORMATION:
; APPLICANT: Labigne, Agnes
; APPLICANT: Sauerbaum, Sebastien
; APPLICANT: Ferrero, Richard L.
; APPLICANT: Thibierge, Jean-Michel
; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST
; TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE
; TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,822
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/447,177
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/432,697
FILING DATE: 02-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495.0137-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ. ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 544 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-467-822-33

Query Match 36.2%; Score 46; DB 2; Length 544;
Best Local Similarity 60.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 KKKADNGTIVBEK 16
Db 167 EKVKGKGSITVEAK 181

RESULT 48
US-08-432-697-33
Sequence 33, Application US/08432697
Patent No. 6248330
GENERAL INFORMATION:
APPLICANT: Labigne, Agnes
APPLICANT: Sauerdam, Sebastien
APPLICANT: Ferrero, Richard L.
APPLICANT: Thibierge, Jean-Michel
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST
TITLE OF INVENTION: HELICOBLASTER INFECTION, POLYPEPTIDES FOR USE IN THE
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESS: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/432,697
FILING DATE: 02-MAY-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495.0137-00000

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ. ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 544 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-432-697-33

Query Match 36.2%; Score 46; DB 3; Length 544;
Best Local Similarity 60.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 KKKADNGTIVBEK 16
Db 167 EKVKGKGSITVEAK 181

RESULT 49
US-08-466-248-33
Sequence 33, Application US/08466248
Patent No. 6258359
GENERAL INFORMATION:
APPLICANT: Labigne, Agnes
APPLICANT: Sauerdam, Sebastien
APPLICANT: Ferrero, Richard L.
APPLICANT: Thibierge, Jean-Michel
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST
TITLE OF INVENTION: HELICOBLASTER INFECTION, POLYPEPTIDES FOR USE IN THE
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESS: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,248
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/447,177
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/432,697
FILING DATE: 02-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495.0137-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ. ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 544 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

; MOLECULE TYPE: protein
US-08-466-248-33

Query Match 36.2%; Score 46; DB 3; Length 544;
Best Local Similarity 60.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 KKMADNGTITVEELK 16
:|:|:|:|:|:|
Db 167 EKVGNKSITVEAK 181

RESULT 50

US-09-198-452A-153
; Sequence 153, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 153
; LENGTH: 544
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 1...544
; OTHER INFORMATION: Xaa=unknown or other
US-09-198-452A-153

Query Match 36.2%; Score 46; DB 4; Length 544;
Best Local Similarity 60.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 KKMADNGTITVEELK 16
:|:|:|:|:|:|
Db 167 EKVGNKSITVEAK 181

Search completed: May 11, 2005, 21:28:01
Job time : 37.4468 secs

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OM protein - protein search, using sw model

Run on: May 11, 2005, 21:23:25 ; Search time 97.3404 Seconds
(without alignments)
85.795 Million cell updates/sec

Title: US-10-712-812-6
Perfect score: 127
Sequence: 1 KKKMDNGTITVEIKLLEQNNLV 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1432185 seqs, 334051727 residues

Total number of hits satisfying chosen parameters: 1432185

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

Published Applications AA.*
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2: /cgn2_6/ptodata/2/pubppa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubppa/US06_NEW_PUB.pep.*
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19: /cgn2_6/ptodata/2/pubppa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 112 | 88.2 | 221 | 16 | US-10-839-729-6 |
| 2 | 112 | 88.2 | 221 | 16 | US-10-839-729-7 |
| 3 | 112 | 88.2 | 221 | 16 | US-10-839-729-8 |
| 4 | 112 | 88.2 | 221 | 16 | US-10-839-729-9 |
| 5 | 112 | 88.2 | 221 | 17 | US-10-699-936-24 |
| 6 | 112 | 88.2 | 221 | 17 | US-10-699-936-81 |
| 7 | 112 | 88.2 | 221 | 17 | US-10-699-936-82 |
| 8 | 112 | 88.2 | 221 | 17 | US-10-699-936-83 |
| 9 | 112 | 88.2 | 221 | 17 | US-10-808-187-214 |
| 10 | 73 | 57.5 | 15 | 6 | US-10-839-729-46 |
| 11 | 55 | 43.3 | 54 | 9 | US-09-864-761-39008 |
| 12 | 55 | 43.3 | 206 | 10 | US-09-873-546-10 |
| 13 | 55 | 43.3 | 206 | 14 | US-10-153-668-214 |

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| 14 | 55 | 43.3 | 206 | 14 | US-10-021-660-132 | Sequence 132, App |
| 15 | 55 | 43.3 | 206 | 15 | US-10-231-913-64 | Sequence 64, Appl |
| 16 | 55 | 43.3 | 206 | 15 | US-10-211-462-79 | Sequence 79, Appl |
| 17 | 55 | 43.3 | 206 | 16 | US-10-408-765A-2022 | Sequence 2022, Ap |
| 18 | 55 | 43.3 | 206 | 16 | US-10-804-491-48 | Sequence 48, Appl |
| 19 | 55 | 43.3 | 209 | 16 | US-10-231-913-66 | Sequence 66, Appl |
| 20 | 53.5 | 42.1 | 336 | 16 | US-10-425-114-69487 | Sequence 69487, A |
| 21 | 53.5 | 42.1 | 486 | 16 | US-10-437-9663-158994 | Sequence 158994, |
| 22 | 53.5 | 42.1 | 512 | 16 | US-10-437-9663-158996 | Sequence 158996, |
| 23 | 53.5 | 42.1 | 523 | 15 | US-10-425-114-57880 | Sequence 57880, A |
| 24 | 53 | 41.7 | 351 | 15 | US-10-282-122A-51553 | Sequence 51553, A |
| 25 | 52 | 40.9 | 206 | 15 | US-10-231-913-63 | Sequence 63, Appl |
| 26 | 52 | 40.9 | 206 | 15 | US-10-231-913-65 | Sequence 65, Appl |
| 27 | 52 | 40.9 | 206 | 15 | US-10-231-913-67 | Sequence 67, Appl |
| 28 | 52 | 40.9 | 545 | 15 | US-10-282-122A-54546 | Sequence 54546, A |
| 29 | 51.5 | 40.6 | 855 | 14 | US-10-369-294-11 | Sequence 11, Appl |
| 30 | 51.5 | 40.6 | 855 | 14 | US-10-369-294-12 | Sequence 12, Appl |
| 31 | 51 | 40.2 | 217 | 16 | US-10-478-245-4 | Sequence 4, Appl |
| 32 | 51 | 40.2 | 626 | 15 | US-10-282-122A-60575 | Sequence 60575, A |
| 33 | 51 | 40.2 | 987 | 14 | US-10-156-761-14515 | Sequence 14515, A |
| 34 | 50 | 39.4 | 92 | 15 | US-10-424-599-219887 | Sequence 219887, |
| 35 | 50 | 39.4 | 174 | 16 | US-10-437-963-186189 | Sequence 186189, |
| 36 | 50 | 39.4 | 300 | 14 | US-10-272-419-26 | Sequence 26, Appl |
| 37 | 50 | 39.4 | 469 | 15 | US-10-417-700A-49 | Sequence 49, Appl |
| 38 | 50 | 39.4 | 516 | 17 | US-10-781-102-1 | Sequence 1, Appl |
| 39 | 50 | 39.4 | 536 | 17 | US-10-781-102-3 | Sequence 3, Appl |
| 40 | 50 | 39.4 | 536 | 17 | US-10-815-390-1 | Sequence 1, Appl |
| 41 | 50 | 39.4 | 545 | 14 | US-10-192-419-2 | Sequence 2, Appl |
| 42 | 50 | 39.4 | 546 | 15 | US-10-424-599-203557 | Sequence 203557, |
| 43 | 50 | 39.4 | 549 | 15 | US-10-425-114-54704 | Sequence 54704, A |
| 44 | 50 | 39.4 | 673 | 15 | US-10-282-122A-76721 | Sequence 76721, A |
| 45 | 50 | 39.4 | 808 | 15 | US-10-104-047-2324 | Sequence 2324, Ap |
| 46 | 50 | 39.4 | 1803 | 16 | US-10-343-509-3 | Sequence 3, Appl |
| 47 | 50 | 39.4 | 1805 | 16 | US-10-343-509-1 | Sequence 1, Appl |
| 48 | 50 | 39.4 | 2477 | 16 | US-10-360-053-28 | Sequence 28, Appl |
| 49 | 50 | 39.4 | 2477 | 17 | US-10-408-765A-238 | Sequence 238, App |
| 50 | 49 | 38.6 | 60 | 17 | US-10-781-102-13 | Sequence 13, Appl |
| 51 | 49 | 38.6 | 123 | 14 | US-09-953-348-132 | Sequence 132, App |
| 52 | 49 | 38.6 | 123 | 14 | US-10-267-255-132 | Sequence 132, App |
| 53 | 49 | 38.6 | 143 | 11 | US-09-978-360A-641 | Sequence 641, App |
| 54 | 49 | 38.6 | 473 | 14 | US-10-354-358-96 | Sequence 96, Appl |
| 55 | 49 | 38.6 | 476 | 15 | US-10-264-049-2925 | Sequence 2925, Ap |
| 56 | 49 | 38.6 | 485 | 15 | US-10-282-122A-51755 | Sequence 51755, A |
| 57 | 49 | 38.6 | 534 | 9 | US-09-883-825-27 | Sequence 27, Appl |
| 58 | 49 | 38.6 | 534 | 16 | US-10-697-894-27 | Sequence 27, Appl |
| 59 | 49 | 38.6 | 643 | 9 | US-09-815-242-11234 | Sequence 11234, A |
| 60 | 49 | 38.6 | 643 | 15 | US-10-282-122A-58503 | Sequence 58503, A |
| 61 | 48 | 37.8 | 159 | 15 | US-10-422-812-4 | Sequence 4, Appl |
| 62 | 48 | 37.8 | 159 | 15 | US-10-612-779-30 | Sequence 30, Appl |
| 63 | 48 | 37.8 | 159 | 17 | US-10-823-397-33 | Sequence 33, Appl |
| 64 | 48 | 37.8 | 206 | 15 | US-10-231-913-6 | Sequence 6, Appl |
| 65 | 48 | 37.8 | 299 | 16 | US-10-437-963-14248 | Sequence 124248, |
| 66 | 48 | 37.8 | 318 | 15 | US-10-282-122A-52263 | Sequence 52263, A |
| 67 | 48 | 37.8 | 401 | 15 | US-10-369-499-10440 | Sequence 10440, A |
| 68 | 48 | 37.8 | 423 | 15 | US-10-369-499-6746 | Sequence 6746, Ap |
| 69 | 48 | 37.8 | 428 | 16 | US-10-437-963-141938 | Sequence 141938, |
| 70 | 48 | 37.8 | 508 | 16 | US-10-686-947-238 | Sequence 238, App |
| 71 | 48 | 37.8 | 508 | 16 | US-10-686-947-266 | Sequence 266, App |
| 72 | 48 | 37.8 | 509 | 16 | US-10-686-947-240 | Sequence 240, Appl |
| 73 | 48 | 37.8 | 909 | 17 | US-10-826-812-13 | Sequence 13, Appl |
| 74 | 48 | 37.8 | 1297 | 14 | US-10-289-776-17 | Sequence 17, Appl |
| 75 | 48 | 37.8 | 1297 | 17 | US-10-826-812-6 | Sequence 6, Appl |
| 76 | 48 | 37.8 | 4437 | 14 | US-10-314-657-45 | Sequence 45, Appl |
| 77 | 48 | 37.8 | 4437 | 17 | US-10-471-193-45 | Sequence 45, Appl |
| 78 | 47 | 37.0 | 659 | 15 | US-10-369-499-2600 | Sequence 2600, Ap |
| 79 | 46.5 | 36.6 | 151 | 16 | US-10-437-963-137765 | Sequence 137765, |
| 80 | 46.5 | 36.6 | 210 | 15 | US-10-425-114-40176 | Sequence 40176, A |
| 81 | 46.5 | 36.6 | 325 | 15 | US-10-424-599-198782 | Sequence 198782, |
| 82 | 46.5 | 36.6 | 428 | 15 | US-10-282-122A-77230 | Sequence 77230, A |
| 83 | 46.5 | 36.6 | 500 | 16 | US-10-437-963-17763 | Sequence 17763, A |
| 84 | 46.5 | 36.6 | 849 | 10 | US-09-899-575-23 | Sequence 23, Appl |
| 85 | 46.5 | 36.6 | 849 | 14 | US-10-190-435-148 | Sequence 148, App |
| 86 | 46 | 36.2 | 137 | 15 | US-10-335-977-9398 | Sequence 9398, Ap |

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|-----|------|------|-----|----|----------------------|--------------------|-----|------|------|------|----|-----------------------|--------------------|
| 87 | 46 | 36.2 | 183 | 15 | US-10-425-114-49684 | Sequence 49684, A | 160 | 45 | 35.4 | 629 | 14 | US-10-128-714-3099 | Sequence 3099, Ap |
| 88 | 46 | 36.2 | 196 | 16 | US-10-437-963-200009 | Sequence 200009, A | 161 | 45 | 35.4 | 637 | 16 | US-10-296-085A-16 | Sequence 16, Appl |
| 89 | 46 | 36.2 | 216 | 17 | US-10-470-048B-286 | Sequence 286, App | 162 | 45 | 35.4 | 638 | 16 | US-10-296-085A-21 | Sequence 21, Appl |
| 90 | 46 | 36.2 | 224 | 16 | US-10-767-701-39143 | Sequence 39143, A | 163 | 45 | 35.4 | 642 | 16 | US-10-296-085A-38 | Sequence 38, Appl |
| 91 | 46 | 36.2 | 315 | 16 | US-10-437-963-116503 | Sequence 116503, A | 164 | 45 | 35.4 | 642 | 17 | US-10-496-179-6 | Sequence 6, Appl |
| 92 | 46 | 36.2 | 325 | 16 | US-10-664-421-143 | Sequence 143, App | 165 | 45 | 35.4 | 643 | 16 | US-10-296-085A-69 | Sequence 69, Appl |
| 93 | 46 | 36.2 | 394 | 16 | US-10-451-467A-510 | Sequence 510, App | 166 | 45 | 35.4 | 643 | 17 | US-10-496-179-1 | Sequence 1, Appl |
| 94 | 46 | 36.2 | 460 | 14 | US-09-759-595-1 | Sequence 1, Appl | 167 | 45 | 35.4 | 645 | 14 | US-10-130-973A-8 | Sequence 8, Appl |
| 95 | 46 | 36.2 | 460 | 14 | US-10-001-254-16 | Sequence 16, Appl | 168 | 45 | 35.4 | 652 | 16 | US-10-437-963A-198055 | Sequence 198055, A |
| 96 | 46 | 36.2 | 460 | 14 | US-10-001-254-28 | Sequence 28, Appl | 169 | 45 | 35.4 | 656 | 16 | US-10-296-085A-39 | Sequence 39, Appl |
| 97 | 46 | 36.2 | 477 | 15 | US-10-335-977-9400 | Sequence 9400, Ap | 170 | 45 | 35.4 | 657 | 16 | US-10-296-085A-68 | Sequence 68, Appl |
| 98 | 46 | 36.2 | 513 | 16 | US-10-437-963-173217 | Sequence 173217, A | 171 | 45 | 35.4 | 660 | 14 | US-10-130-973A-12 | Sequence 12, Appl |
| 99 | 46 | 36.2 | 525 | 15 | US-10-425-114-64587 | Sequence 64587, A | 172 | 45 | 35.4 | 665 | 14 | US-10-130-973A-9 | Sequence 9, Appl |
| 100 | 46 | 36.2 | 533 | 16 | US-10-437-963-200006 | Sequence 200006, A | 173 | 45 | 35.4 | 666 | 15 | US-10-264-227-2631 | Sequence 2631, Ap |
| 101 | 46 | 36.2 | 544 | 9 | US-09-841-132-400 | Sequence 400, App | 174 | 45 | 35.4 | 669 | 15 | US-10-128-714-4099 | Sequence 8099, Ap |
| 102 | 46 | 36.2 | 544 | 11 | US-09-759-272B-5 | Sequence 5, Appl | 175 | 45 | 35.4 | 688 | 14 | US-10-080-334-238 | Sequence 238, App |
| 103 | 46 | 36.2 | 544 | 9 | US-09-809-745-3 | Sequence 3, Appl | 176 | 45 | 35.4 | 778 | 15 | US-10-651-398-20 | Sequence 20, Appl |
| 104 | 46 | 36.2 | 544 | 15 | US-10-289-762-153 | Sequence 153, App | 177 | 45 | 35.4 | 795 | 17 | US-10-130-973A-4 | Sequence 4, Appl |
| 105 | 46 | 36.2 | 544 | 15 | US-10-282-122A-54855 | Sequence 54855, A | 178 | 45 | 35.4 | 862 | 14 | US-10-130-973A-3 | Sequence 3, Appl |
| 106 | 46 | 36.2 | 544 | 15 | US-10-282-122A-55161 | Sequence 55161, A | 179 | 45 | 35.4 | 882 | 14 | US-10-130-973A-6 | Sequence 6, Appl |
| 107 | 46 | 36.2 | 544 | 16 | US-10-470-093-5 | Sequence 5, Appl | 180 | 45 | 35.4 | 887 | 14 | US-10-296-085A-19 | Sequence 19, Appl |
| 108 | 46 | 36.2 | 551 | 15 | US-10-369-493-18994 | Sequence 18994, A | 181 | 45 | 35.4 | 895 | 16 | US-10-296-085A-20 | Sequence 20, Appl |
| 109 | 46 | 36.2 | 551 | 15 | US-10-369-493-20184 | Sequence 20184, A | 182 | 45 | 35.4 | 895 | 16 | US-10-296-085A-17 | Sequence 17, Appl |
| 110 | 46 | 36.2 | 572 | 9 | US-09-986-632-10 | Sequence 10, Appl | 183 | 45 | 35.4 | 896 | 16 | US-10-296-085A-18 | Sequence 18, Appl |
| 111 | 46 | 36.2 | 605 | 15 | US-10-369-493-3541 | Sequence 3541, Ap | 184 | 45 | 35.4 | 896 | 16 | US-10-296-085A-18 | Sequence 18, Appl |
| 112 | 46 | 36.2 | 643 | 15 | US-10-282-122A-67033 | Sequence 67033, A | 185 | 45 | 35.4 | 896 | 17 | US-10-496-179-2 | Sequence 2, Appl |
| 113 | 46 | 36.2 | 792 | 13 | US-10-025-380-1127 | Sequence 1127, Ap | 186 | 45 | 35.4 | 896 | 17 | US-10-496-179-2 | Sequence 2, Appl |
| 114 | 46 | 36.2 | 959 | 15 | US-10-282-122A-68042 | Sequence 68042, A | 187 | 45 | 35.4 | 907 | 14 | US-10-130-973A-5 | Sequence 5, Appl |
| 115 | 46 | 36.2 | 963 | 9 | US-09-815-242-11819 | Sequence 11819, A | 188 | 45 | 35.4 | 1052 | 9 | US-09-060-854B-7 | Sequence 7, Appl |
| 116 | 46 | 36.2 | 963 | 15 | US-10-282-122A-66253 | Sequence 66253, A | 189 | 45 | 35.4 | 1052 | 9 | US-09-891-711-4 | Sequence 4, Appl |
| 117 | 46 | 36.2 | 974 | 15 | US-10-369-493-11758 | Sequence 13758, A | 190 | 45 | 35.4 | 1052 | 9 | US-09-891-711-6 | Sequence 6, Appl |
| 118 | 46 | 36.2 | 974 | 15 | US-10-282-122A-69819 | Sequence 69819, A | 191 | 45 | 35.4 | 1052 | 15 | US-10-665-669-6 | Sequence 6, Appl |
| 119 | 45.5 | 35.8 | 114 | 15 | US-10-424-599-221216 | Sequence 221216, A | 192 | 45 | 35.4 | 1052 | 16 | US-10-829-118-4 | Sequence 4, Appl |
| 120 | 45.5 | 35.8 | 175 | 15 | US-10-425-114-44519 | Sequence 44519, A | 193 | 45 | 35.4 | 1052 | 16 | US-10-829-118-6 | Sequence 6, Appl |
| 121 | 45.5 | 35.8 | 202 | 15 | US-10-424-599-213143 | Sequence 213143, A | 194 | 45 | 35.4 | 1549 | 15 | US-10-369-493-5702 | Sequence 5702, Ap |
| 122 | 45.5 | 35.8 | 422 | 15 | US-10-282-122A-78200 | Sequence 78200, A | 195 | 45 | 35.4 | 1696 | 15 | US-10-408-765A-822 | Sequence 822, App |
| 123 | 45.5 | 35.8 | 492 | 15 | US-10-424-599-212777 | Sequence 212777, A | 196 | 45 | 35.4 | 1720 | 15 | US-10-161-927-8 | Sequence 8, Appl |
| 124 | 45.5 | 35.8 | 603 | 16 | US-10-437-963-161888 | Sequence 161888, A | 197 | 45 | 35.4 | 3432 | 15 | US-10-282-122A-69849 | Sequence 69849, A |
| 125 | 45 | 35.4 | 40 | 17 | US-10-781-102-9 | Sequence 9, Appl | 198 | 44.5 | 35.0 | 159 | 15 | US-10-425-114-43153 | Sequence 43153, A |
| 126 | 45 | 35.4 | 60 | 17 | US-10-781-102-8 | Sequence 7642, Ap | 199 | 44.5 | 35.0 | 171 | 15 | US-10-425-114-47363 | Sequence 47363, A |
| 127 | 45 | 35.4 | 97 | 15 | US-10-335-977-7642 | Sequence 7641, Ap | 200 | 44.5 | 35.0 | 258 | 15 | US-10-424-599-218227 | Sequence 218227, A |
| 128 | 45 | 35.4 | 98 | 15 | US-10-335-977-7641 | Sequence 7641, Ap | 201 | 44.5 | 35.0 | 368 | 15 | US-10-469-993-112 | Sequence 12, Appl |
| 129 | 45 | 35.4 | 126 | 15 | US-10-424-599-147399 | Sequence 51360, A | 202 | 44.5 | 35.0 | 404 | 16 | US-10-437-963-130927 | Sequence 130927, A |
| 130 | 45 | 35.4 | 137 | 15 | US-10-425-114-51360 | Sequence 51360, A | 203 | 44.5 | 35.0 | 410 | 15 | US-10-425-114-81139 | Sequence 81139, A |
| 131 | 45 | 35.4 | 148 | 15 | US-10-424-599-188811 | Sequence 188811, A | 204 | 44.5 | 35.0 | 417 | 15 | US-10-369-493-211136 | Sequence 21136, A |
| 132 | 45 | 35.4 | 210 | 14 | US-10-130-973A-13 | Sequence 13, Appl | 205 | 44.5 | 35.0 | 484 | 17 | US-10-866-527-128 | Sequence 128, App |
| 133 | 45 | 35.4 | 215 | 15 | US-10-312-222-35 | Sequence 35, Appl | 206 | 44.5 | 35.0 | 507 | 15 | US-10-424-599-191824 | Sequence 191824, A |
| 134 | 45 | 35.4 | 216 | 15 | US-10-312-222-33 | Sequence 33, Appl | 207 | 44.5 | 35.0 | 507 | 15 | US-10-425-114-40675 | Sequence 40675, A |
| 135 | 45 | 35.4 | 255 | 16 | US-10-484-298-5 | Sequence 33, Appl | 208 | 44.5 | 35.0 | 542 | 15 | US-10-424-599-218225 | Sequence 218225, A |
| 136 | 45 | 35.4 | 259 | 15 | US-10-424-599-277269 | Sequence 277269, A | 209 | 44.5 | 35.0 | 549 | 9 | US-09-828-311-39 | Sequence 39, Appl |
| 137 | 45 | 35.4 | 260 | 16 | US-10-408-765A-408 | Sequence 408, App | 210 | 44.5 | 35.0 | 549 | 16 | US-10-768-863A-39 | Sequence 39, Appl |
| 138 | 45 | 35.4 | 260 | 17 | US-10-791-155-1 | Sequence 1, Appl | 211 | 44.5 | 35.0 | 619 | 9 | US-09-891-609-4 | Sequence 4, Appl |
| 139 | 45 | 35.4 | 260 | 17 | US-10-791-155-5 | Sequence 5, Appl | 212 | 44.5 | 35.0 | 646 | 9 | US-09-891-609-2 | Sequence 2, Appl |
| 140 | 45 | 35.4 | 273 | 17 | US-10-729-571B-48 | Sequence 48, Appl | 213 | 44.5 | 35.0 | 842 | 14 | US-10-190-403-2 | Sequence 2, Appl |
| 141 | 45 | 35.4 | 277 | 15 | US-10-282-122A-57733 | Sequence 57733, A | 214 | 44.5 | 35.0 | 842 | 14 | US-10-241-009-2 | Sequence 2, Appl |
| 142 | 45 | 35.4 | 325 | 16 | US-10-484-298-8 | Sequence 8, Appl | 215 | 44.5 | 35.0 | 842 | 14 | US-10-190-434B-2 | Sequence 2, Appl |
| 143 | 45 | 35.4 | 329 | 14 | US-10-029-386-32201 | Sequence 32201, A | 216 | 44.5 | 35.0 | 842 | 14 | US-10-190-434B-2 | Sequence 2, Appl |
| 144 | 45 | 35.4 | 356 | 15 | US-10-424-599-165657 | Sequence 165657, A | 217 | 44.5 | 35.0 | 847 | 9 | US-10-190-305A-2 | Sequence 2, Appl |
| 145 | 45 | 35.4 | 440 | 16 | US-10-484-298-6 | Sequence 6, Appl | 218 | 44.5 | 35.0 | 847 | 14 | US-09-476-242-2 | Sequence 2, Appl |
| 146 | 45 | 35.4 | 448 | 14 | US-10-130-973A-10 | Sequence 10, Appl | 219 | 44 | 34.6 | 39 | 17 | US-10-781-102-11 | Sequence 11, Appl |
| 147 | 45 | 35.4 | 462 | 15 | US-10-282-122A-53097 | Sequence 53097, A | 220 | 44 | 34.6 | 68 | 15 | US-10-424-599-161357 | Sequence 161357, A |
| 148 | 45 | 35.4 | 497 | 15 | US-10-104-047-2347 | Sequence 2347, App | 221 | 44 | 34.6 | 74 | 15 | US-10-424-599-146899 | Sequence 146899, A |
| 149 | 45 | 35.4 | 508 | 16 | US-10-484-298-9 | Sequence 174, App | 222 | 44 | 34.6 | 90 | 15 | US-10-335-977-8761 | Sequence 8761, Ap |
| 150 | 45 | 35.4 | 510 | 16 | US-10-484-298-9 | Sequence 9, Appl | 223 | 44 | 34.6 | 117 | 15 | US-10-335-977-8761 | Sequence 8761, Ap |
| 151 | 45 | 35.4 | 535 | 15 | US-10-224-209-2 | Sequence 2, Appl | 224 | 44 | 34.6 | 138 | 15 | US-10-425-114-44012 | Sequence 64012, A |
| 152 | 45 | 35.4 | 535 | 15 | US-10-356-765-1 | Sequence 1, Appl | 225 | 44 | 34.6 | 157 | 15 | US-10-369-493-207 | Sequence 207, App |
| 153 | 45 | 35.4 | 535 | 15 | US-09-882-227-418 | Sequence 418, App | 226 | 44 | 34.6 | 180 | 16 | US-10-767-701-60185 | Sequence 60185, A |
| 154 | 45 | 35.4 | 546 | 11 | US-09-921-157-6 | Sequence 6, Appl | 227 | 44 | 34.6 | 182 | 15 | US-10-424-599-199507 | Sequence 199507, A |
| 155 | 45 | 35.4 | 546 | 15 | US-10-282-122A-58603 | Sequence 58603, A | 228 | 44 | 34.6 | 196 | 16 | US-10-437-963-102544 | Sequence 102544, A |
| 156 | 45 | 35.4 | 546 | 15 | US-10-335-977-7645 | Sequence 7645, Ap | 229 | 44 | 34.6 | 200 | 15 | US-10-424-599-236486 | Sequence 236486, A |
| 157 | 45 | 35.4 | 547 | 16 | US-10-437-963-179668 | Sequence 179668, A | 230 | 44 | 34.6 | 202 | 15 | US-10-424-599-271745 | Sequence 271745, A |
| 158 | 45 | 35.4 | 567 | 16 | US-10-792-517-4 | Sequence 4, Appl | 231 | 44 | 34.6 | 204 | 15 | US-10-424-599-205955 | Sequence 205955, A |
| 159 | 45 | 35.4 | 605 | 14 | US-10-130-973A-11 | Sequence 11, Appl | 232 | 44 | 34.6 | 257 | 15 | US-10-425-114-44806 | Sequence 44806, A |
| | | | | | | | 233 | 44 | 34.6 | 263 | 15 | US-10-335-977-8763 | Sequence 8763, Ap |

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|-----|------|------|------|----|----------------------|-------------------|-----|------|------|------|----|----------------------|-------------------|
| 223 | 44 | 34.6 | 286 | 16 | US-10-437-963-201175 | Sequence 201175, | 306 | 43 | 33.9 | 469 | 15 | US-10-369-493-2943 | Sequence 2943, Ap |
| 224 | 44 | 34.6 | 300 | 15 | US-10-424-559-235900 | Sequence 235900, | 307 | 43 | 33.9 | 477 | 15 | US-10-161-927-62 | Sequence 62, Appl |
| 225 | 44 | 34.6 | 308 | 15 | US-10-369-493-23066 | Sequence 23066, A | 308 | 43 | 33.9 | 485 | 14 | US-10-055-475-17 | Sequence 17, Appl |
| 226 | 44 | 34.6 | 314 | 15 | US-10-425-114-65717 | Sequence 65717, A | 309 | 43 | 33.9 | 490 | 8 | US-08-781-968A-5212 | Sequence 5212, Ap |
| 227 | 44 | 34.6 | 316 | 15 | US-10-425-114-55782 | Sequence 55782, A | 310 | 43 | 33.9 | 490 | 15 | US-10-369-493-5212 | Sequence 5212, Ap |
| 228 | 44 | 34.6 | 327 | 16 | US-10-437-963-135534 | Sequence 135534, | 311 | 43 | 33.9 | 510 | 15 | US-10-369-493-56 | Sequence 56, Appl |
| 229 | 44 | 34.6 | 331 | 15 | US-10-424-559-276035 | Sequence 276035, | 312 | 43 | 33.9 | 521 | 10 | US-09-820-833A-93 | Sequence 93, Appl |
| 240 | 44 | 34.6 | 362 | 9 | US-09-870-759-80 | Sequence 80, Appl | 313 | 43 | 33.9 | 539 | 16 | US-10-375-010-32 | Sequence 32, Appl |
| 241 | 44 | 34.6 | 362 | 15 | US-09-751-708A-80 | Sequence 80, Appl | 314 | 43 | 33.9 | 540 | 15 | US-10-282-122A-47926 | Sequence 47926, A |
| 242 | 44 | 34.6 | 480 | 16 | US-10-437-963-201442 | Sequence 201442, | 315 | 43 | 33.9 | 543 | 14 | US-10-331-061-10 | Sequence 10, Appl |
| 243 | 44 | 34.6 | 484 | 15 | US-10-282-122A-22836 | Sequence 52836, A | 316 | 43 | 33.9 | 553 | 15 | US-10-282-122A-52087 | Sequence 52087, A |
| 244 | 44 | 34.6 | 491 | 9 | US-09-815-242-5671 | Sequence 5671, Ap | 317 | 43 | 33.9 | 550 | 15 | US-10-282-122A-50017 | Sequence 50017, A |
| 245 | 44 | 34.6 | 504 | 9 | US-09-815-242-12692 | Sequence 12692, A | 318 | 43 | 33.9 | 552 | 15 | US-10-369-493-2799 | Sequence 2799, Ap |
| 246 | 44 | 34.6 | 511 | 15 | US-10-282-122A-44428 | Sequence 44428, A | 319 | 43 | 33.9 | 555 | 15 | US-10-282-122A-67921 | Sequence 67921, A |
| 247 | 44 | 34.6 | 530 | 15 | US-10-282-122A-77659 | Sequence 77659, A | 320 | 43 | 33.9 | 567 | 15 | US-10-425-114-69463 | Sequence 69463, A |
| 248 | 44 | 34.6 | 547 | 9 | US-09-738-626-5755 | Sequence 5755, Ap | 321 | 43 | 33.9 | 575 | 15 | US-10-240-280-3 | Sequence 3, Appl |
| 249 | 44 | 34.6 | 547 | 17 | US-10-494-541-84 | Sequence 84, Appl | 322 | 43 | 33.9 | 579 | 15 | US-10-389-566-753 | Sequence 753, App |
| 250 | 44 | 34.6 | 553 | 15 | US-10-369-493-17467 | Sequence 17467, A | 323 | 43 | 33.9 | 587 | 15 | US-10-282-122A-57721 | Sequence 57721, A |
| 251 | 44 | 34.6 | 555 | 13 | US-10-024-809-2 | Sequence 2, Appl | 324 | 43 | 33.9 | 594 | 15 | US-10-369-493-3237 | Sequence 3237, Ap |
| 252 | 44 | 34.6 | 557 | 15 | US-10-424-559-236485 | Sequence 236485, | 325 | 43 | 33.9 | 608 | 15 | US-10-282-122A-71442 | Sequence 71442, A |
| 253 | 44 | 34.6 | 571 | 15 | US-10-369-493-39 | Sequence 39, Appl | 326 | 43 | 33.9 | 625 | 16 | US-10-437-963-152224 | Sequence 152224, |
| 254 | 44 | 34.6 | 718 | 16 | US-10-437-963-196494 | Sequence 196494, | 327 | 43 | 33.9 | 684 | 15 | US-10-282-122A-47915 | Sequence 47915, A |
| 255 | 44 | 34.6 | 726 | 17 | US-10-483-680-2 | Sequence 2, Appl | 328 | 43 | 33.9 | 725 | 15 | US-10-437-963-169845 | Sequence 169845, |
| 256 | 44 | 34.6 | 748 | 15 | US-10-282-122A-48709 | Sequence 48709, A | 329 | 43 | 33.9 | 821 | 15 | US-10-369-493-2791 | Sequence 2791, Ap |
| 257 | 44 | 34.6 | 814 | 15 | US-10-282-122A-52462 | Sequence 52462, A | 330 | 43 | 33.9 | 887 | 9 | US-09-815-242-13179 | Sequence 13179, A |
| 258 | 44 | 34.6 | 1078 | 16 | US-10-437-963-196472 | Sequence 196472, | 331 | 43 | 33.9 | 890 | 15 | US-10-282-122A-74187 | Sequence 74187, A |
| 259 | 44 | 34.6 | 1305 | 11 | US-09-964-956-44 | Sequence 44, Appl | 332 | 43 | 33.9 | 896 | 16 | US-10-474-776-393 | Sequence 393, App |
| 260 | 44 | 34.6 | 1396 | 15 | US-10-282-122A-69535 | Sequence 69535, A | 333 | 43 | 33.9 | 1003 | 16 | US-10-473-276-3 | Sequence 3, Appl |
| 261 | 43.5 | 34.3 | 107 | 15 | US-10-424-559-24488 | Sequence 24488, | 334 | 43 | 33.9 | 1094 | 15 | US-10-296-724-399 | Sequence 399, App |
| 262 | 43.5 | 34.3 | 148 | 15 | US-10-424-559-155154 | Sequence 155154, | 335 | 43 | 33.9 | 1396 | 15 | US-10-296-724-393 | Sequence 393, App |
| 263 | 43.5 | 34.3 | 174 | 15 | US-10-424-559-149808 | Sequence 149808, | 336 | 43 | 33.9 | 1491 | 16 | US-10-437-963-142027 | Sequence 142027, |
| 264 | 43.5 | 34.3 | 269 | 16 | US-10-437-963-203722 | Sequence 203722, | 337 | 43 | 33.9 | 1545 | 14 | US-10-329-079-11 | Sequence 11, Appl |
| 265 | 43.5 | 34.3 | 270 | 16 | US-10-437-963-171875 | Sequence 171875, | 338 | 43 | 33.9 | 5545 | 14 | US-10-329-079-45 | Sequence 45, Appl |
| 266 | 43.5 | 34.3 | 429 | 15 | US-10-282-122A-75835 | Sequence 75835, A | 339 | 43 | 33.9 | 5747 | 15 | US-10-296-724-405 | Sequence 405, App |
| 267 | 43.5 | 34.3 | 473 | 15 | US-10-425-114-55734 | Sequence 55734, A | 340 | 42.5 | 33.5 | 131 | 16 | US-10-437-963-153143 | Sequence 153143, |
| 268 | 43.5 | 34.3 | 477 | 9 | US-09-815-242-13991 | Sequence 13991, A | 341 | 42.5 | 33.5 | 147 | 15 | US-10-424-559-176645 | Sequence 176645, |
| 269 | 43.5 | 34.3 | 490 | 17 | US-10-675-086-24 | Sequence 24, Appl | 342 | 42.5 | 33.5 | 215 | 15 | US-10-424-559-270242 | Sequence 270242, |
| 270 | 43.5 | 34.3 | 495 | 10 | US-09-848-806-1 | Sequence 1, Appl | 343 | 42.5 | 33.5 | 220 | 15 | US-10-424-559-19696 | Sequence 19696, |
| 271 | 43.5 | 34.3 | 500 | 17 | US-10-866-527-38 | Sequence 38, Appl | 344 | 42.5 | 33.5 | 223 | 15 | US-10-424-559-149646 | Sequence 149646, |
| 272 | 43.5 | 34.3 | 501 | 10 | US-09-848-806-3 | Sequence 3, Appl | 345 | 42.5 | 33.5 | 240 | 9 | US-09-974-298-147 | Sequence 147, App |
| 273 | 43.5 | 34.3 | 512 | 17 | US-10-866-527-108 | Sequence 108, App | 346 | 42.5 | 33.5 | 260 | 16 | US-10-767-701-32851 | Sequence 32851, A |
| 274 | 43.5 | 34.3 | 550 | 16 | US-10-437-963-153480 | Sequence 153480, | 347 | 42.5 | 33.5 | 270 | 16 | US-10-437-963-131111 | Sequence 131111, |
| 275 | 43.5 | 34.3 | 619 | 15 | US-10-369-493-19203 | Sequence 19203, A | 348 | 42.5 | 33.5 | 272 | 15 | US-10-140-470-136 | Sequence 136, App |
| 276 | 43.5 | 34.3 | 673 | 14 | US-10-156-761-11243 | Sequence 11243, A | 349 | 42.5 | 33.5 | 278 | 14 | US-10-028-072-132674 | Sequence 132674, |
| 277 | 43.5 | 34.3 | 999 | 16 | US-10-437-963-117353 | Sequence 117353, | 350 | 42.5 | 33.5 | 278 | 14 | US-10-140-808-136 | Sequence 136, App |
| 278 | 43.5 | 34.3 | 2402 | 14 | US-10-203-224-2 | Sequence 2, Appl | 351 | 42.5 | 33.5 | 278 | 14 | US-10-121-049-136 | Sequence 136, App |
| 279 | 43 | 33.9 | 42 | 14 | US-10-029-386-31644 | Sequence 31644, A | 352 | 42.5 | 33.5 | 278 | 14 | US-10-123-904-136 | Sequence 136, App |
| 280 | 43 | 33.9 | 71 | 17 | US-10-472-928-3054 | Sequence 3054, Ap | 353 | 42.5 | 33.5 | 278 | 14 | US-10-140-470-136 | Sequence 136, App |
| 281 | 43 | 33.9 | 83 | 15 | US-10-424-559-194945 | Sequence 194945, | 354 | 42.5 | 33.5 | 278 | 14 | US-10-175-746-136 | Sequence 136, App |
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| 285 | 43 | 33.9 | 170 | 15 | US-10-335-977-6498 | Sequence 6498, Ap | 358 | 42.5 | 33.5 | 278 | 14 | US-10-140-474-136 | Sequence 136, App |
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| 288 | 43 | 33.9 | 172 | 15 | US-10-282-122A-68573 | Sequence 68573, A | 361 | 42.5 | 33.5 | 278 | 14 | US-10-140-474-136 | Sequence 136, App |
| 289 | 43 | 33.9 | 184 | 10 | US-09-873-554-15 | Sequence 1830, Ap | 362 | 42.5 | 33.5 | 278 | 14 | US-10-140-474-136 | Sequence 136, App |
| 290 | 43 | 33.9 | 196 | 9 | US-09-764-877-1830 | Sequence 1830, Ap | 363 | 42.5 | 33.5 | 278 | 14 | US-10-140-474-136 | Sequence 136, App |
| 291 | 43 | 33.9 | 196 | 15 | US-10-242-515-1830 | Sequence 1830, Ap | 364 | 42.5 | 33.5 | 278 | 14 | US-10-121-050-136 | Sequence 136, App |
| 292 | 43 | 33.9 | 210 | 16 | US-10-767-701-36983 | Sequence 36983, A | 365 | 42.5 | 33.5 | 278 | 14 | US-10-141-755-136 | Sequence 136, App |
| 293 | 43 | 33.9 | 304 | 15 | US-10-424-559-280749 | Sequence 280749, | 366 | 42.5 | 33.5 | 278 | 14 | US-10-141-755-136 | Sequence 136, App |
| 294 | 43 | 33.9 | 311 | 14 | US-10-219-810-49 | Sequence 49, Appl | 367 | 42.5 | 33.5 | 278 | 14 | US-10-140-474-136 | Sequence 136, App |
| 295 | 43 | 33.9 | 340 | 15 | US-10-424-559-260951 | Sequence 260951, | 368 | 42.5 | 33.5 | 278 | 14 | US-10-123-236-136 | Sequence 136, App |
| 296 | 43 | 33.9 | 407 | 15 | US-10-335-977-6502 | Sequence 6502, Ap | 369 | 42.5 | 33.5 | 278 | 14 | US-10-123-236-136 | Sequence 136, App |
| 297 | 43 | 33.9 | 453 | 15 | US-10-108-260A-4092 | Sequence 4092, Ap | 370 | 42.5 | 33.5 | 278 | 14 | US-10-123-236-136 | Sequence 136, App |
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| 302 | 43 | 33.9 | 467 | 15 | US-09-875-573-21 | Sequence 21, Appl | 375 | 42.5 | 33.5 | 278 | 14 | US-10-123-292-136 | Sequence 136, App |
| 303 | 43 | 33.9 | 468 | 9 | US-09-875-573-23 | Sequence 23, Appl | 376 | 42.5 | 33.5 | 278 | 14 | US-10-124-819-136 | Sequence 136, App |
| 304 | 43 | 33.9 | 468 | 9 | US-09-875-573-25 | Sequence 25, Appl | 377 | 42.5 | 33.5 | 278 | 14 | US-10-124-822-136 | Sequence 136, App |
| 305 | 43 | 33.9 | 468 | 9 | US-09-875-573-27 | Sequence 27, Appl | 378 | 42.5 | 33.5 | 278 | 14 | US-10-140-928-136 | Sequence 136, App |
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| 539 | 42.5 | 33.5 | 278 | 14 | US-10-140-019-136 | Sequence 136, App | 612 | 42.5 | 33.5 | 278 | 14 | US-10-157-799-136 | Sequence 136, App |
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| 674 | 42.5 | 33.5 | 278 | 14 | US-10-157-785-136 | Sequence 136, App | 747 | 42.5 | 33.5 | 278 | 15 | US-10-157-780-136 | Sequence 136, App |
| 675 | 42.5 | 33.5 | 278 | 14 | US-10-157-794-136 | Sequence 136, App | 748 | 42.5 | 33.5 | 278 | 15 | US-10-157-800-136 | Sequence 136, App |
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| 677 | 42.5 | 33.5 | 278 | 14 | US-10-160-500-136 | Sequence 136, App | 750 | 42.5 | 33.5 | 278 | 15 | US-10-157-802-136 | Sequence 136, App |
| 678 | 42.5 | 33.5 | 278 | 14 | US-10-121-046-136 | Sequence 136, App | 751 | 42.5 | 33.5 | 278 | 15 | US-10-158-784-136 | Sequence 136, App |
| 679 | 42.5 | 33.5 | 278 | 14 | US-10-123-156-136 | Sequence 136, App | 752 | 42.5 | 33.5 | 278 | 15 | US-10-158-789-136 | Sequence 136, App |
| 680 | 42.5 | 33.5 | 278 | 14 | US-10-123-214-136 | Sequence 136, App | 753 | 42.5 | 33.5 | 278 | 15 | US-10-192-011-136 | Sequence 136, App |
| 681 | 42.5 | 33.5 | 278 | 14 | US-10-125-805-136 | Sequence 136, App | 754 | 42.5 | 33.5 | 278 | 15 | US-10-139-963-136 | Sequence 136, App |
| 682 | 42.5 | 33.5 | 278 | 14 | US-10-124-821-136 | Sequence 136, App | 755 | 42.5 | 33.5 | 278 | 15 | US-10-140-020-136 | Sequence 136, App |
| 683 | 42.5 | 33.5 | 278 | 14 | US-10-152-385-136 | Sequence 136, App | 756 | 42.5 | 33.5 | 278 | 15 | US-10-140-023-136 | Sequence 136, App |
| 684 | 42.5 | 33.5 | 278 | 14 | US-10-152-393-136 | Sequence 136, App | 757 | 42.5 | 33.5 | 278 | 15 | US-10-140-809-136 | Sequence 136, App |
| 685 | 42.5 | 33.5 | 278 | 14 | US-10-152-396-136 | Sequence 136, App | 758 | 42.5 | 33.5 | 278 | 15 | US-10-140-865-136 | Sequence 136, App |
| 686 | 42.5 | 33.5 | 278 | 14 | US-10-153-552-136 | Sequence 136, App | 759 | 42.5 | 33.5 | 278 | 15 | US-10-141-701-136 | Sequence 136, App |
| 687 | 42.5 | 33.5 | 278 | 14 | US-10-153-840-136 | Sequence 136, App | 760 | 42.5 | 33.5 | 278 | 15 | US-10-141-754-136 | Sequence 136, App |
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| 689 | 42.5 | 33.5 | 278 | 14 | US-10-156-842-136 | Sequence 136, App | 762 | 42.5 | 33.5 | 278 | 15 | US-10-142-425-136 | Sequence 136, App |
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| 691 | 42.5 | 33.5 | 278 | 14 | US-10-156-845-136 | Sequence 136, App | 764 | 42.5 | 33.5 | 278 | 15 | US-10-143-113-136 | Sequence 136, App |
| 692 | 42.5 | 33.5 | 278 | 14 | US-10-156-846-136 | Sequence 136, App | 765 | 42.5 | 33.5 | 278 | 15 | US-10-146-730-136 | Sequence 136, App |
| 693 | 42.5 | 33.5 | 278 | 14 | US-10-121-048-136 | Sequence 136, App | 766 | 42.5 | 33.5 | 278 | 15 | US-10-146-792-136 | Sequence 136, App |
| 694 | 42.5 | 33.5 | 278 | 14 | US-10-121-052-136 | Sequence 136, App | 767 | 42.5 | 33.5 | 278 | 15 | US-10-158-791-136 | Sequence 136, App |
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| 697 | 42.5 | 33.5 | 278 | 14 | US-10-121-063-136 | Sequence 136, App | 770 | 42.5 | 33.5 | 278 | 15 | US-10-152-405-136 | Sequence 136, App |
| 698 | 42.5 | 33.5 | 278 | 14 | US-10-123-212-136 | Sequence 136, App | 771 | 42.5 | 33.5 | 278 | 15 | US-10-147-528-136 | Sequence 136, App |
| 699 | 42.5 | 33.5 | 278 | 14 | US-10-123-213-136 | Sequence 136, App | 772 | 42.5 | 33.5 | 278 | 15 | US-10-126-103-151 | Sequence 136, App |
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| 701 | 42.5 | 33.5 | 278 | 14 | US-10-123-322-136 | Sequence 136, App | 774 | 42.5 | 33.5 | 278 | 15 | US-10-140-927-136 | Sequence 136, App |
| 702 | 42.5 | 33.5 | 278 | 14 | US-10-123-771-136 | Sequence 136, App | 775 | 42.5 | 33.5 | 278 | 15 | US-10-147-493-136 | Sequence 136, App |
| 703 | 42.5 | 33.5 | 278 | 14 | US-10-123-911-136 | Sequence 136, App | 776 | 42.5 | 33.5 | 278 | 15 | US-10-145-157-136 | Sequence 136, App |
| 704 | 42.5 | 33.5 | 278 | 14 | US-10-124-823-136 | Sequence 136, App | 777 | 42.5 | 33.5 | 278 | 15 | US-10-160-503-136 | Sequence 136, App |
| 705 | 42.5 | 33.5 | 278 | 14 | US-10-125-931-136 | Sequence 136, App | 778 | 42.5 | 33.5 | 278 | 15 | US-10-143-118-136 | Sequence 136, App |
| 706 | 42.5 | 33.5 | 278 | 14 | US-10-125-932-136 | Sequence 136, App | 779 | 42.5 | 33.5 | 278 | 15 | US-10-144-993-136 | Sequence 136, App |
| 707 | 42.5 | 33.5 | 278 | 15 | US-10-127-852A-136 | Sequence 136, App | 780 | 42.5 | 33.5 | 278 | 15 | US-10-262-839-70 | Sequence 70, Appl1 |
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| 710 | 42.5 | 33.5 | 278 | 15 | US-10-131-820A-136 | Sequence 136, App | 783 | 42.5 | 33.5 | 278 | 15 | US-10-147-536-136 | Sequence 136, App |
| 711 | 42.5 | 33.5 | 278 | 15 | US-10-142-886-136 | Sequence 136, App | 784 | 42.5 | 33.5 | 278 | 16 | US-10-431-096-151 | Sequence 151, App |
| 712 | 42.5 | 33.5 | 278 | 15 | US-10-146-728-136 | Sequence 136, App | 785 | 42.5 | 33.5 | 278 | 16 | US-10-152-372-136 | Sequence 136, App |
| 713 | 42.5 | 33.5 | 278 | 15 | US-10-146-786-136 | Sequence 136, App | 786 | 42.5 | 33.5 | 278 | 17 | US-10-931-886-136 | Sequence 136, App |
| 714 | 42.5 | 33.5 | 278 | 15 | US-10-147-499-136 | Sequence 136, App | 787 | 42.5 | 33.5 | 278 | 17 | US-10-158-788-136 | Sequence 136, App |
| 715 | 42.5 | 33.5 | 278 | 15 | US-10-157-798-136 | Sequence 136, App | 788 | 42.5 | 33.5 | 334 | 15 | US-10-425-114-450593 | Sequence 40593, A |
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| 720 | 42.5 | 33.5 | 278 | 15 | US-10-140-863-136 | Sequence 136, App | 793 | 42.5 | 33.5 | 377 | 15 | US-10-425-114-45684 | Sequence 45684, A |
| 721 | 42.5 | 33.5 | 278 | 15 | US-10-141-699-136 | Sequence 136, App | 794 | 42.5 | 33.5 | 383 | 15 | US-10-425-114-48982 | Sequence 48982, A |
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| 723 | 42.5 | 33.5 | 278 | 15 | US-10-141-706-136 | Sequence 136, App | 796 | 42.5 | 33.5 | 424 | 15 | US-10-369-493-232 | Sequence 232, App |
| 724 | 42.5 | 33.5 | 278 | 15 | US-10-141-757-136 | Sequence 136, App | 797 | 42.5 | 33.5 | 429 | 9 | US-09-815-242-10098 | Sequence 10098, A |
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| 726 | 42.5 | 33.5 | 278 | 15 | US-10-142-428-136 | Sequence 136, App | 799 | 42.5 | 33.5 | 429 | 15 | US-10-282-122A-56485 | Sequence 56485, A |
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| 729 | 42.5 | 33.5 | 278 | 15 | US-10-143-027-136 | Sequence 136, App | 802 | 42.5 | 33.5 | 506 | 17 | US-10-866-527-118 | Sequence 118, App |
| 730 | 42.5 | 33.5 | 278 | 15 | US-10-143-115-136 | Sequence 136, App | 803 | 42.5 | 33.5 | 518 | 16 | US-10-437-963-168927 | Sequence 168927, A |
| 731 | 42.5 | 33.5 | 278 | 15 | US-10-144-956-136 | Sequence 136, App | 804 | 42.5 | 33.5 | 546 | 11 | US-09-764-875-1122 | Sequence 1122, App |
| 732 | 42.5 | 33.5 | 278 | 15 | US-10-144-958-136 | Sequence 136, App | 805 | 42.5 | 33.5 | 567 | 11 | US-10-424-599-241719 | Sequence 241719, App |
| 733 | 42.5 | 33.5 | 278 | 15 | US-10-145-632-136 | Sequence 136, App | 806 | 42.5 | 33.5 | 568 | 11 | US-09-764-875-832 | Sequence 832, App |
| 734 | 42.5 | 33.5 | 278 | 15 | US-10-145-749-136 | Sequence 136, App | 807 | 42.5 | 33.5 | 600 | 16 | US-10-437-963-104086 | Sequence 104086, A |
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| 737 | 42.5 | 33.5 | 278 | 15 | US-10-145-878-136 | Sequence 136, App | 810 | 42.5 | 33.5 | 883 | 16 | US-10-441-949-2 | Sequence 2, Appl1 |
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| 739 | 42.5 | 33.5 | 278 | 15 | US-10-147-489-136 | Sequence 136, App | 812 | 42 | 33.1 | 16 | US-10-020-269-30 | Sequence 30, Appl1 | |
| 740 | 42.5 | 33.5 | 278 | 15 | US-10-147-507-136 | Sequence 136, App | 813 | 42 | 33.1 | 44 | US-09-877-843-84 | Sequence 84, Appl1 | |
| 741 | 42.5 | 33.5 | 278 | 15 | US-10-147-535-136 | Sequence 136, App | 814 | 42 | 33.1 | 60 | US-09-97 | | |

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| 864 | 42 | 33.1 | 351 | 14 | US-10-032-585-7371 | Sequence 7371, Ap | 937 | 42 | 33.1 | 1681 | 15 | US-10-398-885A-16 | Sequence 16, Appl |
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| 866 | 42 | 33.1 | 357 | 15 | US-10-424-599-226137 | Sequence 226137, A | 939 | 42 | 33.1 | 1938 | 14 | US-10-171-311-164 | Sequence 164, App |
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| 869 | 42 | 33.1 | 379 | 15 | US-10-424-599-274676 | Sequence 274676, A | 942 | 42 | 33.1 | 1973 | 16 | US-10-341-434-103 | Sequence 103, App |
| 870 | 42 | 33.1 | 383 | 15 | US-10-425-114-53577 | Sequence 53577, A | 943 | 42 | 33.1 | 2014 | 15 | US-10-661-809-22 | Sequence 22, Appl |
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| 873 | 42 | 33.1 | 431 | 15 | US-10-369-493-22917 | Sequence 22917, A | 946 | 42 | 33.1 | 1887 | 14 | US-10-132-382-6 | Sequence 6, Appl1 |
| 874 | 42 | 33.1 | 436 | 15 | US-10-120-801-68 | Sequence 68, Appl | 947 | 42 | 33.1 | 2013 | 14 | US-10-132-382-2 | Sequence 2, Appl1 |
| 875 | 42 | 33.1 | 436 | 15 | US-10-275-595A-16 | Sequence 16, Appl | 948 | 42 | 33.1 | 2014 | 14 | US-10-132-382-8 | Sequence 8, Appl1 |
| 876 | 42 | 33.1 | 450 | 15 | US-10-282-122A-6508 | Sequence 6508, A | 949 | 42 | 33.1 | 2014 | 15 | US-10-220-955-18 | Sequence 18, Appl |
| 877 | 42 | 33.1 | 451 | 15 | US-10-282-122A-67651 | Sequence 67651, A | 950 | 42 | 33.1 | 2014 | 15 | US-10-415-011-8 | Sequence 8, Appl1 |
| 878 | 42 | 33.1 | 459 | 15 | US-10-369-493-18302 | Sequence 18302, A | 951 | 42 | 33.1 | 2040 | 14 | US-10-132-382-4 | Sequence 4, Appl |
| 879 | 42 | 33.1 | 460 | 15 | US-10-417-700A-133 | Sequence 133, App | 952 | 42 | 32.7 | 85 | 16 | US-10-437-963-162000 | Sequence 162000, A |
| 880 | 42 | 33.1 | 462 | 15 | US-10-282-122A-53413 | Sequence 53413, A | 953 | 42 | 32.7 | 98 | 16 | US-10-767-701-53086 | Sequence 53086, A |
| 881 | 42 | 33.1 | 464 | 15 | US-10-369-493-7005 | Sequence 7005, Ap | 954 | 42 | 32.7 | 122 | 15 | US-10-424-599-146448 | Sequence 146448, A |
| 882 | 42 | 33.1 | 481 | 15 | US-10-425-114-53209 | Sequence 53209, A | 955 | 42 | 32.7 | 145 | 16 | US-10-767-701-37553 | Sequence 37553, A |
| 883 | 42 | 33.1 | 481 | 15 | US-10-425-114-59273 | Sequence 59273, A | 956 | 42 | 32.7 | 186 | 16 | US-10-767-701-41740 | Sequence 41740, A |
| 884 | 42 | 33.1 | 481 | 16 | US-10-767-701-45695 | Sequence 45695, A | 957 | 42 | 32.7 | 187 | 15 | US-10-425-114-57345 | Sequence 57345, A |
| 885 | 42 | 33.1 | 485 | 15 | US-10-425-114-46975 | Sequence 46975, A | 958 | 42 | 32.7 | 188 | 16 | US-10-767-701-40973 | Sequence 40973, A |
| 886 | 42 | 33.1 | 485 | 15 | US-10-425-114-47502 | Sequence 47502, A | 959 | 42 | 32.7 | 198 | 15 | US-10-425-114-46763 | Sequence 46763, A |
| 887 | 42 | 33.1 | 485 | 15 | US-10-425-114-47600 | Sequence 47600, A | 960 | 42 | 32.7 | 202 | 15 | US-10-364-337-12 | Sequence 12, Appl |
| 888 | 42 | 33.1 | 485 | 15 | US-10-425-114-53351 | Sequence 53351, A | 961 | 42 | 32.7 | 233 | 15 | US-10-424-599-163137 | Sequence 163137, A |
| 889 | 42 | 33.1 | 485 | 15 | US-10-425-114-59175 | Sequence 59175, A | 962 | 42 | 32.7 | 261 | 15 | US-10-424-599-146446 | Sequence 146446, A |

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963 41.5 32.7 312 15 US-10-425-114-63097 Sequence 63097, A
964 41.5 32.7 345 16 US-10-437-963-204556 Sequence 204556,
965 41.5 32.7 358 15 US-10-464-610-18 Sequence 18, Appl
966 41.5 32.7 365 15 US-10-464-610-4 Sequence 4, Appl
967 41.5 32.7 365 15 US-10-424-599-163141 Sequence 163141,
968 41.5 32.7 374 16 US-10-437-963-118336 Sequence 118336,
969 41.5 32.7 395 15 US-10-425-114-36771 Sequence 36771, A
970 41.5 32.7 413 14 US-10-156-761-15075 Sequence 15075, A
971 41.5 32.7 425 15 US-10-108-260A-4381 Sequence 4381, Ap
972 41.5 32.7 425 15 US-10-282-122A-68661 Sequence 68661, A
973 41.5 32.7 425 17 US-10-959-539-46 Sequence 46, Appl
974 41.5 32.7 438 15 US-10-424-599-265659 Sequence 265659,
975 41.5 32.7 463 10 US-09-988-462-25 Sequence 25, Appl
976 41.5 32.7 470 15 US-10-425-114-70198 Sequence 70198, A
977 41.5 32.7 472 15 US-10-417-700A-67 Sequence 67, Appl
978 41.5 32.7 508 15 US-10-424-599-242297 Sequence 242297,
979 41.5 32.7 517 15 US-10-425-114-65871 Sequence 65871, A
980 41.5 32.7 527 15 US-10-425-114-51766 Sequence 51766, A
981 41.5 32.7 561 14 US-10-032-585-7306 Sequence 7306, Ap
982 41.5 32.7 639 9 US-09-854-731-17 Sequence 17, Appl
983 41.5 32.7 1312 15 US-10-369-493-1804 Sequence 1804, Ap
984 41.5 32.7 55 15 US-10-424-599-235854 Sequence 235854,
985 41.5 32.7 63 16 US-10-437-963-182278 Sequence 182278,
986 41.5 32.3 64 16 US-10-767-701-61024 Sequence 61024, A
987 41.5 32.3 71 9 US-09-982-809-2 Sequence 2, Appl
988 41.5 32.3 71 14 US-10-161-941-11 Sequence 11, Appl
989 41.5 32.3 74 15 US-10-424-599-144538 Sequence 144538,
990 41.5 32.3 99 16 US-10-437-963-168376 Sequence 168376,
991 41.5 32.3 120 16 US-10-767-701-46401 Sequence 46401, A
992 41.5 32.3 128 15 US-10-424-599-251351 Sequence 251351,
993 41.5 32.3 130 15 US-10-424-599-281789 Sequence 281789,
994 41.5 32.3 133 14 US-10-286-421-28 Sequence 28, Appl
995 41.5 32.3 140 15 US-10-282-122A-77767 Sequence 77767, A
996 41.5 32.3 149 15 US-10-369-493-2146 Sequence 2146, Ap
997 41.5 32.3 156 15 US-10-424-599-184133 Sequence 184133,
998 41.5 32.3 157 15 US-10-424-599-226576 Sequence 226576,
999 41.5 32.3 158 15 US-10-389-566-511 Sequence 511, App
1000 41.5 32.3 160 15 US-10-108-260A-3318 Sequence 3318, Ap

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ALIGNMENTS

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RESULT 1
US-10-839-729-6
; Sequence 6, Application US/10839729
; Publication No. US20050002953A1
; GENERAL INFORMATION:
; APPLICANT: Jens Herold
; TITLE OF INVENTION: SARS-CORONAVIRUS VIRUS-LIKE PARTICLES
; FILE REFERENCE: BIOBANK.013A
; CURRENT APPLICATION NUMBER: US/10/839,729
; CURRENT FILING DATE: 2004-05-04
; PRIOR APPLICATION NUMBER: 60/468703
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 221
; TYPE: PR
; ORGANISM: SARS Coronavirus
US-10-839-729-6

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Query Match      88.2%; Score 112; DB 16; Length 221;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 4 MADNGTIVTEELKQLEQNMNV 25
Db 1 MADNGTIVTEELKQLEQNMNV 22

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RESULT 2
US-10-839-729-7
; Sequence 7, Application US/10839729
; Publication No. US20050002953A1
; GENERAL INFORMATION:
; APPLICANT: Jens Herold
; TITLE OF INVENTION: SARS-CORONAVIRUS VIRUS-LIKE PARTICLES
; FILE REFERENCE: BIOBANK.013A
; CURRENT APPLICATION NUMBER: US/10/839,729
; CURRENT FILING DATE: 2004-05-04
; PRIOR APPLICATION NUMBER: 60/468703
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 221
; TYPE: PR
; ORGANISM: SARS Coronavirus
US-10-839-729-7

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```

Query Match      88.2%; Score 112; DB 16; Length 221;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 4 MADNGTIVTEELKQLEQNMNV 25
Db 1 MADNGTIVTEELKQLEQNMNV 22

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RESULT 3
US-10-839-729-8
; Sequence 8, Application US/10839729
; Publication No. US20050002953A1
; GENERAL INFORMATION:
; APPLICANT: Jens Herold
; TITLE OF INVENTION: SARS-CORONAVIRUS VIRUS-LIKE PARTICLES
; FILE REFERENCE: BIOBANK.013A
; CURRENT APPLICATION NUMBER: US/10/839,729
; CURRENT FILING DATE: 2004-05-04
; PRIOR APPLICATION NUMBER: 60/468703
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 221
; TYPE: PR
; ORGANISM: SARS Coronavirus
US-10-839-729-8

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Query Match      88.2%; Score 112; DB 16; Length 221;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 4 MADNGTIVTEELKQLEQNMNV 25
Db 1 MADNGTIVTEELKQLEQNMNV 22

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RESULT 4
US-10-839-729-9
; Sequence 9, Application US/10839729
; Publication No. US20050002953A1
; GENERAL INFORMATION:
; APPLICANT: Jens Herold
; TITLE OF INVENTION: SARS-CORONAVIRUS VIRUS-LIKE PARTICLES
; FILE REFERENCE: BIOBANK.013A
; CURRENT APPLICATION NUMBER: US/10/839,729
; CURRENT FILING DATE: 2004-05-04
; PRIOR APPLICATION NUMBER: 60/468703
; PRIOR FILING DATE: 2003-05-06

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NUMBER OF SEQ ID NOS: 49
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 9
 LENGTH: 221
 TYPE: PRT
 ORGANISM: SARS Coronavirus
 US-10-839-729-9

Query Match 88.2%; Score 112; DB 16; Length 221;
 Best Local Similarity 100.0%; Pred. No. 1.1e-07;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MADNGTIVTEELKQLEQNNLV 25
 DB 1 MADNGTIVTEELKQLEQNNLV 22

RESULT 5
 US-10-699-936-24
 Sequence 24, Application US/10699936
 Publication No. US20050095582A1
 GENERAL INFORMATION:
 APPLICANT: Gillim-Ross, Laura
 APPLICANT: Taylor, Jill
 APPLICANT: Scholl, David R.
 APPLICANT: Wentworth, David E.
 APPLICANT: Jollick, Joseph D.
 TITLE OF INVENTION: Compositions and Methods for Detecting Severe Acute Respiratory
 TITLE OF INVENTION: Syndrome Coronavirus
 FILE REFERENCE: DHI-07986
 CURRENT APPLICATION NUMBER: US/10/699,936
 CURRENT FILING DATE: 2003-11-03
 NUMBER OF SEQ ID NOS: 87
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 24
 LENGTH: 221
 TYPE: PRT
 ORGANISM: SARS-CoV Urban1
 US-10-699-936-24

Query Match 88.2%; Score 112; DB 17; Length 221;
 Best Local Similarity 100.0%; Pred. No. 1.1e-07;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MADNGTIVTEELKQLEQNNLV 25
 DB 1 MADNGTIVTEELKQLEQNNLV 22

RESULT 6
 US-10-699-936-81
 Sequence 81, Application US/10699936
 Publication No. US20050095582A1
 GENERAL INFORMATION:
 APPLICANT: Gillim-Ross, Laura
 APPLICANT: Taylor, Jill
 APPLICANT: Scholl, David R.
 APPLICANT: Wentworth, David E.
 APPLICANT: Jollick, Joseph D.
 TITLE OF INVENTION: Compositions and Methods for Detecting Severe Acute Respiratory
 TITLE OF INVENTION: Syndrome Coronavirus
 FILE REFERENCE: DHI-07986
 CURRENT APPLICATION NUMBER: US/10/699,936
 CURRENT FILING DATE: 2003-11-03
 NUMBER OF SEQ ID NOS: 87
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 81
 LENGTH: 221
 TYPE: PRT
 ORGANISM: SARS coronavirus Tor2
 US-10-699-936-81

Query Match 88.2%; Score 112; DB 17; Length 221;

Best Local Similarity 100.0%; Pred. No. 1.1e-07;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MADNGTIVTEELKQLEQNNLV 25
 DB 1 MADNGTIVTEELKQLEQNNLV 22

RESULT 7
 US-10-699-936-82
 Sequence 82, Application US/10699936
 Publication No. US20050095582A1
 GENERAL INFORMATION:
 APPLICANT: Gillim-Ross, Laura
 APPLICANT: Taylor, Jill
 APPLICANT: Scholl, David R.
 APPLICANT: Wentworth, David E.
 APPLICANT: Jollick, Joseph D.
 TITLE OF INVENTION: Compositions and Methods for Detecting Severe Acute Respiratory
 TITLE OF INVENTION: Syndrome Coronavirus
 FILE REFERENCE: DHI-07986
 CURRENT APPLICATION NUMBER: US/10/699,936
 CURRENT FILING DATE: 2003-11-03
 NUMBER OF SEQ ID NOS: 87
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 82
 LENGTH: 221
 TYPE: PRT
 ORGANISM: SARS coronavirus Shanghai QXC
 US-10-699-936-82

Query Match 88.2%; Score 112; DB 17; Length 221;
 Best Local Similarity 100.0%; Pred. No. 1.1e-07;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MADNGTIVTEELKQLEQNNLV 25
 DB 1 MADNGTIVTEELKQLEQNNLV 22

RESULT 8
 US-10-699-936-83
 Sequence 83, Application US/10699936
 Publication No. US20050095582A1
 GENERAL INFORMATION:
 APPLICANT: Gillim-Ross, Laura
 APPLICANT: Taylor, Jill
 APPLICANT: Scholl, David R.
 APPLICANT: Wentworth, David E.
 APPLICANT: Jollick, Joseph D.
 TITLE OF INVENTION: Compositions and Methods for Detecting Severe Acute Respiratory
 TITLE OF INVENTION: Syndrome Coronavirus
 FILE REFERENCE: DHI-07986
 CURRENT APPLICATION NUMBER: US/10/699,936
 CURRENT FILING DATE: 2003-11-03
 NUMBER OF SEQ ID NOS: 87
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 83
 LENGTH: 221
 TYPE: PRT
 ORGANISM: SARS coronavirus Shanghai QXC
 US-10-699-936-83

Query Match 88.2%; Score 112; DB 17; Length 221;
 Best Local Similarity 100.0%; Pred. No. 1.1e-07;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MADNGTIVTEELKQLEQNNLV 25
 DB 1 MADNGTIVTEELKQLEQNNLV 22

RESULT 9

US-10-808-187-214
; Sequence 214, Application US/10808187
; Publication No. US2005009009A1
; GENERAL INFORMATION:
; APPLICANT: PEIRIS, JOSEPH S. M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: GUAN, YI
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: NICHOLLS, JOHN
; TITLE OF INVENTION: A DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS CAUSING SEVERE ACUTE
; FILE REFERENCE: V9661.0078
; CURRENT APPLICATION NUMBER: US/10/808,187
; PRIOR FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/457,031
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: 60/457,730
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 60/459,931
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/460,357
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/461,265
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/462,805
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: 60/468,139
; PRIOR FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: 60/464,886
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 60/471,200
; PRIOR FILING DATE: 2003-05-16
; NUMBER OF SEQ ID NOS: 2476
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 214
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Human severe acute respiratory system virus
US-10-808-187-214

Query Match 88.2%; Score 112; DB 17; Length 242;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MADNGTIVBELKQLEOMNLV 25
DB 22 MADNGTIVBELKQLEOMNLV 43

RESULT 10
US-10-839-729-46
; Sequence 46, Application US/10839729
; Publication No. US2005002953A1
; GENERAL INFORMATION:
; APPLICANT: JEAN HEROLD
; TITLE OF INVENTION: SARS-CORONAVIRUS VIRUS-LIKE PARTICLES
; FILE REFERENCE: BIOBANK 013A
; CURRENT APPLICATION NUMBER: US/10/839,729
; PRIOR FILING DATE: 2004-05-04
; PRIOR APPLICATION NUMBER: 60/468703
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically prepared polypeptide sequence
US-10-839-729-46

Query Match 57.5%; Score 73; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MADNGTIVBELKQLEOMNLV 18
DB 1 MADNGTIVBELKQLEOMNLV 15

RESULT 11
US-09-864-761-39008
; Sequence 39008, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecm1ca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine ver. 1.1
; SEQ ID NO 39008
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC004837.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.9
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.6
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.9
; OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 3.9
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.4

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.6
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.6
OTHER INFORMATION: SWISSPROT HIT: P11233, EVALUE 5.00e-25
OTHER INFORMATION: EST_HUMAN HIT: A1344679.1, EVALUE 6.00e-24
US-09-864-761-39008

Query Match 43.3%; Score 55; DB 9; Length 54;
Best Local Similarity 41.7%; Pred. No. 2.5;
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 KKKMADNGITVEELKQLEQNL 24
DB 20 KSDLEDKQVSVSEAKRAEQMNV 43

RESULT 12
US-09-873-546-10
Sequence 10, Application US/09873546
Publication No. US20030059771A1
GENERAL INFORMATION:
APPLICANT: Clark, Geoff
APPLICANT: Ellis, Chad
APPLICANT: Vos, Michelle
TITLE OF INVENTION: R1g: No. US20030059771A1el Ras-Related Gene
FILE REFERENCE: NIH-05080
CURRENT APPLICATION NUMBER: US/09/873,546
CURRENT FILING DATE: 2001-06-04
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.0
SEQ ID NO 10
LENGTH: 206
TYPE: PRT
ORGANISM: Homo sapiens
US-09-873-546-10

Query Match 43.3%; Score 55; DB 10; Length 206;
Best Local Similarity 41.7%; Pred. No. 11;
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 KKKMADNGITVEELKQLEQNL 24
DB 128 KSDLEDKQVSVSEAKRAEQMNV 151

RESULT 13
US-10-153-668-214
Sequence 214, Application US/10153668
Publication No. US20030092616A1
GENERAL INFORMATION:
APPLICANT: HONDA, Goichi
APPLICANT: MATSUDA, Akio
APPLICANT: MURAMATSU, Shuji
APPLICANT: ISHIZAWA, Kenya
TITLE OF INVENTION: STAT6 Activating Gene
FILE REFERENCE: 1254-0207P
CURRENT APPLICATION NUMBER: US/10/153,668
CURRENT FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: US 60/293,172
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/316,031
PRIOR FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/328,403
PRIOR FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: JP 2001-157043
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: JP 2001-260681
PRIOR FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: JP 2001-313175
PRIOR FILING DATE: 2001-10-10
NUMBER OF SEQ ID NOS: 488
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 214
LENGTH: 206

TYPE: PRT
ORGANISM: Homo sapiens
US-10-153-668-214

Query Match 43.3%; Score 55; DB 14; Length 206;
Best Local Similarity 41.7%; Pred. No. 11;
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 KKKMADNGITVEELKQLEQNL 24
DB 128 KSDLEDKQVSVSEAKRAEQMNV 151

RESULT 14
US-10-021-660-132
Sequence 132, Application US/10021660
Publication No. US20030152926A1
GENERAL INFORMATION:
APPLICANT: Murray, Richard
APPLICANT: Glynn, Richard
APPLICANT: Watson, Susan R.
APPLICANT: EOS Biotechnology, Inc.
TITLE OF INVENTION: No. US20030152926A1el Methods of Diagnosis of Angiogenesis,
TITLE OF INVENTION: Compositions and Methods of Screening for Angiogenesis
FILE REFERENCE: 018501-000710US
CURRENT APPLICATION NUMBER: US/10/021,660
CURRENT FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: US/09/784,356
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: US 09/637,977
PRIOR FILING DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 135
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 132
LENGTH: 206
TYPE: PRT
ORGANISM: Homo sapiens
US-10-021-660-132

Query Match 43.3%; Score 55; DB 14; Length 206;
Best Local Similarity 41.7%; Pred. No. 11;
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 KKKMADNGITVEELKQLEQNL 24
DB 128 KSDLEDKQVSVSEAKRAEQMNV 151

RESULT 15
US-10-231-913-64
Sequence 64, Application US/10231913
Publication No. US20040005576A1
GENERAL INFORMATION:
APPLICANT: Guo, Xiaojia S.
APPLICANT: Li, Li
APPLICANT: Baturajan, Meera
APPLICANT: Salmate, Richard A.
APPLICANT: Casman, Stacie J.
APPLICANT: Malyankar, Uriel M.
APPLICANT: Tchernov, Velizar T.
APPLICANT: Vernet, Corinne A.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Alsobrook II, John P.
APPLICANT: Edinger, Schlomil
APPLICANT: Peyman, John A.
APPLICANT: Stone, David J.
APPLICANT: Ellerman, Karen
APPLICANT: Gangolli, Bena A.
APPLICANT: Boldog, Ferenc L.
APPLICANT: Colman, Steven D.
APPLICANT: Eissen, Andrew J.

APPLICANT: Liu, Xiaohong
APPLICANT: Padigaru, Muralidhara
APPLICANT: Spaderna, Steven K.
APPLICANT: Zerhusen, Bryan D.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-216
CURRENT APPLICATION NUMBER: US/10/231,913
CURRENT FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: 60/251,660
PRIOR FILING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: 60/255,029
PRIOR FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: 60/260,326
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/263,800
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: 60/269,942
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/286,183
PRIOR FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: 60/313,627
PRIOR FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: 60/318,712
PRIOR FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 232
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 64
LENGTH: 206
TYPE: PRT
ORGANISM: Homo sapiens
US-10-231-913-64

Query Match 43.3%; Score 55; DB 15; Length 206;
Best Local Similarity 41.7%; Pred. No. 11;
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy 1 KKKMADNGTIVVEELKQLLEQNNL 24
Db 128 KSDLEDKQVSVBEAKNRAEQNNV 151

RESULT 16
US-10-211-462-79
Sequence 79, Application US/10211462
Publication No. US2004003495A1
GENERAL INFORMATION:
APPLICANT: Murray, Richard
APPLICANT: Glynn, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Aziz, Natasha
TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis, Compositions and
FILE REFERENCE: 018501-006200US
CURRENT APPLICATION NUMBER: US/10/211,462
CURRENT FILING DATE: 2003-02-13
PRIOR APPLICATION NUMBER: US 09/784,356
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: US 09/791,390
PRIOR FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: US 60/310,025
PRIOR FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: US 60/334,244
PRIOR FILING DATE: 2001-11-29
NUMBER OF SEQ ID NOS: 230
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 79
LENGTH: 206
TYPE: PRT
ORGANISM: Homo sapiens
US-10-211-462-79

Query Match 43.3%; Score 55; DB 15; Length 206;

Best Local Similarity 41.7%; Pred. No. 11;
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy 1 KKKMADNGTIVVEELKQLLEQNNL 24
Db 128 KSDLEDKQVSVBEAKNRAEQNNV 151

RESULT 17
US-10-408-765A-2022
Sequence 2022, Application US/10408765A
Publication No. US20040101874A1
GENERAL INFORMATION:
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Fahy, Boia D.
APPLICANT: Zhang, Bing
APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
FILE REFERENCE: 660088,465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2022
LENGTH: 206
TYPE: PRT
ORGANISM: Homo sapiens
US-10-408-765A-2022

Query Match 43.3%; Score 55; DB 16; Length 206;
Best Local Similarity 41.7%; Pred. No. 11;
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy 1 KKKMADNGTIVVEELKQLLEQNNL 24
Db 128 KSDLEDKQVSVBEAKNRAEQNNV 151

RESULT 18
US-10-804-491-48
Sequence 48, Application US/10804491
Publication No. US20040180375A1
GENERAL INFORMATION:
APPLICANT: Cismowski, Mary
APPLICANT: Duzic, Emt
TITLE OF INVENTION: AGS Proteins and Nucleic Acid Molecules and Uses Therefor
FILE REFERENCE: 60388-A-PCT-US
CURRENT APPLICATION NUMBER: US/10/804,491
CURRENT FILING DATE: 2004-03-19
PRIOR APPLICATION NUMBER: US/09/709,103
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.1
SEQ ID NO 48
LENGTH: 206
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-804-491-48

Query Match 43.3%; Score 55; DB 16; Length 206;
Best Local Similarity 41.7%; Pred. No. 11;
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy 1 KKKMADNGTIVVEELKQLLEQNNL 24
Db 128 KSDLEDKQVSVBEAKNRAEQNNV 151

RESULT 19

US-10-231-913-66
; Sequence 66, Application US/10231913
; Publication No. US2004000576A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Xiaojia S.
; APPLICANT: Li, Li
; APPLICANT: Patnurajan, Meera
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malynkar, Uriel M.
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Vermet, Corine A.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Edinger, Schlonit
; APPLICANT: Peyman, John A.
; APPLICANT: Stone, David J.
; APPLICANT: Ellerman, Karen
; APPLICANT: Gangolli, Baha A.
; APPLICANT: Boldog, Ference L.
; APPLICANT: Colman, Steven D.
; APPLICANT: Eisen, Andrew J.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Zehrusen, Bryan D.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-216
; CURRENT APPLICATION NUMBER: US/10/231,913
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 60/251,660
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: 60/255,029
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/260,326
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/263,800
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/269,942
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/286,183
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 60/313,627
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/318,712
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 66
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-231-913-66

Query Match 43.3%; Score 55; DB 15; Length 209;
Best Local Similarity 41.7%; Pred. No. 12;
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 KKKADNGRTTVEELKQLEQNL 24
DB 131 KSDLEDKQVSVBEAKRAEQMNV 154

RESULT 20
US-10-425-114-69487
; Sequence 69487, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E

APPLICANT: Tabaeke, Jack E
APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5333)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; PRIOR FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 69487
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73003G04_FLI.pep
US-10-425-114-69487

Query Match 42.1%; Score 53.5; DB 15; Length 336;
Best Local Similarity 57.1%; Pred. No. 32;
Matches 12; Conservative 3; Mismatches 3; Indels 3; Gaps 1;

QY 7 NGTITVEELKQLEQ---NML 24
DB 196 NGTISLEELKQALAKDVPWRL 216

RESULT 21
US-10-437-963-158994
; Sequence 158994, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Boukharov, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; PRIOR FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 158994
; LENGTH: 486
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_58414C.1.pep
US-10-437-963-158994

Query Match 42.1%; Score 53.5; DB 16; Length 486;
Best Local Similarity 57.1%; Pred. No. 49;
Matches 12; Conservative 3; Mismatches 3; Indels 3; Gaps 1;

QY 7 NGTITVEELKQLEQ---NML 24
DB 346 NGTISLEELKQALAKDVPWRL 366

RESULT 22
US-10-437-963-158996
; Sequence 158996, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Boukharov, Brad

```

; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 158996
; LENGTH: 512
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_58416C.1.pep
; US-10-437-963-158996

Query Match          42.1%; Score 53.5; DB 16; Length 512;
Best Local Similarity 57.1%; Pred. No. 52;
Matches 12; Conservative 3; Mismatches 3; Indels 3; Gaps 1;

QY      7 NGTIVBELKQLEQ--WNL 24
Db      372 NGTISLELKQALAKQVPMRL 392

RESULT 23
US-10-425-114-57880
; Sequence 57880, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 57880
; LENGTH: 523
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLMO17084F11_FLI.pep
; US-10-425-114-57880

Query Match          42.1%; Score 53.5; DB 15; Length 523;
Best Local Similarity 57.1%; Pred. No. 53;
Matches 12; Conservative 3; Mismatches 3; Indels 3; Gaps 1;

QY      7 NGTIVBELKQLEQ--WNL 24
Db      383 NGTISLELKQALAKQVPMRL 403

RESULT 24
US-10-282-122A-51593
; Sequence 51593, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
```

```

; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: EPIGRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 60/191,078
; SEQ ID NO 1593
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Clostridium acetobutylicum
; US-10-282-122A-51593

Query Match          41.7%; Score 53; DB 15; Length 351;
Best Local Similarity 37.5%; Pred. No. 40;
Matches 9; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

QY      2 KXKADNGTIVBELKQLEQWNLV 25
Db      127 KCIISNGELSLBELKXKMDASNIV 150

RESULT 25
US-10-231-913-63
; Sequence 63, Application US/10231913
; Publication No. US20040005576A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Xiaojia S.
; APPLICANT: Li, Li
; APPLICANT: Paturajan, Meera
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyankar, Urfel M.
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Verneet, Corine A.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Alsodrook II, John P.
; APPLICANT: Edinger, Schlomit
; APPLICANT: Peyman, John A.
; APPLICANT: Stone, David J.
; APPLICANT: Ellerman, Karen
; APPLICANT: Gangolli, Esba A.
; APPLICANT: Boldog, Ference L.
; APPLICANT: Colman, Steven D.
; APPLICANT: Eisen, Andrew J.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Zernusen, Bryan D.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
```

```
FILE REFERENCE: 21402-216
CURRENT APPLICATION NUMBER: US/10/231,913
CURRENT FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: 60/251,660
PRIOR FILING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: 60/255,029
PRIOR FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: 60/260,326
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/263,800
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: 60/269,942
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/286,183
PRIOR FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: 60/313,627
PRIOR FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: 60/318,712
PRIOR FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 292
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 63
LENGTH: 206
TYPE: PRT
ORGANISM: Mus musculus
US-10-231-913-63
```

```
Query Match 40.9%; Score 52; DB 15; Length 206;
Best Local Similarity 37.5%; Pred. No. 30;
Matches 9; Conservative 5; Mismatches 10; Indels 0; Gaps 0;
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```
QY 1 KKKMADNGTITVEELKQLLEQNNL 24
Db 128 KSDLEDKQKVSEAKNRADQNNV 151
```

```
RESULT 26
US-10-231-913-65
Sequence 65, Application US/10231913
Publication No. US20040005576A1
GENERAL INFORMATION:
APPLICANT: Guo, Xiaojia S.
APPLICANT: Li, Li
APPLICANT: Paturajan, Meera
APPLICANT: Shinkets, Richard A.
APPLICANT: Casman, Stacie J.
APPLICANT: Malyankar, Uriel M.
APPLICANT: Tchernev, Vellizar T.
APPLICANT: Vernet, Corine A.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Alsobrook II, John P.
APPLICANT: Edinger, Schlomit
APPLICANT: Peyman, John A.
APPLICANT: Stone, David J.
APPLICANT: Ellerman, Karen
APPLICANT: Gangolli, Bsha A.
APPLICANT: Boldog, Ference L.
APPLICANT: Colman, Steven D.
APPLICANT: Eissen, Andrew J.
APPLICANT: Padigar, Muralidhara
APPLICANT: Spaderna, Steven K.
APPLICANT: Zerhusen, Bryan D.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-216
CURRENT APPLICATION NUMBER: US/10/231,913
CURRENT FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: 60/251,660
PRIOR FILING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: 60/255,029
PRIOR FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: 60/260,326
```

```
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/263,800
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: 60/269,942
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/286,183
PRIOR FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: 60/313,627
PRIOR FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: 60/318,712
PRIOR FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 292
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 65
LENGTH: 206
TYPE: PRT
ORGANISM: Mus musculus
US-10-231-913-65
```

```
Query Match 40.9%; Score 52; DB 15; Length 206;
Best Local Similarity 37.5%; Pred. No. 30;
Matches 9; Conservative 5; Mismatches 10; Indels 0; Gaps 0;
```

```
QY 1 KKKMADNGTITVEELKQLLEQNNL 24
Db 128 KSDLEDKQKVSEAKNRADQNNV 151
```

```
RESULT 27
US-10-231-913-67
Sequence 67, Application US/10231913
Publication No. US20040005576A1
GENERAL INFORMATION:
APPLICANT: Guo, Xiaojia S.
APPLICANT: Li, Li
APPLICANT: Paturajan, Meera
APPLICANT: Shinkets, Richard A.
APPLICANT: Casman, Stacie J.
APPLICANT: Malyankar, Uriel M.
APPLICANT: Tchernev, Vellizar T.
APPLICANT: Vernet, Corine A.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Alsobrook II, John P.
APPLICANT: Edinger, Schlomit
APPLICANT: Peyman, John A.
APPLICANT: Stone, David J.
APPLICANT: Ellerman, Karen
APPLICANT: Gangolli, Bsha A.
APPLICANT: Boldog, Ference L.
APPLICANT: Colman, Steven D.
APPLICANT: Eissen, Andrew J.
APPLICANT: Padigar, Muralidhara
APPLICANT: Spaderna, Steven K.
APPLICANT: Zerhusen, Bryan D.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-216
CURRENT APPLICATION NUMBER: US/10/231,913
CURRENT FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: 60/251,660
PRIOR FILING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: 60/255,029
PRIOR FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: 60/260,326
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/263,800
PRIOR FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: 60/269,942
PRIOR FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: 60/286,183
PRIOR FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: 60/313,627
```

;; PRIOR FILING DATE: 2001-08-20
;; PRIOR APPLICATION NUMBER: 60/318,712
;; PRIOR FILING DATE: 2001-09-12
;; NUMBER OF SEQ ID NOS: 292
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 67
;; LENGTH: 206
;; TYPE: PRT
;; ORGANISM: Xenopus laevis
US-10-231-913-67

Query Match 40.9%; Score 52; DB 15; Length 206;
Best Local Similarity 37.5%; Pred. No. 30;
Matches 9; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 KKKMADNGTIVTEELKQLEQWNL 24
DB 128 KSDLEDKQVSVBEAKSRADQWNV 151

RESULT 28
US-10-282-122A-54546

;; Sequence 54546, Application US/10282122A
;; Publication No. US20040029129A1
;; GENERAL INFORMATION:

;; APPLICANT: Wang, Liangsu
;; APPLICANT: Zamudio, Carlos
;; APPLICANT: Malone, Cheryl
;; APPLICANT: Haselbeck, Robert
;; APPLICANT: Ohlsen, Kari
;; APPLICANT: Zyskind, Judith
;; APPLICANT: Wall, Daniel
;; APPLICANT: Trawick, John
;; APPLICANT: Carr, Grant
;; APPLICANT: Yamamoto, Robert
;; APPLICANT: Forsyth, R.

;; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
;; FILE REFERENCE: ELITRA.034A
;; CURRENT APPLICATION NUMBER: US/10/282,122A

;; PRIOR FILING DATE: 2003-02-20
;; PRIOR APPLICATION NUMBER: 60/191,078

;; PRIOR FILING DATE: 2000-03-21
;; PRIOR APPLICATION NUMBER: 60/206,848

;; PRIOR FILING DATE: 2000-05-23
;; PRIOR APPLICATION NUMBER: 60/207,727

;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: 60/230,335

;; PRIOR FILING DATE: 2000-09-06
;; PRIOR APPLICATION NUMBER: 60/230,347

;; PRIOR FILING DATE: 2000-09-09
;; PRIOR APPLICATION NUMBER: 60/242,578

;; PRIOR FILING DATE: 2000-10-23
;; PRIOR APPLICATION NUMBER: 60/253,625

;; PRIOR FILING DATE: 2000-11-27
;; PRIOR APPLICATION NUMBER: 60/257,931

;; PRIOR FILING DATE: 2000-12-22
;; PRIOR APPLICATION NUMBER: 60/267,636

;; PRIOR FILING DATE: 2001-02-09
;; PRIOR APPLICATION NUMBER: 60/269,308

;; PRIOR FILING DATE: 2001-02-16
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 78614
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 54546
;; LENGTH: 545
;; TYPE: PRT
;; ORGANISM: Campylobacter jejuni
US-10-282-122A-54546

Query Match 40.9%; Score 52; DB 15; Length 545;
Best Local Similarity 41.7%; Pred. No. 91;
Matches 10; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 2 KKKMADNGTIVTEELKQLEQWNL 25
DB 166 EKVKDGVITVEAKSINDELNV 189

RESULT 29
US-10-369-294-11

;; Sequence 11, Application US/10369294
;; Publication No. US20030162170A1
;; GENERAL INFORMATION:

;; APPLICANT: Hahn, Beatrice H.
;; APPLICANT: Gao, Feng
;; APPLICANT: Marx, Preston A.
;; APPLICANT: Shaw, George M.
;; APPLICANT: Smith, Stephen M.
;; APPLICANT: Georges-Courbot, Marie Claude
;; APPLICANT: Lu, Chang Yong

;; TITLE OF INVENTION: Complete Genome Sequences of a Simian
;; TITLE OF INVENTION: Immunodeficiency Virus from a Red-Capped
;; FILE REFERENCE: D6286D

;; CURRENT APPLICATION NUMBER: US/10/369,294
;; CURRENT FILING DATE: 2003-02-18

;; PRIOR FILING DATE: 1998-12-07
;; NUMBER OF SEQ ID NOS: 58

;; SEQ ID NO 11
;; LENGTH: 855
;; TYPE: PRT

;; ORGANISM: Simian immunodeficiency virus
;; FEATURE:
;; OTHER INFORMATION: Amino acid sequence of homologous region of
US-10-369-294-11

Query Match 40.6%; Score 51.5; DB 14; Length 855;
Best Local Similarity 43.5%; Pred. No. 1,8e+02;
Matches 10; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

QY 4 MADNGTIVTEELKQLEQWNL 25
DB 401 MGPNGTITQCRKQIINMQRV 423

RESULT 30
US-10-369-294-12

;; Sequence 12, Application US/10369294
;; Publication No. US20030162170A1
;; GENERAL INFORMATION:

;; APPLICANT: Hahn, Beatrice H.
;; APPLICANT: Gao, Feng
;; APPLICANT: Marx, Preston A.
;; APPLICANT: Shaw, George M.
;; APPLICANT: Smith, Stephen M.
;; APPLICANT: Georges-Courbot, Marie Claude
;; APPLICANT: Lu, Chang Yong

;; TITLE OF INVENTION: Complete Genome Sequences of a Simian
;; TITLE OF INVENTION: Immunodeficiency Virus from a Red-Capped
;; FILE REFERENCE: D6286D

;; CURRENT APPLICATION NUMBER: US/10/369,294
;; CURRENT FILING DATE: 2003-02-18

;; PRIOR FILING DATE: 1998-12-07
;; NUMBER OF SEQ ID NOS: 58

;; SEQ ID NO 12
;; LENGTH: 855
;; TYPE: PRT
;; ORGANISM: Simian immunodeficiency virus

;; FEATURE:
;; OTHER INFORMATION: Amino acid sequence of homologous region of
US-10-369-294-12

US-10-369-294-12

Query Match 40.6%; Score 51.5; DB 14; Length 855;

Best Local Similarity 43.5%; Pred. No. 1.8e+02; Indels 1; Gaps 1;

Matches 10; Conservative 5; Mismatches 7;

QY 4 MADNGTITVEELKQLEQNLV 25

DB 401 MGPNGTITLCGRKQIINMGRV 423

RESULT 31

US-10-478-245-4

Sequence 4, Application US/10478245

Publication No. US20040171008A1

GENERAL INFORMATION:

APPLICANT: INCYTE CORPORATION; TANG, Y. Tom;
 APPLICANT: YUE, Henry; AZIMZAI, Yalda;
 APPLICANT: BAUGHN, Mariah R.; BURFORD, Neil;
 APPLICANT: REDDY, Roopa; CHAWLA, Narinder K.;
 APPLICANT: DAS, Debopriya; NGUYEN, Daniel B.;
 APPLICANT: YAO, Monique G.; ARVIZU, Chandra S.;
 APPLICANT: LU, Yan; GANDHI, Ameena R.;
 APPLICANT: GRIFPIN, Jennifer A.; ELIOTT, Vicki S.;
 APPLICANT: RAMKUMAR, Javalaxmi; LAL, Preeti G.;
 APPLICANT: LU, Dzung Anna M.; LEE, Ernestine A.;
 APPLICANT: LEE, Soo Y.; YUE, Huibin; Catherine M.;
 APPLICANT: KABLE, Amy E.; SWARNAKAR, Anita;
 TITLE OF INVENTION: LIPID-ASSOCIATED MOLECULES
 FILE REFERENCE: PI-0427 USN
 CURRENT APPLICATION NUMBER: US/10/478,245

PRIOR FILING DATE: 2003-11-18
 PRIOR APPLICATION NUMBER: PCT/US02/15688
 PRIOR FILING DATE: 2002-05-17
 PRIOR APPLICATION NUMBER: US 60/292,242
 PRIOR FILING DATE: 2001-05-18
 PRIOR APPLICATION NUMBER: US 60/293,726
 PRIOR FILING DATE: 2001-05-25
 PRIOR APPLICATION NUMBER: US 60/295,346
 PRIOR FILING DATE: 2001-06-01
 PRIOR APPLICATION NUMBER: US 60/303,404
 PRIOR FILING DATE: 2001-07-06
 PRIOR APPLICATION NUMBER: US 60/314,754
 PRIOR FILING DATE: 2001-08-24
 PRIOR APPLICATION NUMBER: US 60/351,262
 PRIOR FILING DATE: 2002-01-22
 PRIOR APPLICATION NUMBER: US 60/368,799
 PRIOR FILING DATE: 2002-03-29
 NUMBER OF SEQ ID NOS: 20
 SOFTWARE: PERL Program
 SEQ ID NO 4
 LENGTH: 217
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc_feature
 OTHER INFORMATION: Incyte ID No: 2715421CD1
 US-10-478-245-4

Query Match 40.2%; Score 51; DB 16; Length 217;
 Best Local Similarity 50.0%; Pred. No. 44; Indels 0; Gaps 0;
 Matches 12; Conservative 4; Mismatches 8;

QY 1 KKQADNGTITVEELKQLEQNLV 24
 DB 34 KKQMVANVEKQLEAKELLEQMDL 57

RESULT 32
 US-10-282-122A-60575
 Sequence 60575, Application US/10282122A
 Publication No. US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangou
 APPLICANT: Zamudio, Carlos
 APPLICANT: Malone, Cheryl
 APPLICANT: Habelbeck, Robert
 APPLICANT: Ohlsen, Karl
 APPLICANT: Zyskind, Judith
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John
 APPLICANT: Carr, Grant
 APPLICANT: Yamamoto, Robert
 APPLICANT: Forsyth, R.
 APPLICANT: Xu, H.
 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 FILE REFERENCE: ELITRA 034A
 CURRENT APPLICATION NUMBER: US/10/282,122A
 CURRENT FILING DATE: 2003-02-20
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/230,335
 PRIOR FILING DATE: 2000-09-06
 PRIOR APPLICATION NUMBER: 60/230,347
 PRIOR FILING DATE: 2000-09-09
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/267,636
 PRIOR FILING DATE: 2001-02-09
 PRIOR APPLICATION NUMBER: 60/269,308
 PRIOR FILING DATE: 2001-02-16
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 78614
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 60575
 LENGTH: 626
 TYPE: PRT
 ORGANISM: Listeria monocytogenes

US-10-282-122A-60575

Query Match 40.2%; Score 51; DB 15; Length 626;
 Best Local Similarity 50.0%; Pred. No. 1.5e+02; Indels 0; Gaps 0;
 Matches 10; Conservative 5; Mismatches 5;

QY 2 KKQADNGTITVEELKQLEQ 21
 DB 417 KQLADEFEELTITLTKQLOQ 436

RESULT 33

US-10-156-761-14515

Sequence 14515, Application US/10156761

Publication No. US20030119018A1

GENERAL INFORMATION:

APPLICANT: OMURA, SATOSHI
 APPLICANT: IKEDA, HARUO
 APPLICANT: ISHIKAWA, JUN
 APPLICANT: HORIKAWA, HIROSHI
 APPLICANT: SHIBA, TADAYOSHI
 APPLICANT: SAKAKI, YOSHIYUKI
 APPLICANT: HATTORI, MASAHIRA
 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 FILE REFERENCE: 249-262
 CURRENT APPLICATION NUMBER: US/10/156,761
 CURRENT FILING DATE: 2002-05-29
 PRIOR APPLICATION NUMBER: JP 2001-204089
 PRIOR FILING DATE: 2001-05-30

PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 14515
LENGTH: 987
TYPE: PRT
ORGANISM: Streptomyces avermitilis
US-10-156-761-14515

Query Match 40.2%; Score 51; DB 14; Length 987;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 10; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXADNGTIVVEELKQLEQW 22
DB 650 KTADDEIDVEDIRAKIEQY 669

RESULT 34
US-10-424-599-219887
Sequence 219887, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J
APPLICANT: Kovalic, David K
APPLICANT: Zhou Yinhua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 219887
LENGTH: 92
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_40586C.1.pep
US-10-424-599-219887

Query Match 39.4%; Score 50; DB 15; Length 92;
Best Local Similarity 47.4%; Pred. No. 23;
Matches 9; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 6 DNGTIVVEELKQLEQW 24
DB 25 NSGFTTEELQALREY 43

RESULT 35
US-10-437-963-186189
Sequence 186189, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yinhua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221) B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 186189
LENGTH: 174
TYPE: PRT
ORGANISM: Oryza sativa

FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_83010C.1.pep
US-10-437-963-186189

Query Match 39.4%; Score 50; DB 16; Length 174;
Best Local Similarity 55.6%; Pred. No. 48;
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 7 NGTIVVEELKQLEQW 24
DB 119 NGVTAEEELRRLRL 136

RESULT 36
US-10-272-419-26
Sequence 26, Application US/10272419
Publication No. US20030087403A1
GENERAL INFORMATION:
APPLICANT: CHEN, QIONG
APPLICANT: THOMAS, STUART
APPLICANT: NAGARAJAN, VASANTHA
TITLE OF INVENTION: BIOLOGICAL METHOD FOR THE PRODUCTION OF ADIPIC ACID AND
TITLE OF INVENTION: INTERMEDIATES
FILE REFERENCE: C1341-A
CURRENT APPLICATION NUMBER: US/10/272,419
CURRENT FILING DATE: 2002-10-16
PRIOR APPLICATION NUMBER: 09/252,553
PRIOR FILING DATE: 1999-02-19
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Microsoft Office 97
SEQ ID NO 26
LENGTH: 300
TYPE: PRT
ORGANISM: Acinetobacter sp.
US-10-272-419-26

Query Match 39.4%; Score 50; DB 14; Length 300;
Best Local Similarity 22.7%; Pred. No. 88;
Matches 5; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY 2 KXADNGTIVVEELKQLEQW 23
DB 20 RMQENPMNTIEDFRSMPDEWH 41

RESULT 37
US-10-417-700A-49
Sequence 49, Application US/10417700A
Publication No. US20040033581A1
GENERAL INFORMATION:
APPLICANT: ECOPIA BIOSCIENCES INC.
APPLICANT: ZAZOPOULOS, Emmanuel
APPLICANT: STAPPA, Alfredo
APPLICANT: FARNET, Chris
TITLE OF INVENTION: Specialized dual condensation/epimerization domain in non-ribosome
TITLE OF INVENTION: peptide synthetase systems
FILE REFERENCE: 3002-14US
CURRENT APPLICATION NUMBER: US/10/417,700A
CURRENT FILING DATE: 2003-04-17
NUMBER OF SEQ ID NOS: 139
SOFTWARE: PatentIn version 3.0
SEQ ID NO 49
LENGTH: 469
TYPE: PRT
ORGANISM: Pseudomonas syringae pv. syringae strain B301D
US-10-417-700A-49

Query Match 39.4%; Score 50; DB 15; Length 469;
Best Local Similarity 64.3%; Pred. No. 1.5e+02;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 10 ITVEELKQLEQW 23
: : |||||||||

```
DB      432 LPLNERKQLEQWN 445

RESULT 38
US-10-781-102-1
; Sequence 1, Application US/10781102
; Publication No. US20050048525A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Fidock, Mark D.
; TITLE OF INVENTION: PHOSPHODIESTERASE ENZYMES
; FILE REFERENCE: PC10350B
; CURRENT APPLICATION NUMBER: US/10/781,102
; CURRENT FILING DATE: 2004-02-18
; PRIOR APPLICATION NUMBER: US 60/177,326
; PRIOR FILING DATE: 2000-01-20
; PRIOR APPLICATION NUMBER: US 09/663,481
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: UK 9922125.1
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-781-102-1

Query Match      39.4%; Score 50; DB 17; Length 516;
Best Local Similarity 55.6%; Pred. No. 1.6e+02;
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY      3 KXADNGTIVTEELKQLE 20
DB      24 KOLENGEINIEELKQLE 41

RESULT 39
US-10-781-102-3
; Sequence 3, Application US/10781102
; Publication No. US20050048525A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Fidock, Mark D.
; TITLE OF INVENTION: PHOSPHODIESTERASE ENZYMES
; FILE REFERENCE: PC10350B
; CURRENT APPLICATION NUMBER: US/10/781,102
; CURRENT FILING DATE: 2004-02-18
; PRIOR APPLICATION NUMBER: US 60/177,326
; PRIOR FILING DATE: 2000-01-20
; PRIOR APPLICATION NUMBER: US 09/663,481
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: UK 9922125.1
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 3
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-781-102-3

Query Match      39.4%; Score 50; DB 17; Length 536;
Best Local Similarity 55.6%; Pred. No. 1.7e+02;
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY      3 KXADNGTIVTEELKQLE 20
DB      44 KOLENGEINIEELKQLE 61

RESULT 40
US-10-815-390-1

; Sequence 1, Application US/10815390
; Publication No. US20050075795A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Pandit, Jayvardhan
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF 3', 5'-CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
; FILE REFERENCE: PC25193A
; CURRENT APPLICATION NUMBER: US/10/815,390
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: US 60/458,946
; PRIOR FILING DATE: 2003-03-31
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-815-390-1

Query Match      39.4%; Score 50; DB 17; Length 536;
Best Local Similarity 55.6%; Pred. No. 1.7e+02;
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY      3 KXADNGTIVTEELKQLE 20
DB      44 KOLENGEINIEELKQLE 61

RESULT 41
US-10-192-419-2
; Sequence 2, Application US/10192419
; Publication No. US20030027266A1
; GENERAL INFORMATION:
; APPLICANT: JACOBS, ANTONIUS A.C.
; APPLICANT: VAN DEN BOSCH, JOHANNES F.
; APPLICANT: NUIJTEN, PETRUS J.M.
; TITLE OF INVENTION: CAMPYLOBACTER VACCINE
; FILE REFERENCE: JACOBS
; CURRENT APPLICATION NUMBER: US/10/192,419
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US/09/544,683
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: EP99201086.8
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
US-10-192-419-2

Query Match      39.4%; Score 50; DB 14; Length 545;
Best Local Similarity 41.7%; Pred. No. 1.7e+02;
Matches 10; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY      2 KXADNGTIVTEELKQLEQWNLV 25
DB      166 EKVGKGVITVEEPKSIDNELNV 189

RESULT 42
US-10-424-599-203557
; Sequence 203557, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Roga Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
```

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FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 203557
LENGTH: 546
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_25838C.1.pcp
US-10-424-599-203557

Query Match
Best Local Similarity 39.4%; Score 50; DB 15; Length 546;
Pred. No. 1.7e+02;
Matches 9; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 6 DNGTIVEELKQLEQWNL 24
DB 477 NSGFITTELEQLREYNM 495

RESULT 43
US-10-425-114-54704
Sequence 54704, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 54704
LENGTH: 549
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: JC-GWFL02220063C09_FLI.dep
US-10-425-114-54704

Query Match
Best Local Similarity 39.4%; Score 50; DB 15; Length 549;
Pred. No. 1.8e+02;
Matches 9; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 6 DNGTIVEELKQLEQWNL 24
DB 480 NSGFITTELEQLREYNM 498

RESULT 44
US-10-282-122A-76721
Sequence 76721, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
```

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FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 76721
LENGTH: 673
TYPE: PRT
ORGANISM: Ureaplasma urealyticum
US-10-282-122A-76721

Query Match
Best Local Similarity 39.4%; Score 50; DB 15; Length 673;
Pred. No. 2.2e+02;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 12 VBEKQKLEQWNL 23
DB 8 IDELKQKLEQWNL 19

RESULT 45
US-10-104-047-2324
Sequence 2324, Application US/10104047
Publication No. US20030236392A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20030236392A1 full length cDNA
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2324
LENGTH: 808
TYPE: PRT
ORGANISM: Homo sapiens
US-10-104-047-2324

Query Match
Best Local Similarity 39.4%; Score 50; DB 15; Length 808;
Pred. No. 2.7e+02;
Matches 12; Conservative 3; Mismatches 8; Indels 2; Gaps 1;

QY 3 KXADNGTIVEELKQLEQWNLV 25
DB 32 KXADNGTIVEELKQLEQWNLV 56

RESULT 46
US-10-343-509-3
Sequence 3, Application US/10343509
```

```
Publication No. US20040101865A1
GENERAL INFORMATION:
APPLICANT: BASF
TITLE OF INVENTION: Pyruvate:NADP+ oxidoreductase and uses thereof
FILE REFERENCE: 0050/51654
CURRENT APPLICATION NUMBER: US/10/343,509
CURRENT FILING DATE: 2003-01-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 1803
TYPE: PRT
ORGANISM: Euglena gracilis
US-10-343-509-3

Query Match      39.4%; Score 50; DB 16; Length 1803;
Best Local Similarity 47.8%; Pred. No. 6.8e+02;
Matches 11; Conservative 4; Mismatches 6; Indels 2; Gaps 1;

QY      1 KKKMADNGTIVBELKQLEQWN 23
DB      963 EKKVADEGLTTL-LAQMLODMN 983

RESULT 47
US-10-343-509-1
Sequence 1, Application US/10343509
Publication No. US20040101865A1
GENERAL INFORMATION:
APPLICANT: BASF
TITLE OF INVENTION: Pyruvate:NADP+ oxidoreductase and uses thereof
FILE REFERENCE: 0050/51654
CURRENT APPLICATION NUMBER: US/10/343,509
CURRENT FILING DATE: 2003-01-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 1805
TYPE: PRT
ORGANISM: Euglena gracilis
US-10-343-509-1

Query Match      39.4%; Score 50; DB 16; Length 1805;
Best Local Similarity 47.8%; Pred. No. 6.8e+02;
Matches 11; Conservative 4; Mismatches 6; Indels 2; Gaps 1;

QY      1 KKKMADNGTIVBELKQLEQWN 23
DB      965 EKKVADEGLTTL-LAQMLODMN 985

RESULT 48
US-10-360-053-28
Sequence 28, Application US/10360053
Publication No. US20030170230A1
GENERAL INFORMATION:
APPLICANT: Caterer, Nigel
APPLICANT: Uttenenthal, Lars O
APPLICANT: Nielsen, Rasmus W
TITLE OF INVENTION: Compositions and Methods for Assembly and Stabilization of Antibio
TITLE OF INVENTION: Fragments via Antiparallel Heterogeneous Colled-Coil Peptide Regi
TITLE OF INVENTION: thereof
FILE REFERENCE: IMX-0028
CURRENT APPLICATION NUMBER: US/10/360,053
CURRENT FILING DATE: 2003-02-05
PRIOR APPLICATION NUMBER: US60/354,376
PRIOR FILING DATE: 2002-02-05
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn version 3.1
SEQ ID NO 28
LENGTH: 2477
TYPE: PRT
ORGANISM: Homo sapien
```

```
US-10-360-053-28
Query Match      39.4%; Score 50; DB 14; Length 2477;
Best Local Similarity 47.6%; Pred. No. 9.8e+02;
Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY      2 KKKMADNGTIVBELKQLEQW 22
DB      1833 KKLSDNTIGKEIIOQLAOF 1853

RESULT 49
US-10-408-765A-238
Sequence 238, Application US/10408765A
Publication No. US20040101874A1
GENERAL INFORMATION:
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Fahy, Eoin D.
APPLICANT: Zhang, Bing
APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 238
LENGTH: 2477
TYPE: PRT
ORGANISM: Homo sapiens
US-10-408-765A-238

Query Match      39.4%; Score 50; DB 16; Length 2477;
Best Local Similarity 47.6%; Pred. No. 9.8e+02;
Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY      2 KKKMADNGTIVBELKQLEQW 22
DB      1833 KKLSDNTIGKEIIOQLAOF 1853

RESULT 50
US-10-781-102-13
Sequence 13, Application US/10781102
Publication No. US20050048525A1
GENERAL INFORMATION:
APPLICANT: Pfizer Inc.
APPLICANT: Fiddock, Mark D.
TITLE OF INVENTION: PHOSPHODIESTERASE ENZYMES
FILE REFERENCE: PC10350B
CURRENT APPLICATION NUMBER: US/10/781,102
CURRENT FILING DATE: 2004-02-18
PRIOR APPLICATION NUMBER: US 60/177,326
PRIOR FILING DATE: 2000-01-20
PRIOR APPLICATION NUMBER: US 09/663,481
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: UK 9922125.1
PRIOR FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.2
SEQ ID NO 13
LENGTH: 60
TYPE: PRT
ORGANISM: Homo sapiens
US-10-781-102-13

Query Match      38.6%; Score 49; DB 17; Length 60;
Best Local Similarity 50.0%; Pred. No. 20;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
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| | | | |
|----|----|--------------------|----|
| Qy | 3 | KWADNGTIVEELKOLLE | 20 |
| | | : : : | |
| Db | 43 | KOLENGEVNIEELKOLLE | 60 |

Search completed: May 11, 2005, 21:43:37
Job time : 106.34 secs